	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
5	GATCITCAAA TGGGACAAAT GCAAGGCTAT TGATCTTATT CCCAGCAAAC AAGTGCGACA	60
v	TETATOSTET ATTITITITE COCAACCEAC TOCTOSTICAA AACOOOCITA AAATCIGACC	120
	TAGITITAAA GOCATCCTTC CAAAGIGTCA CATGIOGICC TCTCGACACT GCAAGCAAGC	180
10	CCATGICAGA GATTITICACA TIGCTITOCTG GTATAGGCAG GTITTICAACG GAATGTAACT	240
	CCTTGAAGIT CCTGATATCC CACAGTCTCA TOGACTTATC TOCTCCOGIN TGTAGCCATA	300
	TAGIAACCIT GOCTATCTAC CGCGACACCA GTGACGGGCC CGGTACC	347
15	(2) INFORMATION FOR SEQ ID NO:59:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 673 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG101712	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
30	GATCTTCTTG GCGTCGGGCA TCAGACAGGC GTAACTAATT TGATCATTCC TGGTGCGGGT	60
	GAGGCTAACT ATGATGCATT GGAAGITAAT CCTTACGAGA CGACGAAGCA AAGGAAAGAG	120
	CAGGAGGITA GATCOCTACT GAACAAATTA CCTGCTGATT CTATTGCATT AGATCCAAAT	180
35	GIGATTOGTA COGTOGAÇAA GOGTICTOOG CAGATTAGAT TGACCOCCAA AGACCTGACC	240
	CAAATCOCAA CIGATGAAGA CATGAAATCT AAGGAGAATA GAGACATICC AAAAGGAAAC	300
	CCTOCTIGTGA AGAGTAAGAA ATTICAGGTCT GCGTACATTC CTCCGTAAGA AGACGCAGAA	360
40	TGTTGTAGAT GAGACGAAGT TGAGAGTIACA GAAACCAAGTTA GAAAACGAAA ACGNINGCCCN	420
	CTTGCGGAAG CANCANGCTG CTGAGGNGAG CTANCAGNAG ATNCGANCTN CCCTGNCGAN	480
	OCGICAGONA GICCACTOGO NMINUNCTCA COCMUNATTO TIOGITINNOM GAMPICACNO	540
15	CANNICACET COCGNICIAN INCTINCOCN NOCINCINITA ACCINCINCINC TOCCNITTOC	600
	NANCOCACNO COCCONOCOC NNCCCCONNON CONNUNNAN NONNOCCOC CTCTNCCCCN	660
	NCCCCCCCAN NCC	673
50	(2) INFORMATION FOR SEQ ID NO:60:	
·s	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 523 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

I

(ii) MOLECULE TYPE: DNA (genamic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1017RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
10	GATCAAOGIT GAAAACGAOC AGOGTGATAA AAAAGAOCAT GACOCCGATG TCCCTGAAGA	60
	GGAATTTAAG ATTAAATATA CCTCGACCTA CTATAAGGTT GAGAATATGA CGCGTGTAGT	120
	ACCACAGCAA TTAAAATATA TTGCATTTCC AAAGGATGAG AGATTTACTC CCGCTCGCAA	180
15	GITTIAAGGGT AGCAATGGGG TTATAGTGCT ATCGGACAAA ACTCCTGACG AGCCGGTCGA	240
	AGTAATCAAA ACCOCTAGAC AGGAAAAAGA GACGGATGCT CCTCTGCCTG CTCCCTTCAA	300
	GGTTCAGGAT GACTTAGAAT TCTGAACTGA TAATTAGGAA GCGTCGATTA TGTTCATTAG	360
20	GAAAAAGGGT ATTITITICTA GAAACGAAAG AACTITACTGA TTGCAGCTCT CTCTAAACAA	430
	GTATATTATG AGGTGATTTA TYTCAACTGA ATCTGGCTAA CGCCCGGCAA CTAGGTCTTA	480
	TOTTOTTGTA GIVACCOTAG AGGIGGIUGT COCCAANCGG CNC	522
25	(2) INFORMATION FOR SEQ ID NO:61:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 493 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1017UP	
35	(A) CREMATER: PASTOTION	
	(xi) SPOUENCE DESCRIPTION: SEQ ID NO:61:	
	CATCHCCATC CACCITITIOS CONCENTRATE CACCICONON GIGACITICAN CONTRATACE	60
40	CGCAATTAAG CCAGGGCCTC TGTATGCGTA CGCAGTGTAG AGTTGCACAA AGTGCGCCCC	120
	CGCTTTGGCA AACTCGATGG CATCCTGGCC ACTACTGATTA CCACCACATC CAACCAAAAC	180
	CAGGITOGIG TOOTTIGIGT ATTIGGIGTAT CGTGCGCAAA GCTTTTAGCG CAAATGGITT	240
45	CACGGGCTTG GCGGACAAGC CGCCTGCCTG GTTTTTCAGC TCCTCATCGA CAGTGTACAG	300
	CGAGTCTGGC CTTTGGATAG TAGTGTTTGG AAACGATGAT ACCCCCAATA CTCGATTTTC	360
	TIESSCOSCO TOTOCCATOG ATTOCAATOO TOSCTOCGTC AAATOOGTIC OCATITTAAC	420
50	ACCAAACTIC CITATOCITA CICCACCAAC AAAATCCCINC CCTCCNCAAA CATTCCCITA	480
	GCANAACAAG NIN	493
	(2) INFORMATION FOR SEQ ID NO:62:	
55	(i) SEQUENCE CHARACTERISTICS:	

5	(A) LENGTH: 523 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1018RP	
10		
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	GATCATOGIC GAGGAGTACA CGCACTOGCT CTGCGCGTGC GTGAACTTCG CCGCGTGACA	60
15	CCCGTACTIC TICGACGCCA CCGTGTTCAG GAACCGGCAC CCGGCCGCGT CGTACAGGTG	120
	CATETIGICE CACGCOGITE COCTCACAAG GIACTGTCCA TOGTCGTCCA ACGACACCCA	180
	CGTGATCGGG CCCTGTTCCT TCTGCGCCAC CTTGAAAGAC TTGACCGCCC GGAACCCCCC	240
20	CAATGIGICT TIGHTCATCC CGATACICAT CCCGCICGIC TIGCAGCFIC CGGICCTIGG	300
	CCCTCTCGCC GCTGCTCTGC ACTGCTGGCT AGCAGAGCTC ACCAAAATTT TTATAGCCAT	360
	GOCCAGGCCA AACTICACTA ACTGOGGAAC CACAGGACCA CAGCAAGCAA TGCCCTCAGT	420
25	ATGICGGTCG GICCCACCGT CCTGGCATCG CTACTAACCC GCACACCTCA AGCAGATGGT	480
	GCACITCAGC GCCGACCICG CGCIGGIGGC GAIGGIGCIG GCC	523
	(2) INFORMATION FOR SEQ ID NO:63:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 770 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1018UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
	CATCOCCTICT ACCACTICAT COCCATOCAC TACCTTATCA CCCACATOCT CCTOCCCCCC	60
45	GACTITICOGT TCATOCOCCA CTACCTOCAG GTCCTOCOCC GCCCCCCCCA GCAACACCAG	120
	TIGIGOGATG CCCOCATGIC TOCCOCTGIG CAACGGGACC ACATTGCCCG ATACACCGAG	180
	CIGCIGATOC TOTATOCOCO GAAGTCTOOG GATGAGAAAA TOCTOCOGGA GCTCTTTOCC	240
50	TCCTTGGTCG ATAGTCTGCC TCGCGGGATG GGCGGAGCCA CTCTTCGTCA GCCATTGCAT	300
	GAAGTCATGA CGTACCTGAT CAGCGAAAAC CAGCCGCAAC AGGTGCTGAA ACTGGTGGCG	360
	GOCATGCGCA AGGCGGAGCC CAATCGGCGG CCGGGCAAAT CCTCCGTTCC AGGCACCTTG	420
55	GCGCTGGTTG TTTCGGCGTT GCGACAGTTC AACAATCCTA ATCTCGTCGT GAGCTTTATT	480

	GIOCAGOCAT ACAGAAAGAC GCAAACGAGA GIOCIOCIOG GACAACICOG OCIATOGICI	540
5	CTGCCATTFT ATCGCCCCCC TGTTCCCCCTC TCTCCCCGAGG CGGCGAAGTC GCCGCAGGAG	600
	CTGCCGCAGA TATCCCCTGT GGACCTGCCG AAGGACCTAA TACTGAAGTC CGTACCTGAC	660
	AGCTGATAAT GTGCGAGCTC TATCAGCGAA TCTATCCCAG AAGCGATCGC AGGTGCCCGC	720
10	GGAGGAGTAC COCGAGATTT AATCCAGCTA TITIGCGCTIT ACCAGGACTT	770
70	(2) INFORMATION FOR SEQ ID NO:64:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 735 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1019RP	
20	(W) ONE-MITEGE: PARTICIAND	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
nr.	CATCCATGAC CCATGCTAGG TGGAAGGAGC CCTTACCCGC TAACTCGGAC TCCCTCTTCA	c 0
25	ATTOCTTAT CASTITUSTA TOCACAGCAC COACSTOSTA CAACAACCAC COCATCACCE	120
	TAGACTIOCC COCATCCACA TODOCTAGAA CAACAACGA CATATOGGOC TTCTTCTCAC	120
		180
30	GTACATATOC AGGGATGICG AATGGGTTCC GCGGGTTAGT GGGCTGCACA ACCTTCTTGG	240
	CCGACGGCTG TTCGCCCTCC TTCGCCCCCG AATCCTCCTC CTCGTCCTCG TAGTTCTTCG	300
	COCCOCCTC CTTGTTGTTG AATTTCACAT CGGCCACCTT CTCGGCCACC TGCTTAATCT	360
35	CAAAGSCTCG CTTCTGGGAT TCCAACACCA CGTCATCCGG CGAGGGCTTC ATGAAATTGG	420
	CACTGOCCTG CTTCTTAGCT CCTTTATAGT TGTTAGGATA AAAAACTGAG AACACCTCCT	480
	CCACTOSCCT CTICACCIGG GITTICCGIG GITCICCGCA TCCIGICTGT CICCACAGAGA	540
40	GCACGCTGGA CAGCTGCAGT GCAGGCGCG CTGCAGGCTT GAAGGACGGC TGACGCTGCA	600
	GAAGAGCCCC CAGGGCCATC CACTGGTCTT GCCGTGCCTC GGTCCTTGCG GGGCGCGCTG	660
	CAACAGGCTT TGCCTCAGCG TCGCCGCGCG ACTGCTTCGC AGAGACGACA GCGTCTGCAT	720
45	CAGCGACGC CCCGG	735
	(2) INFORMATION FOR SEQ ID NO:65:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 740 base pairs	
50	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGIO19119	

	(A) SEQUENCE DESCRIPTION: SEQ 1D NO:03.	
5	GATCOCAGAT TCATCATCOC TGTTATACCA GOCTCTATCT TCCTCGAGGT CCTCGGGACC	60
	AAACOCGOCG CTCTCTTGTG TGCCAAGAGG TGCAGGACCC TCGGCGCGAT CCTCGGCCAG	120
	CAGAGTOSCA ATCTOGTCTT CATCCOCTAT COCTGTCAGC TTAGGCACAA AAGCCAGTTT	180
10	TICCUITTIC TOCCOGICAT CATOCTOCTO CAGOGIOCTO TICICATOTO TGOCACOCTO	240
	TOCANACTOT TIGAGOTOCO TIGOTOCO CTIGICAAGT COCTTAAATO TOAGOGGITT	300
	CTGTTTCTGG CCACCGCTCC CCAAGCTCTG GTCCGGCTCC AGTGCTGTTT CCAGTTCGTC	360
15	GTCCGAATCT TCGAAGCTCA GCGCGACCAA GTTTCTGGAT GTGTTTCCCT TCACGCGCTC	420
	COCCICARGE ACRECCITICA COCTOCTICIT TOTOCOCTICC TOCTOCCIRAC TOCCCACOCA	480
	TACTAGCAGO TOATGCAGGA ACTICIOCIC COOTTAAACT TGCCAAGGGC CATGCAGCTC	540
20	TTAGTIGAACT TCACTOGATC GTATOCATGC ACGCGCGCTA TATTOCATAT CGGCTGCACA	600
	AACITICIET GACATIGGAT GOGGATETIG GTGGATCACT COTTCAGCCG GGGTCATOGT	660
	CITACCICCI ACCGIACITG CICTCICAGA TOCATGATGI GIACCATCOC ATCITICAGCI	720
25	TGACAGACTT CCATATACGT	740
	(2) INFORMATION FOR SEQ ID NO:66:	
30	(i) SDQUENCE CHARACTERISTICS: (A) LENGTH: 537 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1020RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
	GATCGITICCT GITTICTGCGG GCAAAGTTCA GAATTGACCT AGTGCCAGAC ATGACAGTAT	60
	CGTTCAAACT CCTCGGAGAG TTAGOCTTGG ATATCCACCA TGAAGACAAA AACCAGAGAC	120
15	CAACAGOGGA TOCTACCAAA ATGGOCCAGAA TACOGAAAAA CCAGTGCAAT TOTOCGGTTG	180
	CTTCACCTGG GACAGTGAGG TTCATCCCAA ATAGACCCGT AACAAGATTC AAAGGAACTA	240
	ACATTGITCC AATCATAGTG ACCTTTCCCA ACATTTCAGT AACACGATTG TTACACCGGA	300
io	AGGACTICAAC TTOCAATTIGT GCCAAGTAGT TACCATGTGA ACGGGAGAAA ATCTTCTCAT	360
	AGGACAGTAA ATTITIGAAAC ATCOOGAGGA CATGGTCCTG AATAICTCCC AAATAGAGCG	420
	CTATATCAGO TOTTOGITGA GIGCOCTOGA CATGATGATG TTGIATGITO GAGOCTAGOC	480
s	TOSCAÇAÇÃO AGGETOCHET OCOCTAGOCT GCAAGTTOOC AATGITHATC TOGAGGT	537

	(2) INFORMATION FOR SEQ ID NO:67:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 563 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1020UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
	GATCAGCACC GTGCCCTTCG TGTACGCCTG CTTGGACATG GTGTGCGACG ACCGTGTGTC	60
	GCATTICTTA CACGIGAAAG CAATCATCAT CATCGGCTTG TCCACCTTTA TAGACCCGAT	120
20	ATGCCGAAAC TCATCTGCAA TAGGCGGTTT CTGGCTGTTT TGCAGCTGCG GCGAACCGCT	180
	GTGGAACCGA TGAGCTACCA AATGCCCCCC AAACACCGGA CCCAGCACGT ACTGCATGCA	240
	GTTACGGCTT GGGCGGAGTA AACCAGCAAT CCTGAGAGGC CCCATCGAAC GTCTAAGCAT	300
25	TITAAACAGT TATACGTAGT CAGCGGTTTT CCTAAAACAG GACATGAGAG TGCGTCGAAA	360
	GAAGGCGTCA TCTCAAATTT TTCAACTTTA GAAGCGCTGC CCGAAAAAAC ACCGTCACCA	420
	TITATCTATT ACAAGATGAA CAGITAGTOG TOCCOGCAAT TOTGTCAGAT ATATGTCTCT	480
30	OGACATOGAT ACAAGACACT CTCOCCACAG AAGGAGCAGG AGATAGCATC GAAAAATCTTG	540
	CAGAAGGCTG AGCTGGCTCA GAT	563
	(2) INFORMATION FOR SEQ ID NC:68:	
35	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original source: (A) Organism: Pag102111	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
	GATCTCACCC TGCGCACCAT CGACAACCCT GCATACGCCG GCGGTGAGGT CATCGGCAAG	60
50	GCCCGTGCCC GCACACTOGA GATGCGCCTC AATGCCCTGT CCGCTACCAA TGCCGCGGCA	120
	CGAACCCTCG AAACCGTGCC TATGAACATA CGCAAAGGCA TGGTTTCCAA GCACCGCAGT	180
	COCATOCOCO AGCACCAGOA OCTOSCOCOG GACTOCOGOCA COGTOCTOCO CAAGGTOCGT	240
55	CECOGAGAGT TOCOGGAAGAT AGACGCAACC TACAAAAAAG ACATOGAGCG TOGCATTGGC	300

	ALGALLATCA ACOCTOCAGA COGTGCCCCC AAGAAACACC GCGATC	346
	(2) INFORMATION FOR SEQ ID NO:69:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 562 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG102112	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
	CATCTOCOCC OCATOCCTOC CACTTCACCG COCCCAAGAT CTCTCACTCC TCCACAAAAAC	60
20	SCHEGASCHE GARGICCHET TOCASCASCH SCHICHTER GOSGICGSCE GOGGAGATH	120
	TOGGOGGGG CTOGGTCTCT AGGCCCGGGG CCTTGCCGGCT GCGGATGCGG CGCAGTTCTC	180
	GIGGAGAAGG CCCCCITGIAG CCATCIGACG CCCCCCCAAA CCAGATCACG CCCCCCTIAT	240
25	COCCOCCTC GICGICOCAG CIGOCIGAGE COCCOICCAT TICOGACICC TCGICOCATT	300
	CAGACTETIC GGAGCCCCC TCGCCCTCGC TCTCCCGGGTC ACTGTCGCTC TCGGAGGCCC	360
	TOGTGCTTGT GTOGCTGCTT TGTGCAGCAC GGGTCTTGTC TACATATCCC ATATCCTCTA	420
30	GOGAGOCAAA CTGGGGCTCG AAGGCCCTCC CCTGGGACCC GACVIGCTTG NATTIATCTT	480
	CAATTGTCGG TCATCCNGGG GGGTTCTTGG GCCCCANGAA GINININANC ACCAANCCCT	540
	AGUANNANGG TTTTCAAATI CC	562
35	(2) INFORMATION FOR SEQ ID NO:70:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 611 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SCURCE: (A) ORGANISM: PAG1021RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
	GAICCTOGAG TITGTOCOCG GCCGGTCCCG CTCATTTACC TAATCCTGTC TATAGTAAAC	60
50	ACCITICITICIT ATCTACATAG COCACCIGIT GIAACTTACG CIGCACGCAT GCGCGGGCGC	120
	ACCITOCOCCA OCAGOCOCOG GTAGAACOCO TOGOCCOCOCO CAGCATOCAC	180
	AGGCGCAGCC ACGGTTTCAT CGTGATCAGC AGGCCAGTCC ACAGCGGGCC CTGCACCAGC	240
55	OCCATCACCA CCACCIOCOC CACCACCACC TIGOCCACCA CCACTOCOCT GATICOCCGIC	300

	ACTION OF CONTROL OF CONTROL ACTION ACTION OF CONTROL O	360
	TECTTEGGEA GEGETGEGG GAACGTETT TTOGAACCTG ACGTOGGGTA TEGTTATTGC	420
5	TIGGGGICCA TIGGAACGGC TGITIGGGGGI CAGAGGGAGG ATTCCTGCGC TGGITIGGIT	480
	TITTACGAAGA CGACCCTCGG TGAGAATGTC AGTTTGGCCA CTNGGCAGCC CCAGGAAGGA	540
	CCGNGAATTC AAACCACCTG AGTHOGOCGN COGNGTAAAA ACGCTAAGTT AGTOCNNTOC	60C
10	AMACCONCOT C	611
	(2) INFORMATION FOR SEQ ID NO:71.	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDHINESS: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1021UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
	CATCOCOSTIC TYTICTIOCOG CCACOSTICTIC CASOCTTICAT OCTOGTICCCA ATCCCCACOCT	60
	CCATGICTIT TITICTAGGIT GOGICTATCT TOCOGAACTC TOCGCGACGG ACCITIGGOGA	120
30	GCACGETGCC GCACTCCCGC GCCACCTGCT CGTGCTCCCG GATGCGACTG CGGTGCTTGG	180
	AAACCATECC TITIGGETATE TICATAGECA CEGITTUGAG GEITUGTECC ECOCCATTEG	240
	TAGCOGACAG GOCATTGAGG COCATCTOGA GTGTGCGGGC ACGGGGCCTTG CCGATGACCT	300
35	CACCECCECC GTATECAGOG TYGTCGATGG TGCGCAGOGT GAGATC	346
	(2) INFORMATION FOR SEQ ID NO:72:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 438 base pairs (B) TYPE: rucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1022RP	
50	(xi) SEQUENCE DESCRIPTION. SEQ ID NO:72:	
	ANNUMENTAL MANAGETICS COCCETOGING ANTAGTCOCT CITTLCTCCCC COCTCTGTCC	60
	AGAAAACGAG ATTICTICOCGA GTATCTICAAA TTICTITTGTTG CGCCGAGCCG TCTCCGTCTG	120
55	CGTCAAGCGA CAGCGAGTTT OCGACAGGAA CTGAAGCTAA TTTCGTTGCT GGAGGTGTTT	180

5	TOOLOUTING COTTTICAGE CITICAGGAA ATCTAGAGGG GCTGTGTOCT TTGAGGCTGA	240
	AATCAGGGGA ATAGCCTGAA TTTGCGAGGG TGAATTGAGC GGTTATATGG AACTGTGGTA	300
	CATOGRICACA CTIGTACCACG AGGACAGGGA ATATCTGACA GTAGGGCGTC CTTCGTAAGA	360
	ACACAGTGIA TOGOGTGAGA TAGGTGITGA TIGAGTCTAG CGTGCTAGGT ACTCTTTAAC	420
	TTTCAGTOGG TGTTTTTT	438
10	(2) INFORMATION FOR SEQ ID NO:73:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1022UP	
	(xi) SEQUENCE DESCRIPTION: SEO ID NO:73:	
	GATCCASCAG ACGITITAAT CACCGATTIT TITCGGTAACA TITCAAAATAT AATTCTCGAT	60
25	GACAGIGAGA TAGATIGGIGA AACTOCAGCI GGACTIACGG AATCIGGCCG GACTIGCAAT	60
	CTGCTAGAAT TCGCAAAAGC GAAATTTTTT GGCANTGTAG ACGCAGAGC TAATGGCACG	120
	CATAAAAACG TGATTCCAAG CTATCCAGIG GTAAATGAGG ATTTACTAAG TGGGGNANCA	180
30	AATGCATCCA CAAACAAAAT GATAAAATTG TGGGGGATTA TCATCTTCCT GGCACTAAGG	240 300
	TCATIAATGA TGAAGIACGC CAACACTGAA AACATATOGG GTAGTCGAGC ACIATIATGT	360
	TTCTCTTAGA AAAATGCTTC ATGCTTCATG GAATTAAGGC GGCAACAAGT GCAAGGTTAA	420
35	GAACGGAATT TTACTATAGG CCCGAAATTT GTATATATTA T	461
	(2) INFORMATION FOR SEQ ID NO:74:	404
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 213 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOFOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
4 5	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG102311	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
	GROCIAGAAAA CAGAGCITICA GGTCCCACTIG TICITTITICA CIGCGGATIGI CICTIGTICTIGC	60
	TCCACGACCC CCACTITICAG ATTGTGGTGC ATCAAGCGCT GCAAGTGGAC TTCCAGACGG	120
55	GIGICIOSGA TOGIOCAGIA COCAAACTIC TIGIGCTIGI GATCACCOG GICTOTICIO	180

	TGTACCG"AA GCTTGCCGGG CACCAGCTTG ATC	213
	(2) INFORMATION FOR SEQ ID NO:75:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 725 base pairs (B) TYPE: mucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG102312	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
	GTCGAGGGAA GTAACCAATA TATTCACGAG GGCTACCTAT GGCATCAATG AGACGTTCGG	60
20	AACCAAAGAT CGTCGGGTCC TGGGTGATAG CGCTTCTGTG TGGGGTCTTG TGTGCAAGCG	120
	ACAACCTICA TACACGCGAT ACTICCTOGT TAGTGTTAAT CTCAACAGCG GTGAAGTTAT	180
	CTTCGATGAC TTCAAAGAGG AGCGTTTTCT GACGGAGGCT TTGGAGACGC GAATAAAATA	240
25	CACAAACOCG AGTGAAGTTG TOGTCOGAGA TOOOCTTGOC TCAGAAATOG AAAAGGTGTT	300
	TCATACTTCA GATTOCGATA TCACTCTAAA TAGGATOGAG CTOGTOGGGT TGTATGAAGA	360
	AATCTTCAGT GAGCCGCACC CAGCCTTTAG GGGCAACGTT CCTCTGCAAA CAGCGCTCAT	420
30	OCTOGTOCAT COCTACCTAA CAAACTICAA AAATGAGAGT TTACTCTTCT TCAAGGAAAA	480
	CTITAAACCA TICTOCTOGA AGACOCACAT GATTCTTCCC TICTAGCGCT ATTOGAAGCT	540
	TAGATATTIT GOOGACAGIA CAGATAGGAG CAGTAAAGGT CCCCIGITAT GOGINITAGG	600
35	TCAANCTAGA ANAACTAGGG TTAAGGACTT GGAGGACTGG NITGAAAGGC CITINTAATTT	660
	GGICAAGICA ANAGAGITGN GGNNOCCAAN GATTCACNAG GNOCCNATIN TCATGGCICG	720
	GAATT	725
40	(2) INFORMATION FOR SEQ ID NO:76:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 659 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1023RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
55	TOCCCOOCAA OCTTACOGTA CACGAGACAG ACCOCOCTGA TCACAAGCAC AAGAAGTTTG	60

	NGTACTOCAC CATOCCAGAC ACCOGTOTOG AAGTOCACTT GCAGCGCTTG ATGCACCACA	120
	ATCTGAAAGT GOGGTICGTG GAGCAGACAG AGACATCCGC AGTGAAAAAG AACAGTGGGA	180
5	CCTCAAGCTC TGTTTTCTCG ACGCTAGGGA TAACAGGGTA ATACAGATAT CAGATCTAAG	240
	CTTGCCTCGT CCCCGCCGGG TCACCCGGCC AGCGACATGG AGGCCCAGAA TACCCTCCTT	300
	GACAGTOTTG ACGTOCOCAG CTCAGGGGCA TGATGTGACT GTCGCCCCGT ACATTTAGCC	360
10	CATACATCCC CATGINIAAT CATTIGCATC CATACATTIT GGATGGNCOC ACGOCGGAA	420
	GCAAAAATTA COOGTCCTCG CTCAVAGACCT GCCAGCAGCG AAACGCTCCC CTCACAGAAGG	480
	CGITINGATIC TICCCCACGG CGNOCCCNIG TINGAGAATINI AAAGGITAGG ATTINGCAATIG	540
15	AGGINCTCCT TICANTINCT CCCTTTINAA ATCNITGING GICAAGICNI CANATCAAAT	600
	TOCCAACATT AACACCNIGG TIAGGGAAGT TCANNITICN GGGGCCNNGA TIANITICN	659
	(2) INFORMATION FOR SEQ ID NO:77:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 646 base pairs (B) TYPE: nucleic acid (C) STRANDFINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1023UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
	GATCTCAAAC CIGAGAATAT TCTACTICAT CAATCTGGIC ACGITATGCT TTCTGATTTT	60
35	GACCTGTCAG TACAGGCAAA AGGAACCAGA AATCCTCAGG TTAAGGGAAA TGCCCAGTCT	120
	TOOCTIGIOG ACACAAAAGT TIGITCICAT GGCTTCAGGA CTAATTCTTT TGTTGCAACG	180
	CAACACTACA TIGCACCIGA CETCATCACG GGAAATGGCC ATACACCATC CGIGGATIGG	240
40	TOGACATTOG GTATACITAC TTACGAAATG CTCTTTGGGT TCACTCCTTT CAAGGGCCAC	300
	AACACAAATC AAACGITCTC CAATATTTTG GAAGAATGAC GTTTATTTCC CAAACAATAA	360
	CCATATATCT COCACTTOCA AGGACTTOGA TTAAAAAGIT ATTOGGTCAA GAAAGAGAGT	420
45	AAGCGACTTG GTCAAAGTTT GOCOCCAAGT GAGATTAAAA AAGCATCCCT TTCTFFTAAG	480
	ACCOGICCAG 1000COGITA TIGGACOGAA CCAGGAACCT CCCTTITATC CCCGTATTGA	540
	CCCCACATOG GIACCACTIT CCAAACVIAT CACATTAAAG GATGITAAAA AGCCCCCCAA	600
50	TCCGGCCCAC CCGGGTTAGT CTCATATTCA AAGGCCNOGT TCNNCN	646
	(2) INFORMATION FOR SEQ ID NO:78:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 557 base pairs(B) TYPE: nucleic acid(C) STRANDEINESS: single	

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1024RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
	ATINIUNUEN CANNICTORS GORGAROGAN TACTORETCA REANOCTROES CTERRITET	60
	OCOCAGOCOT TOOCATOCTC OCOGATCCTC OCOTCCAATA TACCAGAATG CATCATOCTT	120
15	COCTOOCTICT ATATTICACCT GGTGGCCATA TATCAAAAGG CGGTCCTTCA AGTTTTGTAG	180
	AAACTOGICT GOCTGAGATG GOGTAGOGAA COCAAGGAAG CATTTATTGC GOCATTTACG	240
	ADOCCIOGRA ACACTARCIA OCCOGTROTT CICRICITADO RGIOGRAGOG GOROGIOTOS	300
20	GGAAGGAAGC GGCTCTGGCA ACGTTTTCTC CGCCGATAGA GCATATGGGT TATCCTTGTT	360
	GATGGACTIC AACAGITGIC CAGCATATIC TATCCTGGAC GCATTIGACG CTGGCAAATT	420
	TGACAGGTAG ACACTGGATG OCCOCGTTAG TATCGAATCG ACAGCAGTAT AGTCACCAGC	480
25	ATTCACATAC GACCGGACGC ATGATATTAC TICCTICACA ACTTAANIIN CCCAATCIIN	540
	NECCAGATIN ATTITICG	557
	(2) INFORMATION FOR SEQ ID NO:79:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(11) MOLECULE TYPE: INA (genomic) (V1) ORIGINAL SOURCE: (A) ORGANISM: PAG1024UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
	GATCTAAATT COCACGCCGC TOCGGCGGTT TCTCTGCCGAG TCTTTGCCGT GAAGCACGAC	60
	ATAATCGAGC CCAAACACAG CAAGATCGCA GAGAATCAAG CTTATGTAAG TCTCACGTGA	120
45	CTCGANGCGT GCAGAACOGT ACGGGTGTGC ACTGCAGGTG CCACGGCCATG TCTCACATGG	180
	TIGITAACACG GCGCGACCGC GGITCGGAAT ATCAAACAAA CATATGTTTG CCGCAAAAGG	240
	GACTIGETTICC CGCAGCTICCC ACCCGCACCGC GCACAGCCCC CCAATGCAGA GTCGCGTTIAG	300
50	GENECOGIOG CCCCCATOSC CCAGIGIOSC CCCC	334
	(2) INFORMATION FOR SEQ ID NO:80:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 621 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1025RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80: GATCAGCCCG TTOCCGCCCC CGCCGTTGTA CTTCTGGTTC TGGATGGACC CCGCC	
(XL) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
GATCAGCCCG TTGCCGCCGC CGCCGTTGTA CTTCTGGTTC TGGATGGACC CCGCC	
	CGIGAT 60
GOOGCTOTICS THOOCGTACT COTOGCTOCT GOOCAAGTOG CACTICAGCG CCAC	TAGCAC 120
CASCITICACE COCTICOCAGT COTOCOCAAT THOCOTICACE CACTIGITICI TGAC	GTTCTC 180
CACCGACTOC COCCACTOCA CCCACAAACA CACCATAATC GTGTGTGTGT CCCAC	GTACGA 240
CAGCGATCOC AACCOGTICAA ACTOCTOCTIG COCAGCAGTIG TCOCCACAGGC TCAG	OCTGAT 300
GUCCIGGIUG TCCACGAAGA TGTCATGGAT GTAGITITCG AATACCGIGG GCTCC	GTACAC 360
CTTCCCAAAG TACCTCCCCT GAACACGTTC AACAGCGACG TCTTCCCCCCA AGCAC	eccrer 420
CCGAGGATGA CGATCTTGCC CTCGATAGGA TGCTTGGACC ACGAGCTGGA CCAC	ACAGAG 480
25 CCATCTIGIG TTIGIAGACC TGGIGGIGGG AGCICCTCIG ATGCCAGTCC ACGC	TACAAA 540
TACAGCGITT GAGACGAAAT ACTAGCTGCT ACTGTCCTTT CTCTCTGACG AGGTC	GCACGG 600
CGCATCCCCC TTATAACTGT C	621
(2) INFORMATION FOR SEQ ID NO:81:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 522 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1025UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
45 GATCCCCATG AGAATGAGCG CATCTTGGAT ATGCCGCCGGTGG TAAAA	ACCACC 60
TATATATCTG CCATGATGAA GAACACTGGT TGTGTCTTTG CAAATGACGC CAACA	AAGOCA 120
AGAACGAAGT CCTIGATIGC GAATATICAC CGICICOOCT GCACGAATAC AATTO	FICTGC 180
50 AACTACGACG CCCGCGAATT CCCTAAGGIT ATCGGTGGAT TTGACAGAAT TCTAC	CTTGAT 240
GCCCCTTGCT CAGCTACAGG TGTTATCGGC AAAGATCAAT CTGTGAAAGT AAATC	CGTACT 300
GAGAAGGACT TTATGCAAAT TCCACACCTG CAAAAGCAAC TGATATTATC TGCAA	ATTGAC 360
TUTUTUGACA GCAACTOCAA GCACGGCGGT GTCATTGTCT ACTCTACTTG TTCCC	STTGCG 420

	GTTGAAGAAA ACGAGOCCGT GGTCGAATAC GCCTACGGAA GAGACCTAAT GTCACCTGTT	480
	GAAACCGGCT GGCTATTGGT AAGGAAGGCT CACTAGCTAC GA	522
5	(2) INFORMATION FOR SEQ ID NO:82:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 508 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1026RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
20	GATOCAATTG CTOGTCATAC ATACOCATTA ACAGATTTTA TTACTATGTA TOCAACGTGA	60
	ATTOCTATAT GRACCITATE ATCOCPTICA TANAGATOCT TEATUTCHE ATTCTGAATC	120
	GGAGTCGTTT GACCGGCGCT TAGACTGGTT ATGCCTCTTG CCATCGTTTT TCTCGAAAAT	180
25	GAAAATTCIA GOTTCACGOT CGGCTGCAGG CTTAGTCGTA TCCTGCTCAT TGTTAGTTCT	240
	CCTATGACGG TATCCTGGGA AGGTATCCCA CTGGAATTTG TGCGACCTCT CAAGCTTTAA	300
	ACCATOCTOC TIGOCAACIA CCITACOCTO CCAACAATOC TATOCATCAC COOCAAATAC	360
30	OCACAAAATG ATCCTOCCCA TATCATCAGA TGATTGTTCT TTTTCCTACT TCATATCCGG	420
	AAAGATGGGC AACAACTACC TICTTATTGG CCAGCTTGAT AGTTGTTTAC AGCTATCAAA	480
	AATATOOOGA TAGAGOICIG AGCICICT	508
35	(2) INFORMATION FOR SEQ ID NO:83:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 594 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1026UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
50	CATCTACCAG ACTAGACTOT CTATCCCATO AAGTITTOTGT TTTCAAGTOT CCGTTTCTTG	60
	AGCAACCTGG TGCCCCTATA CCTGTGTCAG ACGCACAGGG AAGCAGACGT CTATCGAGGA	120
	TGTCGAACTT ACAGAGGAAA AAACAGCGCC CGCCAGCTAT TCCAGAGGCA GACGTATCAC	180
55	TOCAGGOTAT CAAGAAGOOG COCATGIOGG CCAGGTOTIC TACCICCOGT AAGTOGGGTT	240
	CTGCCCAGCG TATTAGTGTT GTGCCACGGG CCGCAGCTTC AGAGTCATAT GTGGTTCCAC	300

	CIGCIGGIGC ICCICIGAAL AAAGAGICIG CGGATGACIT ATTICAAACG ACTOCTICCT	360
5	TITIATGAAGG TTACACTATT TOCACACTGA AAGAAATACO GAAAAACATT GCAGATGAGG	420
	ACTICTICCCCG ATATACCGTT AACGAGGATA GCATCACTAT GCCTGACCTT TGCAAACCTC	480
	TATTCCCCAT AGGTGAAGTA TCTGATAATT TCACCGGGG AAAGAAGCTG CAAAAGCCAA	540
10	CATOGAAGCT COGAAGAAGC COCCOCGAACT COGACAGATG CCTAACCGTC AATC	594
	(2) INFORMATION FOR SEQ ID NO:84:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 454 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1027RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
	CATATOGACG TACTICTOCCG TITIGTTCTTC TITOGTCAGCA GGAACGCCGT CCGGCATAGG	60
	CTTACTGACT TTCACAGACA TGATTCTTTT GCTGCAAGTA AAGTATATTA ATGGCGCTGT	120
30	CAAAAATGGT AATAGTACGG AAAGACCAAC CTGAGAAGCG TOCAGGCCCT GCGATAAGCC	180
	GITTITIACCT AGACCAGTOG ATACACCTAA TGITGGAATC AATGCAATOG CTCGTGTCAG	240
	AATTCTCCGT TTCCATGGGG TTATAGTCCA GCGTATATGG CCTCCGCATA CTATTTGTCC	300
35	ACCTATOGTA CAGACAATNO CTOCCGATTG GCCCGAGATT AAGAGTGCGA GCATGAATAT	360
	CETACCIGCC CCICGICCCA AAGIGITGCA TAATACGIGG TGTATCGIGT ATAGATCCCC	420
	ATCCATCCCT TCCCCCCCTAT CATACACTCC CCTA	454
40	(2) INFORMATION FOR SEQ ID NO:85:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 446 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1027UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
cc	GATCAACGAG TAAAAATGCC AGGIGITICC GITAGGTACG TGTCATGAGT GCTAGTTTAT	60
55	OCTITIOGIAC COCTOCTOCO COCCOCTITIC TOCCACCTITIC CACCOCTICAT ACCTITATICTIC	120

	Applied to decide officers, or notice that the second	100
	GATTGGTTCC AGAACGTCGC TGACTGTGTC AAATATGAAA TCATTGGGG AAACTTAGCT	240
5	TOCTACOGAG TOCAGCATOC AGAACOTOCO GCOGAAGCTA GCTGAGOCTC GATGAGACGG	300
	TOCCOGNANT CCTTCGATCC CAGGCCAAAG CAGACGTACC TACCAGCTTT TAATGTGCCC	360
	OCCTACTAAC ATGATATACA GAGAOGITOC AOCTCAAGAG TICATCAACG CITACOCTTC	420
10	TITICITOCA AAGACAAGGT AAGTTG	446
	(2) INFORMATION FOR SEQ ID NO:86:	
15	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 551 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1028RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
	GATCATOCAA ACOGAGAGAA OGAGAAGAAG TCTAACAAAG ACOGCACTAA ACAGAAGAAA	60
	GCCAAAAAGC AGGAGAAAAA GGAACTGAGA AACATCATTG AGGAGTCCGT TGAGCAAAAT	120
30	AAGCTAGCAC TGATAGAAAA GGTGGAGGAA GAAAGAGGCC GCACGAAGGA GAAAGACCTT	180
	CACATCAAGT TCAGGTATCG GGAAGTTTCG CCAGAAAGTT TTGCCTTCAC CACCCGTCAG	240
	ATMITTATES CIGACGACEC TECCTIGAAT GAGTATATIG CCCTCAAGAA ATTITECACCA	300
35	TATAGAGCAA AGGAGTTOCG CAACAAAGAT AAAAGGAAGG TCATGAAGGC TAAGCGTCTA	360
	AAAGAATGGA GGAAAAAGGT GTTCAATAAC GAAAATGGGT TGGCCGATGA GGATGAGGCC	420
	CTTGATACCC AGGCGGCTCC TAAAAAGGAG AAAAGCCGTT CTAAGCACAA GACAAGTAAG	480
40	TAATATTACC GTCTTTATGT ACGITCTGCC GTAATTATAT TITGCTATAC ATATATATTA	540
	ATTIAAACTI T	551
	(2) INFORMATION FOR SEQ ID NO:87:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 628 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1028UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	

	GATCCGCGCC CGCCACAGGC CTGGCAGCAC CCATCGCCGC ATGCTGTGCC TAACATGTCT	60
5	CAGAATTACG COOCCOCTCA GOCCOCCCCCA TGCTTTTIGGG CCAGGAAGCC	120
	TTCCACGAGC TOOCCGACTC GCCTGGCATG TCAATGTACA TGTCGCCCCA GACCCATAGG	180
	CTCAAGGGCA ATGGCGGGTA CCTGTTGCCG ACCGCTTCTA TCTCCGACCC TTCGGTGCTC	240
10	GGTGACACCG GCCCCCTCC GTCTTCTCAG TCATTGACAT CGCACCTTCT GCGTACCCCG	300
.0	AACTITIAACA TGAATGACTA TGTGCATAAC CTTTTCAGCC CCTCACCAAG AATAGACCCG	360
	CCAGGIAGCI CTGGGAATAT ATAGGGCCTC GCACACATIT AGGGCACAGI ATACTAGCIA	420
15	ATCCTACATT CTCTGTCATA GTAATGCCTA TGTCAGCACA CCTGCCGTAT AATTTCATTA	480
.5	TTTCCTGTTT CATAAATGCT CACATATGTC ACGTGGCTGG ATCAGCACGT GATGGCAAAA	540
	TICTTATGAA TGAGOCTGFT CATCTCGTCA GACAATACAT TATACACGCA TCCATCTCTC	600
20	GGTATGATAC GGACTICTCIC ACACTGGA	628
20	(2) INFORMATION FOR SEQ ID NO:88:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 655 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1029RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
35	GATOGIAACA CTCTOGAGAA GIOGAAAGAG CTAGTOOCTC OGAOCTGTAA AOGATOCATG	60
	GATGCOCTTC ATCACAACOG GTACGACACC GCOGAGTTTC COGAGCACAC GCTOGAGGAT	120
	CTCCCAAAAC CCCTTCCCCC CCATCCACTG CTATACCATA TTCCCCCCACT CTCCCAATTT	180
40	COCATOCCAC TOGATCOCCO COTOCTOCAG ACCTCAAAGA ACCTTTGTGT COTATTCTCG	240
	AAGATCGATA TOGTOGTOCA GAGACCGTOG CACATOCCOC AGCACGTAGG TOCATTTTTT	300
	CAGASCTISC TITATCATGA CCISCATGIC AAGATCAGGA ACTICCSCIT CTITICISCS	360
45	CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT	420
	GOCCOCCAA ACGCGGGCAA GTCGTCATTG ATCAATGCCC TGATGAAGAC TGTTGTTTIAC	480
	GARAGICOGO GICTOGTATO CICARAGORA TOCTOTOGGA COCCIGOGGA COTGOCTICOA	540
50	AAAGCGCATT TGGACATCCA TTCTGCGGGT GTGAGCACAA TACCGAACTT CACTCGCCAA	600
	CCCAGCAATA CGATATAAAG GGCAAGATCT CCAGGATTTC CAGGCTACGG CACAT	655
		655

5	(A) LENGTH: 638 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
-	(ii) MOLECULE TYPE: DNA (genamic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1029UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
	CATCTOGTOG TGTTTTOCAA CTTOGTOOGT GACGCGATAT CTCAGGCTTT GCGTOCTGAG	60
15	CATGATTATG AGGTGAACAA GATGCGCCGC GCGCTCTCCT TACTCCAAAA GCTGTATATT	120
	AGGGATAGAA GGACCAATIT CCTCTCCGGG GCCAAGGGGG ACGACTTCTG GGTCATTGGG	180
	GATACCACGG TGAAAAACTG CGACATTACA TCTCTCCTTC TTTACTTTGA TGAGTTCTAC	240
20	AGAGAACAGT TOGATTTGTT CCTGGCGCAG GCCCGTGCTC GCCAGGAGGT CCCCAGGGGC	300
	GATUTUTIAG COTOGGAAAA CGATATAAAA GTAAAGITUT TTAGOGAGAA GTUATUGAAG	360
25	CACGCTTCGT GGGGTTCCCT TGCCCTGCGG AAATTCGAAC TCGTACTGCG CGCTCCGTTT	420
23	CHGITGCCCT TICGCCAGCG GGICGCCTAC TITGAAACGC TGATACACCA CGACCGACGG	480
	COSTTICCACO GACCOCACAC ACCACCACCC TTCCCCCTCC CCCACCTGTA CITCCCGTCG	540
30	TOCCOCCOC ACCUTOCCAT TATCTCCAGE AACAACATCC TOCAAGATGC ATACSAGOCG	600
	TATTATCCCC TCCCCAAGA CTTTAACCAC CACCTCCC	638
	(2) INFORMATION FOR SEQ ID NO:90:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 688 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
40	(ii) MOLECULE TYPE: DNA (genemic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1030RP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
	GATUTOUTTG TTGCGCAACG CTTCCCAATC GATGTCGCTG AGAAAGGGGT GGGCGCGGAC	60
	CTCTGCGCCG TCGTTGACCG CACCGAGGCG GTGCTTGGGA TTGCGGTTCA AAAGGCCCTT	120
50	GACAAAGGAG CGACCTTCOG GOGATAGCAC GTCCCTGGGG AATTTGACCT TGCCAAACGC	180
	AATCTTCTGG TACATCTTCT GGTTGTCCTC TGCAAAAAAA GGCGACCAGC CACAGCACAT	240
	CTCGAATAIC AAGACOCCCA GCGACCAGAA GICAACCATT TICGIGTAGC COGICTCATC	300
55	GAGCAGCAGC TOGGGCGCTA GATACTOGGT GGTACCGCAG AACGTATTGG TGGCATCCTT	360

	TACCTCCCCT TTTCACACCC CCAACTCACA TACTCCCATA TTCCCCTTGC CCTCTAAAAG	420
	GATGITTTCT GGCTTGAGGT CGCGGTACAC GATATCATTA TCGTGAAGGT ATTCCAACGC	480
5	AAGCACCAAC TOSSCAATGT AGAACTTISC COSCTOCTCC GOGAACCGAC CTICTTICTG	540
	AADGTGCCAG AAAAGCTCAC CACCGNTCAG GAAGTCAGTC ACCAAGTATA AGTCTGTGCG	600
	CGTTTGAAAA GAAAATTTCA ACCAACAATG AAGGGACACG ACTTTGAGCA GTACGAACGA	660
10	GATGITGCGC TCACCAATAG TATGIGCA	688
	(2) INFORMATION FOR SEQ ID NO:91:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1030UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
	GATOGATTOC CTGAGCATGT TTTTCCCCTAT GCTGCAGGTT TTACATOGTG ACATTGCGCA	60
	TOCCGAACTA AAGAACCITA TGICTTIGAA ACTOTOGAAC ACTTACOCCG GAATTOCTGA	120
30	ACGCTGGCTA TTCACTACTC TCTACAAGAA ACAGCAAGTT ACCGTAAATG ATACCGTGCA	180
	GCTCGAGTGG TATCCTTTAC GGCCAGAGTT TGTAGAATCA ACCTATTCCC TTTACAGGGC	240
	CACTAAAGAC GCATTITATC TGAATATCGG ACGAAGCATC CTCCAGGCTC TATCAACGCG	300
35	CTTTAAAACG AAATGTGGGT TTGCGGGCAT ACAAAACGTC ATAACGGGAG AGGCCACATGA	360
	TAGGATGGAA TOGITGGITT TGGGGGAGAC CITAAAATAT CICTATCTCC TCTTTGACGT	420
	ATCCAATGAA TTGCATACAC AAAAACGCAC TAACCAAATA TTTAGCACTG AGGCGCATCC	480
40	ACTIGIGITIC ACTICCTICGA TCAACOCTICG CTACGAAAAG AACAAGTACT GTGAAAAACGA	540
	CGTGTATATA CAGAACTTGC GTCGCCTACA GGAGCTTGAC CAGCTGAAAA GCCGTGCCAA	600
	TICATICACT GCAGAGGAAG CCATGATACC AGCTTCAGAT TICAAAACAG AAGACTCOGA	660
45	GEAGTCTTTG AAGGACCOCC TTGCAGCOCC ATACTAGAGG CCTACACGTA GATACGACAC	720
	GTTCGTGGAA CATGCAGACC TTTCGCGACA A	751
50	(2) INFORMATION FOR SEQ ID NO:92:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 646 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
5 5	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIG:	INAL SOURCE	Ε:
	(A)	ORGANISM:	PAG1031RF

5		
·	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
	GATCTTAGTA ATGATCACGT GATTGGATTA CCGCTTGTGC GITTTGCTCT CCGCAAAGCG	60
10	ACATTIACAC GOGAAAAGCG GTGAACTOCC GCCGAAACCC AAATACTCGT ACACTATGAC	120
,	TATAGACGAC AATGICGATG ACGTGAGCAC AGITTIAACTC TAGTGTACAA TCACGTGCAC	180
	ATACCTICIC TOCCACCCAC ACATTAACCA ITTATTITGIG GICACGIGAA ATGAATOGAT	240
15	GCATTITATA ACTIGOAGGIT AGFIGAGOCA TOTOGCCAAC GATGTOCTICO GACAGCATTO	300
	OCCOCACOGO: OCCOTCATICAG TIGATITOGRAGI GAGOCACAGG ACTICCACOGG GOGTIGITITAE	360
	TACTATAATT CGAAGGGGGA AACGTCATGG AATAAGCCCA ACGACACGCC AGTTGAGCTG	420
20	GAACCOCCAC TOGAAGAATG TOOCTOGAAA GTOOCAACGA COGAGGACGG TAACGTGTAC	480
	TATTACAACA GOGAAACTOG CGAAACCAGG TOGGAGAAGC COGAGTTOGA OCCAOCCGAG	540
	GAAGTOCCCC GOGAAGARGA CGAACOCGCG CCGGAGGARG AGAAGAACGA GCCGTCCGCT	600
25	OCTGARGAGO COGGGGTCOG GATCGAACTG CTGCTCAACT CAAACC	646
	(2) INFORMATION FOR SEQ ID NO:93:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 386 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1031UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
40	GATCANOGAN CAGCACOGAC AAATATAACA OCAGCACOGG CATTTGTCTA GTCGGCTGGT	60
	CYYYTGTGTC CACCGTGACG CTGGCGCTGG GCTGGACTGC AAAAACCGGA GCCACAAGCG	120
	TOCOCCTICCG ACOCCGAAAG CTOCCATCCT COCACCACCA CACAATOCCT COCGCACTCC	180
45	AYCYCCCELE CLOCCYCCC GCGCYCCCCC CCYCCCLGCC CCCCCCCCC CLCALICLICC	240
	GOGOGGCATA COCAATICAAG AAGGCACACG CGCGGGGCGCA GCTGGCGATG CAGGTGGCGC	300
	GOCTOCSCOG CCTOCGTGAL GTGCCGCTGC GCCGCGGGGG CGTCCCGCTG CTGGCKGTAC	360
50	ACCCCGGTCT GGTGAACTTC GCGTAC	386
	(2) INFORMATION FOR SEQ ID NO:94:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 775 base pairs (B) TYPE: nucleic acid	

(C) STRANDEINESS: single (D) TOFOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1032RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
	GATCTITIAAC CTCTGGACTT CAATCTTCTG GGTAAAAGCA CAAGTTTAGA GATGTATGAT	60
	CCAAGCACCA AACTACAGTC TOGAGACAGC AAAATAATCC TACTTATATA AACTGAACGT	120
15	TOCAATTCTT TAAAAAATTT ACTAACTTOG ATTAATGOOG COCCOGTGAG COCCTCTGTT	180
	ATTACCTGAG TCATCCTGAG GGTTTCCCTA GGAACCATCC GCTCTTACTA OGTATTTACC	240
	AAGGCACAGG AAAATGTGGT GGTATTCTTG ATTTCGCCGG CGTTTTGTAC ATTACTCCAT	300
20	AGCTICATIOGT CAGCAATCCC GTTICAATIGGA CATTTIOCTCA ATCGTIGAGTIC TTICCACTIGGA	360
	CTICAAATCC CGCAGGCAIT TTCGGCTCCT GGCTCAACCA GGTCGCCCGG ACACCTACAG	420
	CCGAAAAAAT TOCTOCTTOG ACTAGGTCCG CTGACGTCGA CATCCGAGAT GACTTTAAAG	480
25	TGATACATTA AAACCAGGGC TGTATGAACT CAGCAAAGGT CTCTTTTATA CAGTGTGCAT	540
	ATAATATTTC GOGCOCTTGC AATTACCTCA TGCCAGGTAC TCGTAAGATT CGCCGTCCGC	600
	GAGCOCTOTIA OGTATICCTT OCTAATTAAG TIGTOGATOG CCTTCTIGAT AGAGATACCT	660
30	TIGCATITIGA COGITIGIGAG ATTICOGOTIAT GOATTICGICA COAAAGTOGO ATGAGAGACG	720
	ACCOGNITION TITICATAATT CIGAMMATAC AAGCITCAGA ACAATTOOTT TOTTG	775
35	(2) INFORMATION FOR SEQ ID NO:95:	
33	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 720 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1032UP	
45		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
	GATCCCGAAA ATAGACTACA TCTGCCGCAA GCAGCGCGCC CTATCTGCAT TTCTCTTCTT	60
50	OGTOGTTGTC ATGTGGGTCA TCACGTTCAC CATTAGCATT CTAAGGGTAG TGCAACGGGT	120
	CAGITCACTI TCACCCAGAT AAAAGITAAC ACCACAAGIG AAAAAAAACG COGATAAAGG	180
	CATCAGITAT GIAATAAAGA GCTAJACGOC AATAAACATI TAAGTAACIA CCATGGIATC	240
55	TOCAGOGIAT TACTAGGITT COCTGAAGIT TOGAATGIGC CTTCGITACC COGTGITICAT	300

	GENERAL GENERALIA MANGENTE CONCENTIC CALCATINE GEOGGIAM	360
	GTCCTAAAAG TTAGGCAAAT AAACACATAA CCATCCCTCA AAAAGCGCTT GAGCAAGGCT	420
5	ATCOGOGOTIC AGAGCAGGTIG TAATATACAT TAGAAGTIGAG CGATGAACGA TAAATTOCCG	480
	AGASCAGATG ACTITOGAAGC CACTITOGAAC TITIGITOGAGC CCOGTATCOG GCAGATCCTG	540
	OSCOOSCATG OCTOOCCCCA TOCACOCCCA CTOCACAAAC TOCTOTCACC TOCCATOTIAC	600
10	ATOGATOTOT ACACOGOTAT CTACAACTAC TOCOTCAACA AGTCOCOGTC CACCOGOCAT	660
	TITICAGICOG ACTODOCOCA ACOSCAGICOS AACCAGICAT CGATOCTIGGT COGAGOGACA	720
15	(2) INFORMATION FOR SEQ ID NO:96:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 602 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1033RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
••	GATCTTGTOG AACAGGTOGC CCCCGTOCGC CAGCTOCATC GCGATOCATA GGTACTCACG	60
30	TGACACATTIG CAGTICCAGCA COCTICACCAC ATIGITOGGTIGO COCGGGGCACO GOGTICTIGCAG	120
	CACCACCIGG COCOCCAGAT CCICCOCCCOT CATCCCICCC GCIVIGCACC GCICCACGIG	180
-	CACGAACTIC ACAGCCACTA TOGICIGOGG GICIGOGOGC AGOGAGGOGG TITTGAOGAA	240
35	COCCAACCTC COCTOCCCAA TOGTCTCCCC CACCTCTAGT TOCTTAATCT COCCAGGCA	300
	TTCAGCCTGC GACGACTCCA TAGTAGCCCA AAGTCGTTGG ACGGCCTTCC ACGTGGCCTC	360
	TAAGTGCTGG TGATGGTTGG TTGAAAAGTG ATGCCCCCAAC AATAGTGTGA AAAACGGCAA	420
40	AGTOGOCCIT ACOGOGOGAA CAAAACAAGT OCTAACTACA COGAAGCAGG AATTAATTTIG	480
	GEAAGTGGGC TTGGAGCACG GTATAGGAGT ACCGGAGGTG GATATGAGTG TCGAACAGGT	540
.=	GICTOGTOCG CACGCGTOCG AAGAACAGGT GGCACGGTTT GAACGCAATG TOGAGGCGCG	600
45	CA CA	602
	(2) INFORMATION FOR SEQ ID NO:97:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 683 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1033UP

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
	GATCCGCGTC GTCGAAAACA GGTCCTTGGG GTGCGATACC GCCAGCACCT TGCACGACGT	60
	CCGCACCAGC TGGTCGTCGC TCTCCAGCGC CGTGATGATG TCCTCCACCG AAAACACCTC	120
10	CAGCACOGTC TCAAACOGCG CAAGCTTCAC CACTGTGTCC AGCAGCGACA GAAGCCCCCT	180
	ATAGTCCAGC CCACTCATCT CCCCTGCCGT GASCACCTTT TTCATCGCCG AGAGTAGTGG	240
	COGREGATION GOSTOGAGAC GCACCATCAC COCCAGGITOG ASCITGCAGCA IGICCACCAG	300
15	CCCGTTCACC GACCCCACGC CGTGCTCCTC GGGCGCCTCC AGCACATCCG CCAGCTGGCT	360
	CATTOGGTCC TOGATOCTCC ATTOCTCCAT COOGATATOG ACTOTTCCGA AGTAGOGTTT	420
	TOGGGTTTGT AAAAGTAAAG GGCACTTTTC CAGCACTTCG CCACTTAATG TOGTGAGGCA	480
20	CAGAACOGGG GCCCTATGTT GCCGGAGTCA AGGCTTGCCT CGCTATATTC CGACTTCAGG	540
	AACCTCCAAG ACCTCAATCC ACATCGCTTIC CACCCTAACG TICTAACATC GAAACACCAC	600
	CTGATGAACA CAGTGTGGGG GGACGAGCTT CTGATAGAAG GGGGGGACAA GCTGCTGGAG	660
25	CGATTGAGCA CCAAGGAGAC GGG	683
	(2) INFORMATION FOR SEQ ID NO:98:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 653 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1034RP	
40	(xi) SEQUENTE DESCRIPTION: SEO ID NO:98:	
	GATCATATIG GICTIGGCGC CAGCATCGCC TCTTCTGGIT CTGAGCCAGT AGTATGATAG	60
	CATIOCOGOGG ATIGAACCTOG CAATIOGAGAA ACTAGGTIGAG TITGTACATCC CGACGCCAAG	120
45	GOCAACGCCT GAGGGTAACC ACTOCOCCCA TCTGTACTTG TOCTTATCAA TACAATTCTT	180
	TACCACCCAT ATCACTICCAA ACATICCTTCC TACCATICATC GAACATTCCA GTOCCTATICG	240
	TOOGAGTOCC ATACCCATGA CCAGACGTGC GCAGTCTATC CATACGAACG CAGTTGGGAT	300
50	CCCCAATTICC TOCCTCCCCA TITTCGTAGAC CITGTTGTAA AAAATGTACA TTACCCTAGA	360
	CAACACGATC GACCAGCTGG CGCCGATAAT CTGCGCGGTIA AACTGAGCCC TAGGAGAAGC	420
	ACCGATTAAA TGCCCTGTCT TAAGATCTTG CATTAAATCG CCCGCTTGCT GAGCGCCCGC	480
55	CTCAGCTATA CTTCCGGCAA CCAAATTTAT TAATACAGCG GCCTTGTGAT CCCTGGGTAC	540

	ALAALAGUGA AAATGATTIG AGCCAGCTITT CQGATGCCGC TGAACGCGTT GACATCGGTT	500
	TCCCCAAGAC CCGGACGCCC AAAATCGATA GAAAGATGCT ATAAGGAGAG CCA	65 3
5	(2) INFORMATION FOR SEQ ID NO:99:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 670 base pairs (B) TYPE: nucleic acid (C) STRANLEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) Orig inal Source: (A) Organism: Pag1034UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
20	GATCACGCAC AGCGGACACC ACCAAAGCAG AACCACGGTA CCATATCTCT CACACACGGC	60
20	TCCCACTAGC ACAGCGCCTC CACCTGGCCG CCCTGGCCTC GGCCCCCCGT CCCCATAAGC	120
	ACCITOCOCC ACCITATITAC TICCAAAAAT ATIGTICIAA CAGIAATAAT ATCCICATIG	180
25	AGGACATTIC AGTIGITACA CIGAAAAGAA CAGATACTAC ACTIGATCTA AGCCAAAAGG	240
	CAAACAGATT TOGTTTCTAA AAGAAAGAGA AACATGCCTG TAAGAGGGAG GOCCATCGCA	300
	CATTITITCT CTCCTTATAT ACCAAGIAAA ATTIAGAAAA AGAAACGACG COOCTGCTIG	360
30	GLGCOCCCC LCLCCCLCCC VCLCCVCVCC COCLCVCCCV GCVVTCCLCC VLCCVCVCCC	420
	ATGCGATCAA GCTCTGAACG CCCATACCTG CCGCCATACA CGCCGCCATT CGCGAGCTTT	480
	CGTTGAGTTC GTAAGCCATG AAATCACAGT ATACGATTCT CGAGCCCAAG TTAAACAGAG	540
35	CCCACTIGGGC ATACTIGGTAG GGCTACAACT GCGCACCAGC TGCGAAAAGCG GAACTGCAAT	600
	AGITAAGOOC GOOTGOCAAT AGTATCTOCT GCAAGCACCT TCTAGAATTT GGTAGATGAG	660
	TOCGITCATG	670
40	(2) INFORMATION FOR SEQ ID NO:100:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 558 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPCLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG103511	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
	CATCTTTTGT GGAACCAACA TCACCACACA CGAATATGCG ACGCCAAGCG CCGGAACGAG	60
55	CCACACATGG GCCGCGGGGG TAGCGGTGGG CCCAAGCAAG CGTATTTTGA GGACCTGACG	120

TOUTGIOGGI GALCARICCA GOGCALIACTA GOCCCAGGIT GICAGCIGAA AGIGIGITAC	180
CCOGTATCOG TATTACCCCGG CTCGTATAAA TGTTACCCCGG ATATCGTCAAA GCCAAAATTT	240
TOCACOSCGT AAACAACAGG AGAGTGTACG TGCATATGGC GGCAGCAGCT AGTGTAGCCT	300
AGTIGAGAAGA AGGNCTIGTIGA GCTAAGACTA GCGAGGAGAC CAGGATTIGGG CACTIGATTIGC	360
OCCATCTOCA TATTCTCTAC GOOCTGAAG ACCAATCTNC NATATINNOCN COOCCINGTN	420
COCAACCINON OGNOCINONOG AGACINACOGA GVITIGVITINA NOCROCINOOCG CINCANAACCA	480
ANUMINOCN CAATCHOTTA CHATCAANNO CAANTINOON CHINCANCOO CHINGHINAT	540
MANATICAN NOWOLON	558
(2) INFORMATION FOR SEQ ID NO:101:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 604 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genemic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG103512	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
GATCCTTAAA AGCTGGCCTC CGCAGATAGA CCTTCTGCGC AGAGGCTGGA AACCTCAACT	60
AGCAAGTOGC CACCOGAATC AGATAAGCAC TAGAGTOGTT CCAGTAACAG AGGAAGOGAT	120
CAAGGAAGAT AGTAGAAGAG GACACTGCTG CCAGGCTTGA TCGGACAGAG GGTTTAGCTT	180
TCTGTTGAAT TTCAGAGTTT CGGCCTTTG TTTACTTCGC TTCATTCTTT CGTGTAAAQA	240
ACCIGITION AGGATGINAT CATTIONNAS INCONAGGIA COCTATIONA COCOCCACOS	300
AGTOGGTGAA ACAGAGTCAG GACOGAGAAC GCCGATAGAC AGGCGTTTGG TTTGTAAGCG	360
GTGAGAGCTG AAGCAGCTCA AGAGGCCCGC CTTGGTCAGG TTGTGCGGTG GCGGTAGAGC	420
ACAGCAGGGC ATCCCTCGTC GGTGGAGCGT NCGGNCAGNA GCCCAGGGGC NTGGAACAGG	480
GOGGIGITTAT NANGANCNAC CGACCACAAA CACGCININA TICGNACCGG CGGCCAGTIN	540
CCTCANCNTG GITCCCGNGA CITGITTINN GAGCCNATCC TTGGCNCTCC GCCNNAGNAA	600
AAAA	604
(2) INFORMATION FOR SEQ ID NO:102:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 480 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: INA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1035RP

5	(xi) SEQUENCE DESCRIPTION: SEO ID NO:102;	
	GATCITAAAT TGTTGCATTG TGACCTGAAA GTTGCCCCGT AGACGCTGCA TATTCAAGGT	60
	TICCATTICC ACGGGACGIA ACGIAATCGG CIGCACHITIC GACAAACGAC TAATGIATCT	120
10	GTTCTCCGAC TCTCCGCTCAT TCCCATCCCC ACTCCACTGT ACTTGTCCTG ACTGTACTTG	180
	TIGACUTE ACCITATOR COTOGAATGA CICCAGTAGT ACTIGATITIC GICTICCAAT	240
	COTTICTATO CACCOCCTICA ACACOGAACO TOCCTOCOCC TOCCAGGACT CCAAAAACCCC	300
15		
	CCGCTCCTCT GCAGAAGOCG GGAAATAAGA CATAACTTGC TCATCGCGTA GGTAAATCTA	360
	CGTCATTATC CGCGTCCACC ATGTTCGGCT GGGATAAAAT GGTGTTTCCT CCACGGGGGG	420
20	GOGAATACCA COCACTOTICC AATOOTOCCC COGITANIGA ATNONTTINI TNATGOOGNN	480
	(2) INFORMATION FOR SEQ ID NO:103:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1035UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
	GATCHOCCET ACOCTACOCA TATATTICAA CICACCIACITATI CCHIAGAACA CCTACCITICA	60
	GIGGITCCAC GCTATATIGC GITGCAAATA IGITTIGCGIA CCCTICTGGC TIATCAGIGG	120
40	CATTAAAGAG COCOCTAATG COCACTATCT CTTTTACTOG CCCAGTOGTC TOCAAGAAGG	180
	AAGCATTCTC AATATATTTT CCGTGGTTTT TCAGGATGCC ATAATCTGGT ACACTCACAA	240
	ACAATTIATG TTOCACTOOG TGAGATGCAG GOGTATTAGT ATTTOGAATC ATGTGOGTGA	300
45	TTGTCCCGGA TGGGGTGCGC TTCACAACCG CAGAGGAAAA AATATCCCCCA GGGGGATATT	360
	ATTNETICGAA GCAAGAATCG CITCGAGTAG GCATTGAAGA TITCTTCTTG ATACITAAAG	420
	CTGAATTOGT TCANATOOOG TCCAACGAAN GANTAOGNIG GATGENCCCT TNEGOGGGGG	480
50	α	482
	(2) INFORMATION FOR SEQ ID NO:104:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 645 base pairs(B) TYPE: nucleic acid	

(C) STRANDEINESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1036RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
	GATCATATIT CAATOCAAGA GCICCATTAA TAGGTATTGT CTTGAGACAT GCGCTCAAGT	60
	CATTAATGIC ATGGGAAAAA TGCACCGTTC CACCTCCTAT CTCCAATGTA TATTITTAGCA	120
15	TITCAAAATC ATGFFFTCTG TTIACTATAA AGTGCAACCC ATTCAGGICT GCGGCTTTCT	180
	TAGTAAAGCC TCTAAAGCCG TAATCCTGCT CTTGTATACT CCCTACCTGT GCGTCAAAAT	240
	CGGTAACAGG CTGTCGAAGA AGAGCGGTAA ATTGTTTCAG AAATTCGAGA TGCAATATTG	300
20	GTATGCCTTT AACAAGTOCA AAACAAATAC TITTTCOGAA TCTTCGTCAT CTTCATGOOG	360
	TCTTAATAAT ATGATGTGTA GTGGGCCTCC GAAAAACAGG TCACCACTCG TATTCCTAAC	420
	CCTTAATTAC CTCAAGCAAA GCAGGGCTTC TTGTAACAAA GTTTCGGGAC CTGGACTCCC	480
25	CATGOGCCCC TCCAATIVICA TTOGNOGGAT MIGNINCOCCT TCCNGATANA GGNCTGGATG	540
	COCANODGAA NOONICCTAG TGATNICCON CCCCTTCAGT GNINCONCIN GAGGITTOGA	600
	NESCANANTT TOCANAINECE GENANINITETE GNAACCINCOC COINT	645
30	(2) INFORMATION FOR SEQ ID NO:105:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 613 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1036UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
45	CATCCCCTTT GETAACCAGA GETGTCCCCT TGTATTCACC GCACATCCTG GECTATTTGT	60
	CATTACTOTG GCCCCGTCCC AGAGACCTAC AGGTATAAAT TCCCCATCAA GTGCCACCAG	120
	AAAGATATGC TATACTGGIT TTGAGCTTGA GCGACTGTTA ACTGCAACCA GCGGGACCGA	18C
50	ACCOCCUTAGO TITTACTICAT TEATTGAGOC TAAATTGGAA CCAGACATCA CAATTCTGCT	24 C
	TCAGTOCGAA ATOGACGCAT ACAATCCAAA ACGCCAGAAG TATACTGAAA TAAAATCCTC	300
	TGTGGACTTC AATGTACGAA ATGTCCGGCA CCTGAGCAAA CTGCTTAAAA TATGGGAACA	360
55	AACAGGGGTG GTCCCATCCA CTGATATCTT GTAGGGGTCA GAGACCCATC AACCCATGTG	420

	TIGAAACAGN COOCCCTTAT GOGTOGTCAA ATCGNAGGAA AATCTTTTTA GOGTOGNOON	480
_	NAGOCANCAC TIMITTIANI TATOOGAGIG CAANATOGAA ATAANCATOG TNAATITOGA	540
5	AGGTATTTCC COGOGNICAAC CANCOGENING AANNWITTIN NGGOGTINGAA AGANTCAAAT	600
	TAAATNOOCC NOT	613
10	(2) INFORMATION FOR SEQ ID NO:106:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 606 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1037RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
	GATCATCATT ATTICCTOCS TICGICCCCA CGATTCGAAG GOCGOGGICG GTITCTICAA	60
25	GGATTICAGG CGTATGAATG TIGCTCTCAC CAGAGCAAAG GCCAGTCTCT GGATCCTGGG	120
	TCACCATAAA TCTTFATACA AGAACAAGCT ATGGATGCAT TTGATTTCAG ATGGGAAAGG	180
	GOGTGACTIGC CTCCAAATGG CATGTCCCGGG CTTCCTTGAT CCACGGAACA GAGCCGCCCA	240
30	GGATGCTCTT CATAGGTTCA AAAATCACCA TAATTATATC GAGAACGCAG ATGATTATGG	300
	OCCIGAACOG GTCATGACTA AATCAAGAGG ACGCAATAGA TCATOCAGAA AACGCAAAACA	360
	TATOGAAGAT AATCCAGATG ATAACTAGA TCCCTTTCCC GAATTGAAGA GAAAAACAA	420
35	AACAGAAAGC AACACAGOCA CCGGTGGTTA CCGTGCGCAT ACATCTAACC ACAGATTIGGC	480
	ACCITECTAGE AACGATAGCA AGAAGGCCAA GACGTGCTCC AATGCCGCCG GTATTTICCCA	540
	GOCTACTICA NARGATOGIG ATCGAAGTCA GAAAGGACAT GCAACTAAGA AGARTCITCC	600
40	ATATTC	606
	(2) INFORMATION FOR SEQ ID NO:107:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 553 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
50	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1038RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
	GATCAAAAAA AGAAATTACA ATTGACTGIT GCACCCACAC ATTCAACGGT TGCACCCACA	60

	CATTATGAGA TOCTTGATTT GGCGCGAACT GCGCTTTCCA ACTACAGTCC CGAGACTTTG	120
5	GGTGCCAACC GAAGCAGACT TCAACAGTGG TGATAACCAT AGTGTCGAAG TCTAGCGAAT	180
3	CTANGGATAA TACCAACAGA CAAAGCATAA TOGTATGTGC ACAGGATGGG GCGAAGTGTG	240
	GICTAGAGCT GICGGTGCGA GCAGAATACG GTGCGGCGAA TGAGGACGCC GCAGAGGCGG	300
10	AGOGTIGTIGGG CAGCTICACGA GGGCCCGAGC GCTTCCAAGC GGTCAGACAG AGTACTAACG	360
,,,	CATTOCAGAC AAGATOOCTIC ACGAAAACGT TTGOOGTICTIC CCACCOUNAN AAACTACOGT	420
	AAGGGTCCC CCACTGCGCG TGTGCGCTTC GNCTCTTGTT GGTCANAAAG TACGGGTTGG	480
15	ACATOTTOCO CAATOGITCA NAGAGAAGGO CACGACATTG GITCCCAAAT CCCCTAAGAG	540
,0	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	600
	TATTITICNA NACCOCNITT TITANITINA NACNOGEINO COAGNACITT GON	653
20	(2) INFORMATION FOR SEQ ID NO:108:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 609 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
23	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1038UP	
30		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
	GATCGGITCT COCCCTTCTT TAGCTGCCCG TTATTCAACG AGTCATCGAC TGAGAAAGAG	60
35	ATAAAAGCGG TCGATAGCGA AAATAAGAAA AATCTCCAAA AIGATATGTG GCGCCTTTAC	120
	CAGCIGOGIA AGTOCCIGAC CAACCCCATT CACCCGIACC ACAAATICIC TACTGGAAAC	180
	THIGAGACHT TAIGGAGATH TOOGAGATHG AAAGGOGHCA AGGHOOGHGA TGAGCHGCTG	240
40	AAGITCIACA AACOGICATA TICIGCAAAT CICATGAAAT TAGIGATCIT GOOCCOCGAA	300
	GATCHAGATA CCTIGGGICA GIGGGCATAT GAGCIGITCA AAGACGICCC TAACCAIGGG	360
	ACCAAAGTGG CTGAGTATCA OGGOCAGGGA TTCACGGCCG AGACCTGATG AAGGTAATTA	420
45	AAGIGAAGCC GVIAAAAICT TAAGAGIGIG GAATTCATNC GVGGGGCAGA TTTGGTTAGN	480
	ATGGAGGCAG CAGTOGTATG NGGATTTATO GCCAGAGCAA GGTOCTOCCG NICTGGAGAA	540
	AAAGTOGAAN CONONOCOT NOONVICCOO TINAAAGCAA AATINOCOONG AANNOOCITIN	600
50	ANNAACENT	609
	(2) INFORMATION FOR SEQ ID NO:109:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 643 base pairs (B) TYPE: nucleic acid	

	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1039RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:	
	GATCATTICT CITCAATCCC ATTGACGIGA ATGATGAACC GCATTATCTT TITAACAGCG	60
15	ACAACATOCC ACOGIATATA ATTOTOCTIA OCTOGIGATA TOCAGAACCA GGIGITTAGA	120
	CTGGCAATAT CCCTAAACTG GTGTAATATG GTCTTCAAAA GTTTTGTGCT GTCCGAATGA	180
	GGGCAATITA GTAAATTAAC CTCCAATITG TCTAAAGTAT CGCCACCOC ACATCTITTA	240
20	AACCOCACCA OCOCCCCCT TTTTATTOCC CATCOCCCCT GTCAATTACC AAGTTCTAAA	300
	GGGCTACTGA ATACGACGCC ATGCAGCTCT TCATCGATAT TCACAACCTC GTAATCATCC	360
	AATTEGITAG CTTGGATTTT BONEBOCATA TCTCTTATCC CTAAAAAGTG GGTTGGATGA	420
25	TGGATAAAAC TGATCTTCAT CATATAGAGA AATTTGGGCT CGCCCCAACG CAGACACAGN	480
	CAATGTAGTT TCTTGTGGCA NAGTINGCIN CGCAGGNATT ACTCGCANCC GGGCAGGINT	540
	CACCCCGGAG ACAAAAATTC CCCCTTTTCT MTGGAAATCG INGTAGNNCC TANCAAGGAT	600
30	GGGTCAAGGA CCTGGTTGCC ATTCCANTTT ACCATTTTIN CCC	643
00	(2) INFORMATION FOR SEQ ID NO:110:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 635 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1039UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:	
45	GATCCTTCCA ATAACCCCTA AACATCCATG TGCTGGTTTT AACTATGAGG GAGFTGGAGT	60
	AATTICGCGG TCTCGCAAAG TAAATTGACA GAAAACCCTC AGATCGGTAA CGAAACAGCT	120
	GAACGACOGA GATTAAAAGG AAGAOOCAAA TAAOCTATAG ATAAGATCGA TAAATATTGA	180
50	GGGGGGGATG GATATATTAG AAACTAGCTT TAGACTTGAA GATGTGCTTT CACGCTATTA	240
	TAGAGTIGAA AAGGTOGTOC GAGTCAAITTA TCAACAGTIC GTACCGAGGA CTCCAGATGA	300
	TCAATGGTGT ATCCAATCCG ACCTTCTTAA TCCGCAAGAA GGATCCGAAA GCCTGGTGG	360
55	COCUTTITUD GOOGGAACTO TOGIOCTITI AGCATCAATG ACCAGGACTI ACCCATTICCO	420

480

GROSTTOGAA GRGATAGROG AACCCCCCNC CTCGGAGAAG AAGROCCACT TTACGRCAGG

	CTITICCAAC GONAACCIGO AACGCONVIG GATCITITIA AAGCNIGGGG GGATGVICAA	540
5	TRANDATTON GACCOCONAGA ACCTITICOCA ATTICGAAAAN MANTITICOCC CANAGAAAGC	600
	NNAGOGANCC CCCCGGGNCN NATTTTTTGGA ATGNC	635
	(2) INFORMATION FOR SEQ ID NO:111:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 648 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1040RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:	
	GATCCAGTGT ACCAGGIAGC GTCAGGCACT TCTAGCGCAA GGGCCGCCGT AAACCTTGGC	60
25	CTCTCACASC ATTIGGGATG AGTATIGGGCC ATCTTTAGGG CACGTGAGTG ATCATGATGG	120
	GIACAAAAAG AAATGATTIC GOCCAGGATC GAACTGGGGA OGTICTGUGI GITAAGCAGA	180
	TGCCATAACC GACTAGACCA CGAAACCACT TICIGCAGOC TCTTATTIGGA CAGGTGATGT	240
30	TAGOGCAGAA GAACATGAAC GIGATAATAA TICAGAAACC TOTTATGOTA AAGTGAATTA	300
	CTATICCTTA ATAACCIGAA GGGAATAGGC ATTGCCAGTA TIGAAAATCG GGCTTTGGGT	360
	THATTOSCTA ATTATATTAT TANCAMIATA TATATATACC AACAAGSTGA AGAATOGMIG	420
35	TOUNIGETIT GOOGGOCATA COONAGAACO AAAGTAGAAG TIGACAAGIT GGIGGNAGNG	480
	GITCAATTCA GNACTICATG GCAACNITTA CNATNVITIN NINAGAACCC CCNATTANIC	540
	TTINNCTICG GOOGGICTON NONAACOGGA AACAAINITN CNGAACIGAG TINGGOGGAN	600
40	GITCNICGGT NITTICNNCC TTIGGGICCA AATTGGGCCG GAANCCCT	648
	(2) INFORMATION FOR SEQ ID NO:112:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 613 base pairs (B) TYPE: nucleic acid (C) STRANDFINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1040UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:	
	GATCAGCAAC CTTCTCCGCC GTCTGTGTCC TCGCTTTACC GAGGATACGA AAATAGCCGC	60

	GOCTICTIGTT CAAATGOOGA TOCTGACGAG CAAACCACGT CITCTGATGC AAGCAGTACT	120
	AGTTACATTA TTCTAGAGAT OGAGOCAATG COGACAGCTC TGCGTCAGTA TTTGAGGGCA	180
5	ATCTGCCAAG ATGCAGAGGT ATCCGCCAGT CTGTCCCTAA CGAAATTCCT ATTCAAGAGG	240
	ACCATACACA ACCOTOCTIT TACCOCAGAA ATOCTOCAAG ATATICAATC TOCCCACCTT	300
	ATGGATGTAT ACAACCTCGA AAATCAAGTT AAATTCCAAA AAATGGCGT TTGGATAGAA	360
10	CTGTGAAGCT ACAAGTCCTC GCTAAAGTCC CTAAAAGAAA AAATCTTGCA AGATATGACT	420
	ACATTATGAG GITTITCCNCC AATTTAAGGA GAGGAGGATC CCAGNGACNA TITTAGCTCTC	480
	AGAGATTUTT CONTOCOGAA AATTITTTING GTACCINATIC ACCTTOCOGG AATNAATGIN	540
15	NATINITIAC ANTOGOGONG AAATATOCTO ANAGNINAAG TTTGGGCACC CCCCCCCNCCT	600
	ATGANGTITT GTC	613
	(2) INFORMATION FOR SEQ ID NO:113:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 649 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1041RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:	
	GATCCTCCAC CAGACCGICG GOGICCCCATA CCTTCTGTTC ACGCAGTGGC GCGTTCTTGT	60
35	AGAAAACOCC CAACAGTTGT TTGTAGGTGA ACTOGTCOCG GAATTTCTGG GCGCGAATTC	120
	SCICCASCIC CICTICOGAA ASCITTICAC GEODOCACCA GCITCICATC COSTICAACC	180
	ASCISCITUTE GIOGAGIOCE COCTIGUICOS COCCUTACIOS COCAGEAATA TETECOCOCCA	240
40	GATGCCGTAC GCCCTCCGCC ACTICATGAC GCATGACGCC CTGCCGCTCT TCTGTGAAGA	300
	ACTOGRAGIC CAACCCASCT TOGAACAAAC AACTGCTTCA OGRATOCOCG OCATACTTTC	360
	ATOGACGICT CCAGATAGIC COCCOGGACGA GOGGCAACAA ACAACGCCAG COGCCGGGT	420
45	THOUSECATE TETCANGING SCHOOSCCTE COCCTTCACC AACCACCAAT AATGITGCAT	480
	TINGCCCING TCCCINIGGCG GNINCAATCA GAATGCCGGN TCAACCNAAN CAAAAGGCAC	540
	AATINIOCOGG AACCAAGOGG GITOCANOCC GAAAGTGTTT ATTINIOCONAC TINITOCOGTA	600
50	NAATTITINI TINICNCIGG GENIGIENNI NACCNCCACC CCNAAATAA	649
	(2) INFORMATION FOR SEQ ID NO:114:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 645 base pairs(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1041UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:	
	GATCTOCTTC CTGAAAAATG GCGTCTCTGT CTTACTGGTA CTCTCAAATA GCTACGTCTA	60
	OCTACAGOGC CATTICCOGA TOCCAGCCAC GOCTCCACTG CAGGAGGTAC AACAGGATAT	120
15	COCACOTICTIC GCCCTGCCCCA COTICACTTTGG ACCCTCCCCGT TCTCGTCCTG ACGTCTCAAT	180
	AAGGIACGOC GITTCTCTTC GCCGATGGAC TGCGCTAACT GTATGGCCTG GCTACAAGTC	240
	TGTTGGTTTC GAGCAGCCCA CTTCTTTATC CACCCTCAAG GTTTACCGCA ATCCAGCAAT	300
20	TTTGGGTCCT GGCACAGCCG GATATCATGT GACTTAATTA CGTCAACGTT CAAGAGTTGG	360
	COCCENTES COCCANATITA ACCESSOCAN COCTOSTCCC CCCCCATCGC COCCENTES COCCASCATA	420
	GOCNATTANO ANICCANIGO COGOCAAATO TINGITTACA NAAAOCAAGO ANANTCATAG	480
25	TEATFICOCC GAANANCOCA ACCITINICOC CNCCANCICNI CAAANICNCC CNITINITITT	540
	TOCOCOTA TARACCOCORDA CONTINUOS ACCOCOCARO CONCOCARA TITICOCONT	600
	TINIPAGGIGAG TONNTTNOGG GGGGANNONG CCANAGGAAG GVOGT	645
30	(2) INFORMATION FOR SEQ ID NO:115:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 682 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1042RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:	
45	GATCCGTGCT GCGGACAACC GCCAGAGCTC GCCTACAGCC CGTATATATA CGCCGGCTGC	60
	COSCCTOCCO CATGCGATTT GICCCACCTC GCTCTGCTTC GICCCGCCTG CCGTTGCTCC	120
	ATGGGACCTT TCATTTAGTG TCTCGGGAAC GTTTCGAATG TACCCTATCG TGGTACCACG	180
50	TIGOCTICOCG TIGOCGITTACT ACATOTICTIA GOGCGGACTIG AGICACATGT CTCCCCCCCC	240
	ACTOCITITO TOTAGATAGT CAGACGACAG ATAGTOGATA GITGGAGATT TOGOCAACAA	300
	TAGCOGTOCC CATTACOCCT GCCCATTGTT CCCATGTCAT TGGGAGGCTG GGNCCCACCC	360
55	ACCOCAACTC TINCCCCTTT AANCCTNANA GNCCCNOCGA ATGNAAAACN CTTTCTTTNG	420

	ADDINATED. ACORPORA (TRODUCT) DITTACRES VIII DESCOUR PACCATOR	480
	AGTINGGAAGG GEGCTINNAAA AATINGCTCCG GGCCANNCCT NCCCAAAGGT TTINAAAANCN	540
5	GCIVITAAATINA GCCINCAGAAG AACCINCOGGA GGAANCANAC ANAAANINGG CCCCINCCIGA	500
	AGCAAAGGGG CVGNVNTGGG GVCCAANCCC CNGNAACGNT NTTTCTTAAA GCANAACAAA	560
	NOGTINCAAAA AAAATGOOGG NC	582
10	(2) INFORMATION FOR SEQ ID NO:116:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 649 base pairs (B) TYPE: nucleic ació (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1042UP	
	(xi) SEQUENCE DESCRIPTION: SED ID NO:116:	
05	GATCOCCTCC TCCACCCACT TCTGACCCTC AACCTCCATA COCTGATCCT CCTCCTCATC	60
25	CTOCTOCTOC TOCTOCTOTO CTCTOCCCTG COCTATGACC TOCCCTGTTG CCGTTCCCCT	120
	GTTGCTGCCG ACAGCAGCAC CTGTATCCGC AATGCCCGAT ATGCTAGAAT GGAGCAAATT	180
30	AATOGACTOG TCTOCATTCT TOCAGAGOGG AGCCTCGCAC ATOCTGCATA TOCTTACGAG	240
	ATCGCCGGAG GATCTTTATG TCTGTTTCGC TATTCACCAC GTGGTCGTGG CAGTGCTGTT	300
	GITICATGAC CAGCCCGIAT CITCANAGGA GICGIAGTIC ACGCATIGIT GOGCAAAGCC	360
35	AGTOGAAGGA GOCCATOCTO CACGGTOGGG GAGTOCOOGG GGCACGTTTC CACAAGGCAA	420
	GGTACCTAGA AGATGAATCT TTTTTGANTC ANCNGTTGGG CCNCTNGGCA ATTTNAAGTC	480
	GUAANIGNIG AACTICGGAA AGTIGGAAAT TOGNOONAGG NOTTCTTCCC COCNOCNONT	540
40	TNGGNAAGCA AAAANAAANA ATTAATTOGN CCCCCCCCG CAAATTITGNG GTCNGAGAAA	600
	TITICCAAACC TIGGGITAAT AGUAAGGNCC CCGNIGNCTG GGCCGNCCC	649
	(2) INFORMATION FOR SEQ ID NO:117:	
4 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 648 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1043RP	
55		
	(vi) SECTEMES DESCRIPTION, SECTED NO. 117.	

	GEATCOUCEA TOUCHATAAA AEAATTOCTIC COTGATTIGAT TIGTTIGTTOGA AGGAGATOCA	60
	GATGGATTGT CCAGAAAAAC CGGTTTTAAG ACTCGTTCAT CAAACTTGTT AAACCATTGC	120
5	CCATCOCCTT GCAGTATATT GCCCAAGGTT TCGCGGATAT TTCTTCTGTC TAATGATAAT	180
	COCCCCACAG GCTGGTCAGC GCCTGATGCA GACCGCGAAG AGGGTCGGTC TATCATAGGA	240
	GCAAASCTIT CITICATCCOS OGASCCOGTC GOSCIGIOGG TTAAAAAATGG AGGTGCGTCT	300
10	ARTCANGACA THAGCHOGAC AGGICHAGOG GCTTCANTAT CANALTCATC ATCCGITTCC	360
	TECTIGITETT CHACOCACCE TIGTETTTATIG TITTAAGATET CAAGCATACE COCAGGAGTA	420
15	CCTCCAAATA TGATAACGGT GAGAACCACA ACTACCAGCA CAGTGGCCAG AAGAGGCGAA	480
15	CTTGGANCTC GCCCININICA CCCINTABOCA GNONCACTOC AANACNAACC CCINAANCCCG	540
	NOCHMANDE NAACANOCIN NAITTNEWN TOCATHICCC CHANNANINN AAAACCCCCC	600
20	CCCCGGCAIN TIMMOGGANC CCMMANNCCC MMAAANGGAN AAAANNAC	648
	(2) INFORMATION FOR SEQ ID NO:118:	
25 30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 419 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
<i>35</i>	(A) ORGANISM: 1043UP (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:118: GATCAGATIG TOTIGIGATE GAGAACCIGG COCATCAGTA GAGTGCAGAG AAGACCCATG	60
	COGAACAACT GIACCACCCA GOGACTOCCG TOTTCCCGGA ATGTTGCGAA AAACAACAGC	120
	ACGCCTGAG TCACITACAG TCGCAGTGGG TTGGGAGGGG GACAGATTAA AAGAAAAAGG	180
40	CTCGGGGTTT GTGAACAGNT CAGACCAAAA CCCAGGTCCT GGCTCGCGGA ATTCCTCGCT	240
	TACCITICACA TNICAACITAG TGTGTTCOCT GTCCNAAATA TACTCCAAAA TCTTGATCOG	300
	COCACCTCTG TGGTTCATGT CCTGCACAAG TTGACCACTG TATTCCAGTT TGACATCAGA	360
45	GGGCGAAATC ATCAGTGTGT GGCGTTCACA GAGCAAATAA ACTCCTTTAC TTCCTGCAC	419
	(2) INFORMATION FOR SEQ ID NO:119:	
5 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 606 base pairs (B) TYPE: nucleic acid (C) STRANDFINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) Original Source:	

(A) ORGANISM: PAG1044I1

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:	
	GATCTCCCGAC TOCCCCCCTC TGTACCCCGTC ATCCCCCTCT GTAGTCCCCCG TCATCCTCAT	60
10	CCTACCCAGO COCACCAACO AATOCTCCAT GCAAGCTCAA TOCTCOCAGO COOCCACTOC	120
	TGTATACGTG CTGGCTTAGG GTGGGCACGT CCCTTCACGG CCCGGCCGCC ATTGCAGTCC	180
	ACCAACCGCC GAATOCTCTT GTGACTGTAA CACCCATACA TTGCACCCCC TACATTTCAA	240
15	CGATGGGACG CGAGTGCCTC GGGAGCTGGA CGGAGACGCA ACGGGGGAGA CCAGGGGGCC	300
	COCCOCAAT CCCCACCCC ACCCACCCCC CCACCACCCC CCCCCTACCC CCACCCCACCCC	360
	ACCOCCACACO COCCCCCC CITTTCATG AAAAATATATA TOCCTACAAG ACCCATACCT	420
20	TOCATATACC AGAACTCACT COTAAGAGAT AATTAAGCAG ACGAAATGGT TGTTTGGAGG	480
	ACGITCGTAT CCCGAATCAC AATAATTIGA CAAAAGGITT TIGANICOOG GAGGICONIG	540
	TTGTTGTOGG NGCNAGACCG CCNTATTANA NGAAGNGANG GNAACNCAAG ANNGOGOCAN	600
25	occurre .	606
	(2) INFORMATION FOR SEQ ID NO:120:	
30 35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 632 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG104412	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:	
40	GATCTACAGA ATOCAGGAGA COCTOCTTGA CACAACACAA ACOGCTGAGA COOCAGOCOC	60
	COCCEACCOC CTICCAACEACE COCEACACACAC COCEACACACACC ACTICCACACACAC	120
45	COTOCTOCAGO COTTOTOCAGO COCACTACOS COCOCOCOGO TOCCCOCOTOG CCACCATACO	180
	CLIVICAVCECC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	240
	GIADGAGGIG GGGCAGCAGA COGTGCCGGT GCCGCTTTCCT GCCGCGGCATG GGCACGGCAG	300
50	CGATCCAACA GOCTCGTGAC GOTTGGAGCTG AGCGCGGGAGG ACCTTGAGGAG CGCGGCTGGCG	360
	ACCECCACA ACCCACCECT TOCOCCAACCC CGACCTTTTC TOCCTACNOC TGTTCAACTN	420
	AGANICOGGA CCCINTINCT INTOCTINING NACTININGING TOMINIACON NEAGCTGAGN	480
	TOCAGGICAN GIVAGINNIC CINNONICON ACCOCCINCCA ACCONNICAN COCINITITI	540
55	NUMBER OF THE PROPERTY OF THE	600

	ANITHICATT TICOCCCCTT CONACCNITN NT	632
	(2) INFORMATION FOR SEQ ID NO:121;	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 626 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1044RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:	
	GATCGOCTIGC CTAGTICCGAC CTCATICCACC CCTTICGAACT CCCCCCCAC CCATICTCACC	60
20	ATCHITATCT TOCTOGACOC TGTGACOGAG TAAACAAGCA COGTCATCCA CGTCTCAGOC	120
	TTCCCACATG GATGITCAAA CAGCCAGGCA TGGTCAATGC CTCGTTTGTC AACTATCTTG	180
	TOGTAATGTT GTAAGTTOCT CGAATGAAGT AGCAGTAAGC ACTTGGTCGT CCCCACGAAT	240
25	ATTGTCCGCA GCCGTTCCGA GTACAGCAGC TCTTCTACAC CATAATTCCG GCCAAGCAAT	300
	TOTOTATATO TOTOAACTAG ACOCAGOCCT CTOTOGTOCA TACTOGAGTA CACCAAGAAG	360
	TCCCTATTAT TTCCCACCAC CACAAGITGT CGAACCCCAT CAACCACACG GACACACTGA	420
30	OCACCITOGO ACOGAÁTOGO ATTIACIAGO TOAGOCCTAA GOATCITATO ATGAGOGOTO	480
	CCCTTAGCIT CCTCAGTCCT TCCCCCTCCC TCCTTGTGGT TCGTCCGGTCC TTTCTTAGAA	540
	CCATTOTICA AAACCATGAT GAIGGGGIIT GGICCGGCCN GGIGATITGA AGATTIAAAC	600
35	COCTINCCAAG GAATTGACON TOCCOG	626
	(2) INFORMATION FOR SEQ ID NO:122:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 545 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1044UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
55	GATCTCCTTG ACCGCGCGTG GCGCTCTCTT CTTGAAGGTG ACACCGTGCA ACTGCTACTG	60
	TTAGTATOGG TOCOGTOTOC GGCTCOGCTC CACGCAGCAG GGAGCCCTGC TCCGCACTCA	120
55	ACATACCCTC TTGTGCAAGT TAATGGTGTA CTCGCGAGTA ACAACGTCCT TCAAACCAGC	180
	CATTICGOCT OCTIAATIAT CICTIACGAG IGAGTICIGG TATAICCAAC CIATCCCICT	240

	TOTAL STATE TOTAL TOTAL STATE OF THE STATE O	200
5	CTASCOCCCC CCTCCCTCCCC CCCTCCCCTCC CCCCTCCCCAT TOCCCCCCCCC CCCCTCCAVIC	360
	CCCCONNOCE CTCCONNCCAE NTCCCCACGA NTCCNCNCCA TNCNCGAAAT GTACGCNTTG	420
	AANCNITCNI GINAAAGGCA NAAAAGAATC CCCNNINGGI GCNITNNAAN NNNGGCNNNN	480
10	NUMBOGGAN GNCCCACCIN ANIMACAANT TTAANAACNG NUNTNUANA TNUMINGATN	540
	NANAA	545
	(2) INFORMATION FOR SEQ ID NO:123:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 723 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genemic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1045RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:	
	GIGGATCCGT AATGIGGGTT TGTAGGCCAG AGGGCATTCG AGGGTGGCTG GGGGCCATTC	60
30	TOCCCUTTAA TTAGATGCCA CCCAATTGTT TTCACATCCC AGGCGAAGGT TCGCATACCG	120
	CCCACATACT TGGGTAATTG ATAATGCCGC CACATGACGG GATACTAAAC AAAGCAAAGT	180
	GICACATTCT TATTTTCIGT TGTGGICAAA AATOGGGGGG TAGGCGATCA ACTTGCATAT	240
35	ACAACACGAA AGGGGATCGG AGATTICTAG GTCACAGGAC AGTTIGGGGT TTTTATTGGG	300
	TGICTITGIG AAACCATAGG CACTIGACAT AGGAGCCCTC TTTAGAGTAC AATAAGCAAC	360
	TGCAGCAGC CCTACAGCTT GGGCTAAACT TCTCCATTAT GTGAAACGGG AAAGACGACA	420
40	ATGCCTCTGA ACGCTTTCAC GCCACTTTTG GTGGCCCAAT TGCATHCRVIT COCNAANTAN	480
	NIVITININ THOOGRAFT THOORNAA AAAACCINIA AAAAAGGGGG GGGGGGAINA	540
	AAACCANGA TNYITTITI NGGGNVGGGG GGGGCCCCCT TTINIIAAAN CCNNOCCCC	600
45	CHARAAM COMMINM COMBAAAA TIMMMIM NITITINGG MICHMMIT	660
	NCCCCCCCUA MIGNOCAMIC COMMINITY THIMINIMA MAAAMONCO CAMOCAMICO	720
	(2) DESCRIPTION FOR CITY AND 124	723
50	(2) INFORMATION FOR SEQ ID NO:124:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 502 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (coenomic)	

	(A) ORGANISM: PAG1045UP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:	
	GATCTAATAA CCACCCGTTG TATATTIGGG COGTTAACTA TATATGGGAA TCATATAAGT	60
10	CCTTAAAAAC ACCTCACCCG CAAGGGGGTC ATCTATAAAC AAGCCATAGT GTGTGTATCT	120
	TIGOCTACAT AGCATCATGA CIAIGITIGOG CACGOGICAT TIGCACTGTT TTAGCATGTA	180
	ACTOOCAGAG CCAGCAACGA ACAGAGCTAA TITTIGGAGGC TTACCATACT GITGTCGCTG	240
15	GATGITCAAG CACGGCTGTT GTGGATAAGT TTAGAACCCG TCGCCAGCAC ATTCATACCC	300
	TGAAACTACC AGTTCCAGGG GACATGITCT TCGTGGCTTT GACAGAATTA TTATTGTAGT	360
	CCAGTTAGAT GTACTACCAT TGTTGCGCTA ACATAATCAC CATTGTCATC TCTGGAATCA	420
20	CGTGTCGCCA AGCATATTAA TGTTTGTACT TAAACTCGGT ACTCCCTTTA TCGAAAGGCA	480
	TCACOGAATC GCCCTTCACT AT	502
	(2) INFORMATION FOR SEQ ID NO:125:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 515 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1046RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:	
	GATOGOGOCO GCAAGOCCOOT GOOCGAGCTIC GAGCAGGTTC TOGAGGTCGC GOGGCAGCGC	60
40	GTCACACGAG TAGGCGTAGG GATAGAGGAT CTCCTCCGAG TACGAGTGCA GGTCCAGGTA	120
	GOOGTAGATIG TOCAGOTTOGG COTTOGGTOTT GTTCACGTAG TOCTTCCAGO TOCOCCGCCTC	180
	CACOOCCTOG AACOOCTOCT GOCCOCTATA GTCGCCCGAG CACOOGTIAGG CGTGCTGGCC	240
45	OSTOCACTOS TAGTOGAACS AGTOSTCAAT GTOCACOCCA TOOCAGCOG GCATGTACGT	300
	GGGCTGCCGG TTCTTGCGCC ACAGGCGGTC GTGCGTCCAC GTGTACGCGT AGCCGTCTGG	360
	GTTGAACACA GGGATCACCA GGAAGTGGAG GGGGTGCAGG TAGGGGGTGT CCTTGGGGGG	420
50	CCCCCATAC CCCCAGAGCA GACGCTCCAC GACAAACCAC GCCGTGCTCA CCCCAATCCA	480
	CTCGCCAGCA TGCACGCCGT CCGTAATTAC CACCG	515
	(2) INFORMATION FOR SEQ ID NO:126:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 561 base pairs	

(vi) ORIGINAL SOURCE:

	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1046UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:	
	GATCCGGGAG CTCCATCATT AGAGGGTCTG GACTTCGGGA AGACACGCAG TGGTATGTCT	60
15	GUAACUTTOC AATUTCAAAT TAATUCTCCT TUCATCGTAG TUCGGGCUGC TOGGCCGATCT	120
	CCGACACAAA CCCCTGACTC CCTGACACAA ACAAAAACTC GACTACCCAA AACGACTAAG	180
	CGTCGCAGAT GCTATATATA TACAACTIGG TTCCTAATTA GGGTTAGATC CTTGCCAGAA	240
20	ACAGACGTIG ACCTIGIGCA CTICACAATT TTAGICCCGT CTCCGAAGTT TCCAGCCAAC	300
	ACGAATAACA ACACATATIG CCATGGCATC GGTAACGTTT AAAGACAATG CGGAAGTGAT	360
	AATGATAGGT GAGCAGGATC GGAGAAGAGA GCAAGGTATG GCCAGGCCCT GGATAACGGG	420
25	ATTICATIONAC GOOGATATICA TOTOGICAAAA GGACOGTICCO TAACTICATAG TAGACATCOC	480
	CAAAGAGAAC TICGACAGCT TATATIGACA TICGTCCTCT TOCTCTACAT TGTTGAGGCA	540
	AAGATATAAG AGAGTATOGT G	561
30	(2) INFORMATION FOR SEQ ID NO:127:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 685 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1047RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:	
	CATCCACTAG ATGTTCCCCCA CCCCTCGCAT CTTCACGTCC CCGTACGTCA GCATGAACTC	60
45	OCCAATOCTG GTATCCAGOG TGAACCOGTT GACGCCCTGC CCCGTCGTTA GCATGACGTG	120
	CCTCCACCCC CCCTACATCC CCTAACACCC TCCCACCATC TCCCCGCCCCC ACCCCCACCAC	180
	ATCCTTGAIT GTCCCCCTCG AGTCCCGAGT CACCTTGAAA ATCGAAACGA TOGTGCCCAC	240
50	CGACACACOG GOGTICCAGGT TOGACGACCC GTCAATCGGG TOGCAGCACA COGCATACGT	300
	CCCACCOGTC TCCGGGAACA CGATCAGGTC CTCCTGCTCC TCCGACACCA GCACCTTGAC	360
	CITCCCCCTG CCCTTCATCG CATTGATGAA GATCTCATCG CCCAGCACAT CCAACTTTTT	420
55	CTOCTOGTOC CCAGTOGOGT TAGACOCOGC GGAGAGCCCA ATCAGGTTCA CCAGCTCCGC	480

	COCTOTGATO GIOTCOGAGA IGAACTIGAA CCCAAACGAO ACTGAGITGA CCACCAGGIT	540
5	GAACTCGCCC GTCGCGTTTT TCGCCCGAGCT GCGCTGCGAC TCCAGGATGA AACGCGCCAG	600
	CGTAATGATA TOOGTGTCGA TAGOCTCTOC GGAGTCGCGT CTCTGTGGGT TCACGGTAGC	660
	CATTICTECT TEAGROCCET GIGGT	685
10	(2) INFORMATION FOR SEQ ID NO:128:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 678 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1047UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:	
25	GATCACTCCC CTCGCTTGAA ACAATGCCGT ATAGCGGAAT CTGGCCGAGC ACCAAGAAGA	60
23	TCAGCAGCGA GACGGCTGTC CAGATCAACT TCTGGTTGTA TGGCACTTTG CGCTCGGGCG	120
	CGATCACCTC GGGCAAAAAA GCCTCGAAGG GTTTGAATAG ATCCAACAGA CGCCCACTCA	180
30	TTTCAGGCTC ACAATGTTTG TAGGTAGCTT GCTGGGCTTG GATTGGCTAC ACAGTTGGAA	240
	CCACACAAAG TCACTATTGG GCGAGATGGT ACTCTAAATG ACTGCAAGGA GAACTGGTCG	300
	GITTOGITTO CIGAACAGOT TAATIGGACT GAGITGCAGT AGCIGIACIG AAAGGAACAC	360
35	GIATCITGAA AAAAITATAA ATCTCAGTAC CACGIGACCG GATACGACGI CCIATTCCAT	420
	CTCCCTAGAG CACCTATATG CCTAGTCCCC GTACCCTTCG TGAGTAAGAA TACCTCTCTT	480
	GGACAATAAT COGTGATGAC CITATTATGC TATAAAGCTA TITITACATAG CAATGGATCT	540
40	COGTIGUTUAG ACCUTUGOGO COCCAAAAGA CCAAGUACAT CAGCACCGAG AACAGCAGGO	600
	AATOGOCAGG COCTTGTGGA GCTOCAGAAG ACATGCTGGA TGCAAACCGG AAGAACGGG	660
	NTCCCAGTAC AGTTCCCC	678
45	(2) INFORMATION FOR SEQ ID NO:129:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 638 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genemic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1048RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:	
	GATCGTCATA GTCCGCCTCG TCGTATTGGT TCCTTCTGCG CCGGCCGCTGC ACCCGCATAC	60
5	CCATCGCGTC CACCTGCATC TIGICATCCG CGTCCATCTC GTCGTCCAGA AACACCTGGC	120
	TATCCTCCAG CATCCTCTCC COCOCATTCA OCTGCOCCTC CATCCCTCOC COCTCCCCCA	180
	ACGACAGCIC CICGIGCICC OCGICGICCA COCCCICATI TICATAGAAG TCCTTGTTGC	240
10	GATTOSCOST ATASTOCOCG TACATOTOGI COCCCACCAS GIOGACCICG TCTATOCOCT	300
	CTTCTGCGTC ATCCAGGTCG TCTTGCAAAC TCGATGCGCT CGTCGCCGTC GGTAATCGGG	360
	GITCTOGAAG TOGATCITOG TOCOGGGAC COCAGGGGG ATTAITCCCC CATAGGGGAA	420
15	GCGGGGCCCG CTCCCAACTT GTGGGAAGAT AGTGGGTGCT CCGAGGTTCT TTTGACCTGC	480
	TGTAATAMIC CNCTGTCTTT TICGGTTCAA CINTAGCCCC CNGGGCCNGG TINACCCCCC	540
	ATCCCGTATG GAAGCANCCA ATAACAAATG CCTCCGAAAA NITTGFTNTT TTCCNATTTT	600
20	GGAANAAGNA AGITCINANA ANGAATTIIN NANIINN	638
	(2) INFORMATION FOR SEQ ID NO:130:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 621 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1048UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:	
	GATCGCGCTC CTCAGCCATG GCTTCCTCTA ATAGTAACAC ACGCCCTGCT TCGTAGTCGT	60
	CGAGGTGCAC ACCTACCCGC GCAAATAATG CCTCATCTGA CAGCTGCACC TGGTAGAACT	120
40	GTGAGCACCG GAAGTGCAGC TTGCTGCAGA ACCTTGTGAG ATATTTGTAG GGGTTGTTCT	180
	GIGICAGAAA GITOCTCACC CGTCGATTCT CGTAGGGATC ACGGATACGA CCTIGGCTCT	240
	GCCCGCACAG CGGGTACCCG CATACCTTGT TTAGATTGCG CTCATCTATC AAGTCTGAAT	300
45	ATGROSCIT GOGGAAAGAA OCTROCCACG TATTITAGIG ICICOGGIGI GCATICITGI	360
	CTTOCGAAGA OCAGTICOGA GCAATICGAC CGICAGAAGG TCCCCCTCCT TTAGTGAAAG	420
	NNOCGATGIT OGTGATAGGA ACTTAAAACC CGITTTGGVT TNICNCAATA GNAOCCANNA	480
50	CCTTANGTAC GGININCOGT TCTTAACCCC GCCGGGICCC NGGGNGGTTT CAAGTICTIG	540
	GIBSGANAAG GINCCONINC CCGSSGGINC GCCTACTTAA GNGANGCCAN AAGGNAAAAG	600
5 <i>5</i>	NCCCCCNGAA AAGIGGNITT T	621
	(2) INFORMATION FOR SEQ ID NO:131:	

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 480 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG149RP	
	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:131:	
15	GATCTFTCAG CTTTGGCGTG CTATGGCAGG CAGCCTGCGC CTTTATGGCC TCAATGCCTC	60
	CCTGACCACT CTCATGTGCC TGTGGGCAAT CTGGTCACGT GGGTACTATC CAGCGACGGG	120
	ACTOCCTATG GOTGTTGCAG ACAAAGOGAA ACTCAGCATG CTCTACGTGC CCTACTTCCT	180
20	GATTOCTCTG CGCCTCGTCT TTGTGTGAGG TCTGGAGCAA TGCAGAAGTG CAACACTCTA	240
	TATATAATCA CCTGACTATG TACCTATTTC TOOCATAGCA CGTTACGTTT TGTCACGATT	300
	CCAGTCAGTT AGCTGCCTCG AGCAACCGGT GAGCTCCGAA AAGGGAATTC GCTACAAGGT	360
25	CITAGOGCAT AGNOCTIGGAA CTGGCTTTGG CTAGGTCAAT TGGTTTTCTT GGAACCANTC	420
	TIGGIATAGA CICTIGOGIA TIGATOSSOC IGAGGAGIGI TITINGNOGNA GWCAAACACC	48 0
	(2) INFORMATION FOR SEQ ID NO:132:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 477 base pairs (B) TYFE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1049UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:	
	GATOGICTOC TOGGGGACAG CGCCTTCTAG ACCCTOGAGG GGCGACACCT TGATGCTGCT	60
45	CTCGCTCTCA AACSTACCCA GACCCTTGTA GTAGGTGACG CCGTTTTTCT TGAAGAGCAT	120
	CTCAATACCG CCAGTCAATT GCTTCACAAC GGTGTCCTTG GCCTTTTGGA ACTGGGGCAT	180
	GITCACAGIG ACCIOSCOCT IGACGIOGAT ACOGCGCIGC TIGGCATCGA GITGCATCIG	240
50	GIGCAGCAGG TGCGAGTTGT TTAGCAGCGC CTTGGATGGG ATACACCCCA CGTTCAAACA	300
	OGTGTCACCT AGACOGOGOG OCTTCTCCAC ACACOGOGOG TCGAAAACCA GTTTGTTOCA	360
	OCCTICEATE COCCCACNN TITAACCACCE COCACCACCACCACCACCACCACCACCACCACCACCACCA	420
55	GETTTICITT TETTOGCAAT TCAACCAGGC CONCTITINT GGGACGACON CITIANING	477

	(2) INFORMATION FOR SEQ ID NO:133:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 443 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (v1) ORIGINAL SOURCE: (A) ORGANISM: PAG105CRP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:	
	NNNTTINIOS TOCOCCGIGI AGANTACTOS TOCOCCOCOCOCACATI CICCATOCTO	60
	ACCACCACGA CAGACTOGAA GTACAGGAAA AGOGACATTG TOGTOGCAGA GATGTGGGAC	120
2 0	GCGGCGTTCC ACTTCCCAAA AGCACACACC GTTGCGGACG CCAGCAGTCC AAGCCCCGCA	180
	ATTGTCCCCG TCCCCCACTT CACAGGTGTT TCGCCCACGG TCCCGCCCGTT CGTGAAGTCC	240
	GICTOGATOC ACCACACCIG GICGITICGAC TOGGITITCGT GIACCATCAC CITGAGGIAG	300
25	GOGICATTGI COOGCACCIG GIACGICACG COGGGAATCI TNITIGIGIT CICOGGGCIC	360
	ACATACTOCA COOCCTOGAT CTGAATOTCA CCOOCTOTCA CAGGACAAAA CTGCTTCTAG	420
	COGATOCCAT ACATOTOCTT COC	443
30	(2) INFORMATION FOR SEQ ID NO:134:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1050UP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:134:	
45	GATECTTTCG TATGAAGTAT GCAGCTGTCG ATATGCTTAG TTAACTTCTG CCCAGCTATT	60
45	TAASCTSCAA TTGAATCGGC GGTGACTCAG CTTGCAAAGG GTAGCAGAGA GGACGCGATG	120
	OSTITATICS GARAGGATAS ASSIGNACOS ATACCIGAST TICOSIGITA COTOCIAGAS	180
50	ACCINERACCO ATCTOGTOCC CINTONCAGOG GATTCTIATAC AACCTTGTGA TCGAGCOGAC	240
÷ =	ATATINGGAG COGATACTAG GOCAGNICCC TOGGATAGGT GAGOCTINTAG ACCOGGGCCT	300
	GACCOCCCC TITICAGCCCC CAGACCTACC CCCCCCCCTT CCCGACCTCA TGAACCCCTT	360
55	CCAGGAGGG TACGACTCCC GGGGACAAAA ACGCAGGCCC	400
	(2) INFORMATION FOR SEQ ID NO:135:	

5	(A) LENGTH: 713 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1051RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:	
15	GATCAAATTT GACATGTAAT TAATATATTG AGGTAAAATC TAGATAATAA ATACTGCCAG	60
	CAGTOCTGAC CAACTTCCAT TAGCAAGCAT ATAAGAGGTC TTAAATCAGC CGAAGGTATA	120
	TGCGAGGGAA GATAGATCCC CCGGGCTGCA GGAATTCGAT ATCAAGCTTA TCGATACCGT	180
20	CGACCTOGAG GCCCGCGGTACCCAATT CCCCCTATAG TGAGTCGTAT TACCCCCCCT	240
	CACTOSCOGT CGTTTIACAA CGTCGTCACT GOGAAAAACCC TGGCGTTACC CAACTIAATC	300
	CCCTTCCACC ACATCCCCCT TTCCCCACCT CCCCTAATAC CCAACACCCC CCCACCCA	360
25	GCCCTTCCCA ACAGTIGCOC ACCCTGAATG CCCAATGGAC CCGCCCTGTA CCGCCCCATT	420
	AACCOCCCC CETETECETCS TTACCCCAS CETEACCCCT ACACTTCCCA CCCCCTACC	480
	SCCCOCTCCT TICSCITICT TCCCTICCTI TCICCCCACG TICCCCCCCT ITTICCCGICA	540
3 0	ASCICTAAAT CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	600
	CAAAAACTTG ATTAGGGTGA TOGTCACGTA GTGGGCCATC GCCCTGATAG ACGGTTTTCG	660
	CCCTTIGACG TIGAGTOCAC GTICTITAAT AGTGGACTCT TGTTCCAAAC TGG	713
35	(2) INFORMATION FOR SEQ ID NO:136:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 703 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1051UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:	
50	GATCTATCTT CCCTCGCATA TACCTTCGOC TGATTTAAGA CCTCTTATAT GCTTGCTAAT	60
	GGAAGTTOGT CAGCACTOCT GOCAGIATTT ATTATCTAGA TITTACCTCA ATATATTAAT	120
	TACATGTCAA ATTTGATOCA CTAGTTCTAG AGCGGCCGCC ACCGCGGTGG AGCTCCAGCT	180
55	THIGHTOCCT TRACTICAGES TRANTICCCC COTTICCCTA ATCATOCTCA TACCIGNITIC	240

	Clothann Tightalett Cleanafie Geanacht acanteda attainabí	300
	GTAAAGCCTG GGGTGCCTAA TGAGTGAGCT AACTCACATT AATTGCGTTG CGCTCACTGC	360
5	CCGCTTTCCA GTCGGGAAAC CTGTCGTGCC AGCTGCATTA ATGAATCGGC CAACGCGCGG	420
	GGAGAGGGG TITIGGGTATT GGGCGCTCTT CCGCTTCTCG CTCACTGACT CGCTGCGCTC	480
	GGTCGTTCGG CTGCGGCGAG CGGTATCAGC TCACTCAAAG GCGGTAATAC CGGTATCCAC	540
10	ACARTCAGGG GATAACGCAG GAAAGAACAT GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA	600
	CCGTAAAAAG GCCGCGTTGC TOCGTTTTTC ATAGGCTCCG CCCCTGACGA GCATTACAAA	660
15	AATCGACGCT CAAGTCAGAA GTGGCGAAAC CCGACAGGAC TAT	703
13	(2) INFORMATION FOR SEQ ID NO:137:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 595 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
25	(vi) Original Source: (A) Organism: Pag105211	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:	
30	GATCTCCGCT TCAAACCAGC TAGGGACGAC CGGAGGTCGT TCCAGAGAAA GTCAACAATC	60
	AATATOCTOG GTAAAGCTAG CACCOCCGAA CTACTTGCTC TTGGCACCAC CGCAAAGGCA	120
	CACAACGAAA ACTGGGAAGA TGAACTGAAG AAACAACAAA CGGTCACCGT TGATGACCAG	180
35	GTIGITITOOC CAGAAGATTIC GOCCTITIOCA GAGCCAGTOC AGGAACCAAA GACCTICAGTIG	240
	TCCCCCTACA TCAACACCAA ACTATCCCTC AACCGTGATA AATCCACAAG ATCCAATCGT	300
	TCGCAATATG ATAGGITACA GGACTAGATA TGGATGTTAA GTATAGAAAA ACTGTATATT	360
40	ATTIGACCIG CTCCCCCTTA CCCAAACATA TAAAGATITA ATTACTCATG CCCCGATGCT	420
	ATTITITCAT GOOCCCCACT GGACTCCATT TGGGCAGTTG GAGGACGAAG TAGGAACCCA	480
	ATTOCTOCTT ACAAGOGCTC GGTTTCATGT ACCCTATACA CAAGTATCCA TTATTNGGGC	540
45	TTATIGATIT GIGICINIOG GCCGGACITI TANCITICIC ACTOCCGGAN GICCI	595
	(2) INFORMATION FOR SEQ ID NO:138:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 625 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM PAGI05212	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:	
5	GATCTGGGTT GCCCCTGAAG ACCACCAATG CGATGCACAC GAGTATCATG ATCAGCAAGA	60
	TTAAAGAAAA GACAGOGTTC AAAATAAAAA ATACCCATGC CATAATGGAG CTGACGCTTG	120
	CAGGCTGTCC AAAGAGCCCT GAGAAAAATA AGAAGAGGAA CGAATTAACA AGAGTAACAC	180
10	TOGATATCAT AATGITCAGG ATGTTAGTOG CGCGGTCGAG GTACGGCCTG CATTTAGCCA	240
	GAGCIGCCAG GININITATI TCANIGACAA ATAGACCGAC GOCCIGGGIT TIACCGGAAT	300
	TGTGGGCAAA TGCAATAAAT ACCOCTTTCA ACAAAATATG COCGAGGATC ATGCAGGACC	360
15	ACCAGINGIG TGICOCACTG TACATIGIGI AGAACAAGCC GIATITGIGI AGCACATTIT	420
	CATTIGCCOCA TAGAATOSCA GOTOOGITOG AGTOCACACO AATOGAAGOO CITICCACNGT	480
	AGATAGTOGG GCAGGCAGCC CANCOCATAA TTGACAAGAT AAANGTNGAG CTAAGNCTGC	540
20	CAGAAGGACC NCCCCCCCC ATCANCGITC ANIGATICCC CACCAGCAGA GATCGCIVATT	600
	GANIGACCCC GGCAGTININ CGCAA	625
	(2) INFORMATION FOR SEQ ID NO:139:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 486 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1052RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:	
	GATOGOGCAC GOGTGGGCGC AGAACCTGGC GTGGAGCATG GGGCTGATCC GAGTGGAATT	60
10	CATGCAACGC ATCTTCCGGT GGTACGTCCA GGCGAGCGGC GGCGAGCGGT CGCTGCATTT	120
	GACGICAACG ACCACGICTG TGCTIGCCCA ACGCICACIG GATGCGCTAG TGGGCCCCCC	180
	CGTGAGCAAG GCGACACAGT CGCTATTTGC CAGCACACAC ACGATGATCT TCAGAGGGAT	240
5	COGTAGACTG GOOTACOGTG CGAACATAGA GAGOTCATOG GITGTGTGTA COGGGOTAAC	300
	GITCITCCIT CIGITCOOCT ATTIGGATIG GOGIGGOGGT TIACATTIGT TCAAGCGGGG	360
	CTACTCGGAG CTCCTTATCC COCATGAAGG TCAATGAACC CAGGTCCGGG TCCCTAGACT	420
0	TOCAAGAAAA ACGTGOGTGA TIGNOCICAA AGGTGTTCTT TIGGGGTANA TCTTCCCCCG	480
	NGTTCA	486
	(2) INFORMATION FOR SEQ ID NO:140:	
5	(i) STYLENITE CUMPACTEDICTICS.	

5	(A) LENGTH: 468 base pairs(B) TYPE: nucleic acid(C) STRANDEINESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1052UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:	
	GATCCASCTC TTGCGCGGTA TGAACTTTCC CGCCGGCACC GGCGCCTCGC ACACCGAAAT	60
15	CGACCGCACC TCCGTCTGCG TCTCGTAGTT CCAAATTTCC GCGCGCCCCG AGTACAGCCT	120
	GATCAGCACC CACCOCICGC TCGCGIGAAA GICAATGCCC TTCACCCTGT CTGTCCTCCA	180
	GACAAACGIT TICTACTCAC GITAGIACTT OCTOGGGGC CTGGATAGCA TGGTGGAGCT	240
20	CTGCGGGTCC GCCCCCTCCG TGGGTGGCAA ACATGGTCTT CAAACACACC GTAATAGGCC	300
	GTGCGCCACC ATGCAGCCC CATTCGTCCT CGGACACACA CATACCTTCG TTTCCAAACT	360
	TCATTGGTCC CCACTTGGGA TTCCTAGTAG CTGTTCAACT CGGCTTTTTG GGTTCTTGTG	420
25	GAAAANIAAT ATTCCCNIGG ATTATTIAAA TAGGGGICCN TTTINITT	468
	(2) INFORMATION FOR SEQ ID NO:141:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 672 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genamic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1053RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:	
	GATCATAGIG ATTGATATOG OGAGAGOGIT TOGIATGIGA CAGOCIGIAT TCACGTATOT	60
	GETCCTTCAC TECATATATE TCTTGTGGGA GCTGTGAATA TATCTCCATG CETTCTCTGT	120
45	TOCATTITIC GIGCATTITIC TOCAATOCAC COCACTICIC GIACGITGAA GIACOCTICG	180
	GTACTAACGA TOCCTGAACA GOGAGGAGGC ATGTTGCGAG GGAGAATATT AAGGAATCAT	240
	ATCTCATTIT TACGTCTGAG ATAACTAGTA CTAACTGCAA TGCGGCGTCC AAATACCCGT	300
50	CGTAGTAATC GTATAGGAGC AAAGUTTCAT CICTTATACG ATGTGGAGTT GATTCAGTCC	360
	ACTICACCC TIGGIATITA COCACCATIC CATCATATIT GGACTGATAA TATICGAAGT	420
	TCTTCCACCC GECCTTATAC GGATCAATTA CTGATTTTAC AACATCGAGT AATATOGAAA	480
55	GATATAACTC TOGATTOCCC TGTATGACTT CCAGCACGCC ATGGAACATA TCCCCCAATGC	540

	COLCUMENT ARETHOGO TOTALATED CICTICACT GICCATOGS	600
	TEAGGTAGGT ATCTTCAGGT AGAATCAAGT CAATGAGCGA TAAACTCACT TGCTTGAATC	660
5	GICCCAAAGA GI	672
	(2) INFORMATION FOR SEQ ID NO:142:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 609 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1053UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:	
	GATCTCGGCT CGCTGCTCGC GCTCGAGCCC TACTGGGCAG ACCGCTACCC AATAAACAAC	60
	GCCCTAATCG GCGGTGCAGA TAAATTGCAC AAGCTCTACT CAACCGATTT TGCGCCCCATC	120
25	GTOGOCGOCA GGACTITICGG CTIGAACCIC GTOGACAAGC TTOGACCGCT GAAAGACCIC	180
	ATAATOGCAA AGGTCAGCGG CCCAAATTAA TAGTCACGTG TACATAAAGG TTTTCCTAAT	240
	AGCTATACAG CTTGCCCGCG TCCTCAGCTT GCAGCGCGCA ACCGGCGTGC ACCCATGAGC	300
30	GTOCTACTOG AAACTACCAT TOGOGACCTT GTAGTAGACC TOGACTACAA GACATOCAGC	360
	GCCGAGAGCT ACAACTTOCT CAAACTCTGC AAAACTCGCT TCTACGACTG TCAGTGCATC	420
	TACCGACCTC CATCCTGAAG GCTCAGCACG CCCTCGGGCGA TCCACAGGTG GCCTTTGCAT	480
35	TOCOCACOGA TITIOCCIGIA CACAATACCT CGATOGAAGG CC10CCCCGAC ACACCOCCGG	540
	TCACCCCGAA CCTCATTGAA GCCTCCGTTG CCGCTCAACC CGCAGAGCGC TTCGGACAGG	600
	TOCCCITIC	609
40	(2) INFORMATION FOR SEQ ID NO:143:	
45	(i) SPQUENCE CHARACTERISTICS: (A) LENGTH: 594 base pairs (B) TYPE: nucleic acid (C) STRANDEUNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1054RP	
50		
	(xi) SPQUENCE DESCRIPTION: SPQ ID NO:143:	
	CATCOGTOGC COGTCOGCCA ACCACAGCTC CTCGTGCTCC GCGTCGTCCA CGCCCTCATT	60
55	TTCATAGAAG TCCTTGTTGC GATTGGCGGT ATAGTCCGCG TACATGTCGT CGCCCACCAG	120

	CICCACCICG TCTATCCCCT CTTCTCCCTC AICCACCTCC TCTCCAAACT CCATCCCCTC	180
	GTCGCCGTCG TTATCGGGGT TCTCGAAGTC GATCTCGTCC GGCGACCCCA GCCGCGAATT	240
5	ATTECCCATA COCCACCOC GOCCOCTOCC AACTTOTOCC GACGATOCTG GCTOCTOCTA	30C
	SCICIGIGAC CIOCIGICAC TACICOSCIG CICIGIATOS TITICATOTO TAGOCCITOT	36C
	GCGCCCGTGT GAACCCTCCA TICCGTTATG CGAAGCCATA CCCAAATTAC CAAATTGCCC	420
10	TICCIGAGAT CHIGAATACT ATCICCCAGA IGTTIGACAG ACGCGCAGCT TCTCACGATA	480
	CGAAATATCG TGATTTTACG TGACTTTCAA TACCTCATTT CGATTCGATT	540
	AGATTITICAG TCATATIGAA AAATTATITIC CAAACAGGGC AATTGGATGA GCTG	594
15	(2) INFORMATION FOR SEQ ID NO:144:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 545 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOFOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genamic)	
25	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1054UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:	
30	GATCOTCOCC TTOCOCADOS CTOCCCAACO AACCCTTGAC ATGTCAAACC GCTTGAAAGA	60
	AGAGGIGATA TOOOCCACCC ACGAGGCCAA GIGGGAGCAA CIGCIGGCIA CIGGGACCCI	120
	TCCCCCAGAT GOOGCCAAAA GCGACTGGAA GCCTGGCGA GCATGGCTGG AACCATATGA	180
35	GGCCGCGTTT CGGAACCAGC TTGCAAATCG CAAGCGCACG AGCCAGAAGC TCAAGCGCTA	240
	TAGTOCCCAA ATCAGCAAGG TACACCTCCC GTATTACATT AAGTGCAGTG CTOCTATOCA	300
	TACCOGTOGC GCCAAACGCT TCGAGTGITT CCAGAAAGAG CTCCACACGG TTAATCCATT	360
40	OGITOCAGGO AGAGATOTOG GTTOCCTACT CTCCAAGTGG CGAATGGTGA ACGGAAAAAA	420
	CTACTATOCC TGAATGTATA TAGTTTATAG TCCTATTCCT TCATCAGGTC TCCCAGCAGA	480
	GGCGGCCGCT CGGTCTCAAC TATGCGCACC TCGCTCAGGC AITCGCTGAG GTCCTTCTGA	540
45	GTTCG	545
	(2) INFORMATION FOR SEQ ID NO:145:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 532 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1055RP

5	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:145:	
	GATOCOTOGO COGTOCOCCA ACGACAGCTO CTOGTOCTOC GOGTOGTOCA COCCCTCATT	60
	TTCATAGAAG TCCTTGTTGC GATTGGCGGT ATAGTCCGCG TACATGTCGT CGCCCACCAG	120
10	GIOGACCIOG TCTATGCOCT CTICTGCGIC ATCCAGGICG TCTGCAAACT CGATGCGCTC	180
	GICCCCGTCG TTATCGGGGT TCTCGAAGTC GATCTCGTCC GGCGACCCCA GCCGGCGAATT	240
	ATTICCCCATA COCGAGCCOC OCCCOCTCCC AACTITETOCC GACGATOGTG OCTOCTCGTA	300
15	SCICIGICAC CICCIGICAC TACICOSCIG CICIGIATOS TITICATCIC TASCOCITICI	360
	OCCCCGTGT GAACCCTCCA TTCCGTTATG CGAAGCCATA CCCAAATTAC CAAATTGCCC	420
	TICCICAGAT CITGAATACT ATCTCCCAGA TGTTTCACAG ACGCGCAGCT TCTCACGATA	480
20	CGAAATATCG TGATTTTACG TGACTTTCAA TACCTCATTT TGGATTGGAT	532
	(2) INFORMATION FOR SEQ ID NO:146:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 553 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1055UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:	
	GATCGTCGCG TTCCCCAGGG CTGCCCCAACG AAGCCTTGAC ATGTCAAACC GCTTGAAAGA	60
	AGASCIGATA TOCOCCACCC ACGAGGCCAA CTGCGAGCAA CTGCTCGCTA CTGCGACCCT	120
40	TOCCCAGAT GOGGCCAAAA GOGACTGGAA GCCTGGCCGA GCATGGCTGG AACCATATGA	180
	GGCCGCGTTT CCGAACCAGC TTICCAAATICG CAACCCCACG ACCCAGAAGC TCAACCCCTA	240
	TAGTICCCCAA ATCAGCAAGG TACACCTCCC GTATTACATT AAGTICCAGTG CTGCTATGCA	300
45	TACCCGTCGC GCCAAACGCT TOGAGTGTTT CCAGAAAGAG CTCCACACGG TTAATCCATT	360
	CGTTCCAGGC AGAGATCTCG GTTCCCTACT CTCCAAGTGG CGAATGGTGA ACGGTAAAAA	420
	CTACTATCOC TGAATGIATA TAGGITATAG TCCTATTCCT TCATCAGGIC TCCCAGCAGA	480
50	GGCGGCCGCT CGTTCTCAAC TATGCGCACC TCGCTCAGCC ATTCGCTGAG GTCCTTCTGT	540
	AGITECTICAL CCG	553
	(2) INFORMATION FOR SEQ ID NO:147:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENTH: 556 base pairs	

	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1056RP	
10		
	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:147:	
	GATCATCAGO GOGAGOTICO AATTIGIGGG CITITOTGITG ACATACATOO TOCACACCIO	60
15	GCATGCGGCG COCCAGGGCT COCCCTTTIGG CCTCGGCCTG ACCTTCACGG GATACGGGTIA	120
	CASCATGATT CCTASCGACG TGACGAGCAA GGTCGGCAAG GACGGCGACA TCGCGGGGGT	180
	GGAGCTGGAC GACCCCAACG AATTCGAAGA TICGCACCTG TACTCGCCGC TGGCGCAGCC	240
20	GOCCOCACGAC COCTICGAAT CACACCTCTC GCACGGGCTG ATGGAAAAAAC GGCGCAGAAT	300
	TCCCCCCCCC CCCATCCTCC TAGAGATTIT CCCCCCTCCA ATTATCTCCA AAACCCTCTA	360
	CGACTACATT GTGGTCAAGC GCATGGAGGG CCGCATCTTT ACTGGGAGGG ACAGCGAGAG	420
25	CCCCGCATAG ATGITCATAT AACTTATATA TCCCTCATTG ATCTTCGCTT GCGCCCCGTC	480
	TAGOGAGCAG ACCAGCAGIT TCTTCGITCG CCCTNAAGTC GATGCCGCCA GAGAGACCAG	540
	ACCCCCACC CCCCTIA	556
30	(2) INFORMATION FOR SEQ ID NO:148:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 550 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pag1056UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:	
	GATOCAACCC AGGACTITCTC GAAAGATAGA ACTOCGAACA CAGCCACCGG CAGGAACTITC	60
45	TCATCAGCTA GCAGCAATAC TAAGCAGACC TTCAGCGAAA ATGAAGAAGA ATCTGATGCT	120
	CAGITCCAAG ATGTATAGIT GTACCCGTAT ATTCCATTIT TTTTTTTTTT TTTTTTTTTT	180
	TTTTTTTIGA GATGICAAAA GCTCATCTCA ACTCCATGAC CAGCCAGTAG TGACTAAAGC	240
50	AGTGTGTCTA GTTCTTCTAA GTGATTTTAA GGACTATGAG CTTTAATGAG AAGGTGAAGT	300
	OGGIACTAGG CACTOCTGIT OCGACTCTAG TTACGATAAA GTCTGTCGAA OCCGIATATC	360
	OCCICTATION AGICTAAGNAG AACANTAGNA GGAGNATTTIN TOOGGAGNAG AAGGACGTAA	420
55	GACTIGGCCAA ACGGATTICGT GAGTCTAGGG CGTACGATGA GGAATTATAT CGGGAGCAGT	480

	TAGCTCOGAA CTACOCATTT TOOOCGAAGA COGTATOOCA CGACTACAGG AACAGTACTC	540
	ATATOGTOOG	550
5	(2) INFORMATION FOR SEQ ID NO:149:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 653 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1057RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:	
20	GATCACCCC AAATCACTCC TAACTACAAA CACAAACCCC CAACTATTAA OCTGACACAG	60
	CGTTACAGGT GCATEGATAA TACCGCAGGT ATATATCAAG GCGCACAGTG AACACATTCT	120
	GCAGACGATA GATATGTCTG AGACGAAGTA GGTTGAGATA TTTACGCACA AGCCTCATTT	180
25	GTAAGATAAA TGGTCATTAC TAACGTTTTT GGGTTTAGCA GCAGCAGGGG GAGCAACAAC	240
	CAGOGOCAGO AGCACOGTIGO TOGTIGGACAG GGTTCCAGGAG TOGAGGATTOG CGGGGAGGCA	300
	CGGCCCAGGG CGAACACGCG CAATGTGACT GTGGCAATCC AGTACTCGTG GCTCCACGAC	360
30	ATGAGCAATG TCGGGGGAGA GGGCGAGAAA CGGGGACAGGG CCCGGGGGAGA AACGGAGATA	420
	CGTTCGTGAT GASCTTCACG GACGTGCCGG ACTCGACGTC GAACGATCGG TTTCAGGAAG	480
	TGATCGGCAT TGCGGCGCAG TTTGCATTGA GCCGCGTGGC GCGGCGGATC AGCCTCCTGC	540
35	GGGGGCTCTC GAAGCAGTCC TITGAAAACT CCCTCTCAGG AAGCTCAGCG AGCTGGACAG	600
	CCACCIGIOC AGIATATOCI ACCACCACTI TCAAGACGAC ACGICGATCG GGI	653
	(2) INFORMATION FOR SEQ ID NO:150:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENCTH: 668 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1057UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:	
	GATCTAGGGG TTCTTCTTGC CGCGCTACGG GCGCCCCTCG CAGCCTCGCG CTGGCTCCCC	60
55	COCCAGAGOG CATCOOCAAG OCTOCTOGGA GCCGCACACT OCGTCTATGC CTGGACCGTC	120

	COCCONDICTO CALIFORNIA CALIFORNIA COCCONDICTO TOTOCOCCOC GOLDENIACI	100
	CTOSCOCTOG TGTTGAATTT TCCTAAAACT OGTGAAATTG TACGGGCTCG CTGCACCCCG	240
5	COCCTGTCGA TTGTACACGG GAATAGCCGA TCAATTGGAT GOOGACGCCA GTGTTACCCC	300
	CEAAACCGTIC COCACCGCT COCCCCCCAA COCCTGACCT CCCCCTGCCC CCCAAACCCCC	360
	ATTTOCTOTC CACTOCAGAG CTGCAGGAGAC TGTTGAAGGC GCAGGACAAG TTGCAGCTGT	420
10	CAAAACCAAA QAQGAGOTED DOQAAACCCO AQAGGAGAA QAQGOTOTITO QOOCOOTOCA	480
	ACCTOCCTGA AATACGGGAA ACCTTTGCGG GGCTGGAAGG GGAACGACAG CCCCTGCAGG	540
	ACCOCCTOGA COSCIATICAS ACCITACITATO TOCOCTACO TGAACCCTOC CACCOCCTIAR	600
15	ACCOCCCTCC CCCCCCCTT ACAACCACCC CTTCTCCCCCC CCCCCCTTCCA CAACAAATGC	660
	SCECTIGOG	668
	(2) INFORMATION FOR SEQ ID NO:151:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 614 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG105811	
30		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:151:	
	GATCTICACA TICOCATOCA OSTICIPICITE STIPTITIASTA SCACCOTOCO SOSCOTIGITE	60
35	990CTTCAAC TIGAGITCAT COGCACTIGG CTTGATAAGA CCAGCITICA AGTACACCAT	120
	GATGICGICG TCATCACCGT GCTTAAAGCA ACAGCGCTIG CCATAGCGGC AGIAGCCIGT	180
	CITACIOCAA TIGATACATG GOTTOGIGOG GAATTIGICO GACOGOTOCT IGAACTITAA	240
40	CTOGTOGAÇA CCATOGGCAA ATTOGCACTT GTTATOGTAC TIGCAGGCCC CCGTAGTCGC	300
	AAATGATTOG CATAACTCTG TCTTGTAAAG CATCTTGTTG ACCTTCTCCT GCGATGGCTG	360
	TGOCTGCTGC TGTGGGGTGG CGGGGGGGGG GACTGAACCC GGCAAAAGTT CGGCTCCGGC	420
45	TOTOCOCCTG CTCOCCCTGG GCGCTCGGGT CCTCCCGACG GATGCTGCAG GAGCGCAGGT	480
	THOGOGOGI CAGOGRAGIA TOCCATIGGT AGGCCGNIAA TGAGAGITHA TOCCCACCIC	540
	NAAGGTAGGT TOCCOGTTOC GNAGGGCCAA GOGNAATCAN TNGCCGCCCA AACCGTNAAC	600
50	באננסמבונה פופה	614
	(2) INFORMATION FOR SEQ ID NO:152:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 634 base pairs(B) TYPE: nucleic acid(C) STRANDEINESS: single	

(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG105812	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:	
	AAGCITGCAT GCCTGCAGGT CGACTCTAGA GGATCTTGCA AAGTATGGCT TOGTAGTGTG	60
	GIGATOGITA TCTOCAGTIT CAATTOCTTT GTTAGTTAGT GTATCACATT CTTCTOCCTT	120
15	TOCCCGATTA GAGTOCTOOG CCTCATOGAT GOCCATCTCC GGTGTATACA CGTATATTTA	180
	TICICITICSC CCAAGIGGCG GAGIACAATT TICCTCTAGC TGGACCTATT TCGGITGIAT	240
	TICAGIAGIG AAATAAAACI ATCAATTAAG TACAGCITIC GTATGACICI GCCACAGGAT	300
20	GAGAGCAGAC ACTICTOCAAA GTACCOGATT TCAAATAAAT GTTTAGGAAT AAAATCAAAG	360
	COGRACATT ACATAATTAT AAAATCCTCT CGTACCTATG TCTTTCCCCCT CTTTTTTTTA	420
	TUTTAAAGIG AACATUGAGI CITIGICUTTU TTAQUIGITT AGATGACAAG CITIACATOCC	480
25	TOCHENICAN ARACAGITING TOGRATOCOT OGGRICOTON OCRNGTAGNA AGGNANITACG	540
	INCAGCAÇAG TCATTACCNC NACCCACCGG CTTGCCANCC NAVITNCTIN GGNNGNACNG	600
	GENNEGRAL LENYCONYNN LLLENNCCAL NECC	634
<i>30</i>	(2) INFORMATION FOR SEQ ID NO:153:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1058RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:	
	GATCATTCTT GAGAATOCTC ATAGTTATGG TTTAACGGTT CTTCAAACGG AAGAGTATCT	60
45	TCAATTACAG AGTAGTTTOG AGAGAGAACA GGTAACGTCC TACAACATTG COGAGAAACC	120
	AACTACAATT GOCTACGITG CACTTCCAAG AACCGAGTAC GATGAACTTG TAGCTTCGCA	180
	ACCITICTACG AAAGAACAGA ATTITIGAGGT ATACOCCOCC GAAAATOOCA ACGICATACT	240
50	GGATAAATCT GAGTATCACG ATTTGAAGAT CAAAGCTATC CCAGTGATTT CACCATTGCC	300
	TCAAATGAGC AAAGAGCAGA TOGTTGAAAA GOCCAAGGAA CTTGGAATGC TAGCTTTGCT	360
	CCATTGACGA GTATGAGAAG TTAAAGAGOC CTATTTCCCG ATAACGCTTT GGATTGCAAC	420
55	AGOGAAGGAC COCGGAAAGG TIGGTCTCCT AAAGGAGGAG TACAACCCCT TATTG	475

	(2) HAPOREMITON FOR SEQ ID NO:154:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 476 base pairs (B) TYPE: nucleic acid (C) SIRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genemic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1058UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:	
	CATCIBBOBO COCCACABOO IRCOCABOTIC COCCIBCATO COCCOCTOCT OFFICACACTO	60
	GTCGAGCCCC AGCTCCTGCC GGAAGCTAGC CCTCCAGCTC ATGTACCACT CATGCCTTAC	120
20	CTICGITCCC COCAATTICT TCTCCTCTTC CACCTCCCCT TCCCGTACCT CCCCCTCGTC	180
	CICCTICICI COSCOCICAA GCICCTICIG AAACCACCAC TOCGCGICCT CCTTTAITGA	240
	CGAGATCAGO GCAAAACACA TOTGTATTOC CAGGAGGATG TOCTOCTOCA OCTGTOGCAT	300
25	GGACTGGCTT GGAAAGACGG TOCACCTCGC COGTCAAAAT GAAATGCTTG TCCGGAATAT	360
	TCTCCAGTTT CGCAACACAA GGGTTCCCCC GTGCTCGTCC GGACTTCCTN GTTCCTCAAT	420
	CCCNCCTCAA CCTGCTCGGN TTTCGGCGGG GAAGGINCCA NCGGGCTTAA TGTCAC	476
30	(2) INFORMATION FOR SEQ ID NO:155:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 644 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1059RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:	
45	GATCTGTTAC OCTOCAGCOC GAAACCTCCA ATOCTCTOGG CCAAGGTTGG CGOCTGOGAT	60
	TETTOSSETE ACTOCATOCT TEGGTTTTCA AGGAACGACT GGAGAATGAA TACOOCTEGA	120
	AACTCATTAT CACACAACCC ACTGTTCCAT ATGTCGTGGA GTACTCCGAT GGGACCCAGA	180
50	TAACAGTAAC AAATCCAGAT GACTTTCCTG ACCTGACACT TOOGCGAACC AAGATAAAGA	240
	ATTTCCAGGA GCCATATGTA GAAGCTATAA TGACTCTTCC ACAGGATTAT CTCCGAAGGG	300
	TTATCACTCT CTGCGACGAC AACCGTGGCA TACAGAAAGA GATAACGTAC ATTAACACCA	360
55	COORGEARGE GATGCEGARA TATGATATCC CATTORCACA TCTAGTAGAC GACTITITITG	420

480

GTAAGCTCAA GTCTGTCACG CATGGTTATG CTTCCCTAGA CTACGANGAT GCAGGCTATA

5	ACCOSTOTICA CATTOTICAAC ATOGACTITOC TITOTIAAATOG AAAACCTOTO GATOCACTITO	540
	CACAAGTGAT GCATCOCTCC CAAACCGAAC GARIGOCCAA AGAATGOGTT ANGAAGTTCA	600
	AGCAATATGT CAPATCCCAG TTATACGPAG TGGTTATCCA GOCC	644
40	(2) INFORMATION FOR SEQ ID NO:156:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 649 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1059UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:	
	CATCCTCCCC GACCTCTTC TCCCCACCCC CCACCTCCTC CTCAACATCT CCCCCTACCA	50
25	REALECCARE GCGCCGCCC ARCCCCCCT GRECCTGCRE CCGCRCCACA TCARCCTCAR	120
	GCCCCTCCAC CTGGAGTCTG TGCCCAAGTT GCCCGACTAT AACGGCGACA TCTAGTCCCC	180
	GCGCCCCCC CGCGCGCGCA CCACGGGTAT ATATACACAG CCGGTCTCCG CGCGCCATGC	240
30	CCCCCCCCC GACCCCACAC ACAGCCCCC ATCTTGSCGC CCCCCCCC ATCACCTCCT	300
	GCAACOCTO: TGGCCCGTAC CCTGCTAAGG AGGGTAATCT CCCACCTCAG TACTATAAAA	360
	AATTITTAAG TTAGCCACTT TCGAGTTACA ACTCCCCGCC TGTCGGGTAA CGGATCTCAA	420
35	CTICICAACC CCCTAACCCT CCTCTACTCC TTTTCCCCTA ACCCAATATC CCCCCATGTC	480
	TICCTCOGAT ATCAATCTCA COCTTGATIC GITTATIGAT AGGITGAAGC GGAAGCAGAT	540
	TACTOSCACG TACAATGTGT COCTOGAGAC GITACAAATT CTGATOCGTT ACGTATCTGC	600
40	CATCOGETGG TOGACGAAGG ACGARCTCAT TGAACAGATC CGTCTACTC	649
	(2) INFORMATION FOR SEQ ID NO:157:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 641 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
5 <i>0</i>	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1060RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:	
5	GATCIOCICA TACTGAGOGG CCAACTGGTC GTACTCCGTA TGCAAAACAT CTGTGGTTTC	60

	CTGGAAGTGC GCCACCTTGA GCGATATCTC ATTAAACTTG GTAACCAGCT CTCCCAACTG	120
	ATGATTGACT GCACTOGTIT COGTCASCAG GTOCTCCAGT TCGCCAGTTC TGGTGTCCAC	180
5	TICCOCCACS TATOCOCTOT ACAATGIATA CTOGTOGTTC GCAGACCOCA GARCAGAAGC	240
	TOGOCOCCAC TOTOGOCOCCA GCAGOTCAAT TACOTGAGGT TOAATOTOTG TITCAACOGT	300
	TGCCAACAGA GTGTCTACTT TTTGCCGTAA CGAACTATCC CCAAAAAACCG GAGCCACCTC	360
10	AFCGTGAGAR GARGCACCGG GATITIOCCGC TACATOCTGT ATGACTGART TCTTCCGGCT	420
	CCTAAGCATG GTGCAGTTGC TGCCTCAACG GCTTTCTTCC TGGTGCARGT CTGCAGTGGT	480
15	TOGTOCTTAT GOCCAAGCAG AATACCATGT TGAGCCGGCG AAATCTCATC ACGTGATCAT	540
,,,	CATCTIGCAA COOCTCOGAR GACRCIGATG CACIGITCCA TAGOCTTAGG GCGCAATTAT	600
	ACGCTAGCTA GITATATTCA TAATATGTAC ATGATGCCTT C	641
20	(2) INFORMATION FOR SEQ ID NO:158:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 649 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1060UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:	
	GATUTTOCCO TOCTTOTTOT COASCITOTAG CICCOGATGA GOGTACOCCI COCTCAGGIA	60
35	CICCAGCOC AGCICOCCOC TCICCATGGA COCCTCCAGG ATCGAAGGCG CCGGCACAGC	120
	CTCGCAGGGG AGGGGGGGT GCAGGAGGGG CATCTCCTGT CGCTCCTGGT GCATCTGCAG	180
	COCCOCAGOS CTOGOCTOCA GOCCOGACTO GAAGTACTIC ACATTOGTCA GOCCOGACTO	240
40	GIACAGATIC AGGATGCAGC CCTTGAGCTG CGCACGGTGC AACCGGTACG CAGTCGCGAC	300
	ATACTOGTIAC COGCTOGTOC COCCTOCCGT GAAGTGCGGC CGCTGCGATC CGATGGAAGA	360
	CAGTGACOCT GTTGGCTGGT GCCTGTATCG CCCCTCGCGC GCCGGCGCTG CGCCCTGCGC	420
45	CTTGTTCACC CACCCCACCC GAAACACACT CCCGTCGTAC GTCTCCCCGT TCAGCCCCCC	480
	TOCACGTOGC ACCOCCCARC COGCOCCCTG CGARCAAGGC GACACCTGCT CCTCGCAGGG	540
50	COCACCCOCC TICATGICCT CACATGICAG CGTCCGCTTG TGCGCTTGCC CCGTCNGCAC	600
SU	CTGTTAACTG CATCOGCGTC TGTTGGCTGC TGCTGCTTGC TGCTTGCTT	649
	(2) INFORMATION FOR SEQ ID NO:159:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 570 base pairs(B) TYPE: nucleic acid	

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	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1061RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:	
	CATCIGCTIT TGTAAGTATT CATCAGCTAA ATACCGTAAA GCTGGTTTGA ACGGAGGTCC	60
	TOCCTTGTGC TCATATATTA TAGAAGTATC AATGACGAGG GGATOCCGCA TTTTCAAGAC	120
15	GITCAAGTCG GCCTGCAATG AATGGCCGAT AAGCACATCT GITGCGCTTA TCATCCGCAA	180
	GAGATOCIGI TOGAOGICTT GCAAAGTOGT GGTCAOCCCG ACCAACTICT CCTCTGTAAT	240
	ACCOCTOTAC TICCTCAAGT ACTCCACAAT GOOCTCATCT GOCTTGACAA ACTTGTCATA	300
20	AACTAAGTTA CAATCAAAAT OGACGACGCT CACACGGGTC AACACGTATC CGTTTTTAGA	360
	AADOCACATC TCACAGTCGA TGGCAAACGT GTGAGAACCG TCGTGTTGGA AACTGACAGT	420
	GTOCACCCAC CCACTGCACT TCTCCTTATT CTGATACTTT AGCAACAAAG CCTTTTGGGT	480
25	ACTOCICCGA TAAGOCAGGI GIGTITAGAT GGATGOGGIA CTCATTATGC AATAAGICAA	540
	CAACOGGCAT AGCAAATCAA GCAAGTGATT	570
	(2) INFORMATION FOR SEQ ID NO:160:	
3 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 522 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1062RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:	
	GATCTCGGTG ACGTGGCCCT GGTATGCCTT CATCCAGTCG CCCTTCAACA AGAAGTTTCT	60
45	GTTAACGTCC AAGTTACAGC TOGTGAAGGA ATCAACCTCT GCGCCCACGG CCTTGATCAC	120
	CTCTGGTGTG TTCAAATACT CCTCACTGTA CTTCATGTCA TCGTAGCAGA GCTGGCCCTC	180
	ACACTOCTTG CCAACGTCGT ACACGTTCTT ACCACTTCTC TGGAACGGCG TCAACTGGTT	240
50	CCCATTACAC TACAGAGAGG CICCAACACA CGACCACACG TICTOCAGGG TGTAGCATGT	300
	OCCIONANA COCAACCACC CTOOCAACCT CTCGTTCATT CCCCAACCATT CCTCTGGGCC	360
	AAGAATGGCG GCTTCGCCGC CACCACCGCA GGCCATACGC TCGTVAGTAGG GGTACTGTGT	420
55	CAACESSTET GTCAACCCGT TCCCAATTAG CACAGAGCTC AACTTAAAACG AGCGCTCCTC	480

	SCCTOBOTOC GACAAGATCT COOCAOCAAT AGCAGGAATG TG	522
	(2) INFORMATION FOR SEQ ID NO:161:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDERNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1062UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:	
	GATCCTOGTT GTATCATAGA GAATGAACAT ATTGATAAAA AAATGCTACT GTGTACAGTA	60
20	AIGICIGAAC ACCAACAIGC ICTITICIIG IATIAAAIGA IGGGATAACG AACICIIIGCA	120
	AGAATOCTOG GOGGAAATAG TAGACATGIT TAGAGAGATT TITGTAATGG CTAGAGTOGG	180
	TITTGATGOC CGAAAAAGAA GTOCCAACAT TTAATTICGA AGGITTATCA GGTAGGTCAG	240
25	GGAATATACT ATCCTCGTAT AAACCCTTGA TIGTACTTOC AAGGAOCTCC AAGTCGTCTG	300
	AGITAGOOGA TOGTICATOT TTAGTGICAG CATOGAOGAG GAOOTCACAT GTGATTOCTG	360
	AGICANTICC ATCINICACC TOTOCATTCA CAATCAAGOC CATGOGTCCA ACCTCCTTGA	420
30	GAGCCCCCTT GATAAGCTCA GTACGCAGCT CGACCGAAGT ATCCAACGTA ACTGACTCCT	480
	TTATTTCGAA TTGCAGATAT TCGGGCCGCA CTGCATGTAT AGATCCCCCA TGAATAAAGG	540
	AGAATTOCIG CACAGTAGTA AACOCAAATC CCCCGTAATT AGTTOGTTOG CTTCTTAGGA	500
35	AGICAGIGAA COGATIATIT GOGICCIGAT CCT	633
	(2) INFORMATION FOR SEQ ID NO:162:	
40	(1) SPQJENCE CHARACTERISTICS: (A) LENGTH: 505 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1063RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:	
50	GATOGACTIG ACOGICACCC GGTACTOGIC GTACTIGTCG ATGAACTGGT CCTGTAGTIC	60
	CCCCAGTTCG TAGATGAGCA COCCCAGTTT GTCGGTCACG TCGGACACAT CGTCGTCGTT	120
	GTOCATOCCC CACATOGACA SCTGCCGCGC AGCGCGCGC CGCTCATTIGG CCACCACTTC	180
55	CAGOGCACGT ACCACOCCCT TITTCOGTICTT CAOGAACGAA GACAGCTTCC GTGCCAACTC	240

	GGGCCAAAG TTTCCCGCTG CATTCTTGCG GAACGAGGAA GCAATCCCGG CACGCCCAAA	300
5	GAACTTOGAA COTOTOGAAG AGOOTOGOOG AGOOGOTGAC TOGAGOTCTG ACGCAGTAGG	360
	COCCITCTOS TITCTCAAAS ASTATSTICT STOCATATIC TOSISCITAS ACTOSICTOS	420
	CAGTOGGTAT TYGTAGGTOC GATAAGATYC TCAGACGACA GCAAGTAAAG TACAACOGTG	480
10	GROSGIBOGC CICCAACGIC TITTI	505
	(2) INFORMATION FOR SEQ ID NO:163:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 631 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1063UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:	
	GATCTITAATA GCAATAGTOG ACTACAGGAA ACACAAGCTT TCATAATGTO GAAATCTITTA	60
	TCATOGGATA CACTAGACTA TACTCTACAA CCATGGATTC GTACTGCTGT TGATGCCATG	120
30	CCITATGAGA CCATGACACC TGTACAGCCA TCGACGATCC CGCTATTTGC CAGAAACAAA	180
	GATGIGGITG TAGAATCIGI GACCGGITCG GOGAAGACCG TGGCATTTGT CATACCTGTA	240
	TTOGAGAGAG TGATACAGGA TGATGCCAAT AGTTCAAAACC TCAAAAAAAGG CCACTTCCAC	300
35	ACCATAATAA TCTCCCCTAC GCGGGAGCTT GCATCACAGA TACAGGGCGT GATTGAAGCG	360
	TITUTGACAT ACTATOCAGA TOGAGAATAT OCTATAAAAT CACAGITGCT TATOOGTAGO	420
	AATACCAGTA GIGICAGAGA TGATGITIGCA GCGITTITTIGG AACATAGACC GCAAATTITA	480
40	GPTGGFACGC CTGGAAGGCT ATTAGACTTT CTTAAGATGC CAAACATCAA GACGTCTTCA	540
	TGTGGCGCAG CTATTCTTGA TGAGGCCGAC AAGTATTGGA TATGAATTTG AGAAGGATGT	600
	CCAGACAATA CTOGAGATOC TACCAAGCCA A	631
45	(2) INFORMATION FOR SEQ ID NO:164:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 626 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG016411	

561

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:	
	SCAGGAANTG GOTAGCCAAG AACCCGGCAA GACCTTCCCG ACCTACAACC GCCTCATCTC	60
5	GUAGGTGTTT GOCATCTGCG TCAGCATGGC CGGCTGTATC GGGTACGGCT GGGGAATTCA	120
	ATTICACTAT CACATCOCTA TOGTOCTATT CTTTTCTTTC CTAATGGCGT TGGGTATGAC	180
	STOGTOCTET AACTCCACCA TGACCTTCCT TACOGAGICC AACCCAAAAA GACCTOCCGG	240
10	TACCATTOCC GTAAGCAACA GCTTCCGCAA TATCGCTGCC GCCATCAGCT CCGCCATTAT	300
	TITICAAACTA TOCAACOCCA TOOOCOTTOG ATOOTOTINIT ACACOCTTOG GTCTAATCGA	360
	CITIOCTATCC ATGITGAGCG TCTATTACTT GATCCGTAAT GGGCGCGAGA TTACAAGGAT	420
15	AGCTGCTGAG CTATGATATC ATAACACATC CGCATTTTTA CGGATTTAGA TAACCAAAAC	480
	ASCATANITA GCATGITTAG AATCTATCAG AAGAACCICC CTIGITCCTT TAATCATTAA	540
	TITIGAACAGT CATTGATTCC GTCTTTCGAC CAAGAAGTTA GCACGTGATA TCCGCTGACG	600
20	CCGAAACOGC GTOCCTIGIC TITCAC	626
	(2) INFORMATION FOR SEQ ID NO:165:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 394 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(11) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG106412	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:	
	AAAAATCATT TITATCACCA CICAAGATGC AGICTGATTG AAGIGIAAAG CIGCAGIAGA	60
	AGAGACAAGT AAGCCATCAT GAAGGTATGT TATAGGTGCT AAGTTCCCGA TACNAGCACA	120
40	GIGGGCATGC TAGGGCTGCA GAGACAGGGC ATGGGCGTGT TAGGATAGCC GGAGACTCCG	180
	ATTOCCOGO: TACCOGGAGG TTACCOGGGC GTTGAAACGA TAATGOGTGC CACGACGCGC	240
	SCCACGGGG CACTGATGCT TGTATTGTTT GGCATGAATC TGATACTAAC ATTCCTGTAG	300
45	TIGAACATTI CITACCCAGT TAATGGIACG CNAAAGACCA TIGAGGICGA TGACGAACAC	360
	CGTGTCCGTG TCTTCTACGA CAAGAGAATT GGCC	394
	(2) INFORMATION FOR SEQ ID NO:166:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 559 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) NOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: PAG1064RP	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:	
	TAGIGGATOC AGCATCCOGI CTOGACCAGI CCTGAGITTCC GCCGGCTCTA TOCTAGACCG	60
	CCAAACCCA CCTTGAACAC GTACTGCGAG ATCGTGAAGG AACCAAACCT CACTATATGT	120
10	TUCCTGAGGA CAGCGCTAAT GITCGCCACC TACTATGGGT TCAGCGTCAC GTTCGCCCAC	
	TACTIGAAAC TIGACTATOS CITICAGTAAC CITIOGATOG GCOCGTOCTA TGCCTGTCCA	180
		240
15	OCCIOGCOC TAATCATOOG CTCCCTCTTG GGCGGTCACA TTTCCCGACCG CTTCCCCACG	300
	AAGTGGGTAG CCAAGAACCC CGGNAAGACC TTCCCGAGCT ACAACCGCCT CATCTCGCAG	360
	GIGITIGGCA TCTCCGTCAG CATGGCCGGC TGTATCGGGT ACGGCTGGGG AATTCAATIT	420
20	CACTATCACA TOOCTATOGC OCTATTCTTT TCTTTCCTAA TOOCGTTGGG TATGACCTGG	480
	TECTOTAACT CCACCATGAC CTTCCTTACG GAGTCCAACC CAAAAAGAGC TGCCGGTACC	540
	ATTOCGTAAG CAACAGCTT	559
25	(2) INFORMATION FOR SEQ ID NO:167:	
30 35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 611 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1064UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:	
	CATCHETTICT COCCCCCCTA TOCCCCCTCC CTGCCGGCAG ACGCAGATCG TCCTGGTCGG	60
40	CCTAGGCTAG GCACGGCCCT AGCCGGAGCT TGTCCTGCGG AGCCGGGGCC GGCTGAGCCC	120
	COCTOCOCAG GCOCOCAGOC COTGAGAGAG TAGUGGCCCG CCTAAATGOCT CCTACOCAGC	180
	GACCGCGCAG COCACCTOCA COTTAGTAAA AAATCATTITT TATCACCACT CAAGATGCAG	240
15	TCTGATTGAA GIGTAAAGCT GCAGTAGAAG AGACAAGTAA GCCATCATGA AGGTATTTTA	300
	TAGGIGCTAA GITCCCGATA CAAAGCACAG GTGGGCATTC TAGGGCTGCA GAGACAGGCC	360
	ATCCCCTTT TACCGATACC CCCCACTCCCC CCCATTCCCC CCCACTCCCC CCCACTCCCC	420
50	COCOGNETT GGAAACGAAT AATGOGNTGC CANGACOCGG GCCACGGNTGG GACTGATGCT	480
	TGTTTTGTT TGGGAAINAA TCTTNATACT AACAATCCCN GINGGNIGGA CAATTCTTAC	540
	CCCNGTTAAT NGGTACOCAA AAGACCATGN AGGTCGGNIG ANGACAACCN NNTCCCNNNT	600
55	THE THE YEAR A	611

	(2) INFORMATION FOR SEQ ID NO:168:	
5	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 615 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(11) MOLECULE TYPE: INA (genomic) (Vi) ORIGIJAL SOURCE: (A) ORGANISM: PAG1065RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:	
	CATCTCTAGT TTCCCACTCC CTCATCCCGT CCCCCACACC AGGCAGCCCG GCCCAGGGTC	60
	TOCGCAAGGC AGGCGTIGIG TCACCGCGGA GCCACTCTGT GGGCAGGCAG TTCCACGCCT	120
20	CCTGAACGAG CGCGGGCATG ATGGGGGCCCA GAATGCTGCG ATAGGCATGC AGAATGTGGA	180
	ACADOGTOGT CTTTATOOCC AGACOCCTCT TATTATGTOG GOGTTOCATG TAAAACCGTGT	240
	CCTTCGAAGC ATCAAAGTAG AGGGACAGGT CGTTGCTCAT GTGGTACAGA ACAAAGACTG	300
25	ATGACATTGG AGTAGGTCTG GGATTCCGCA CAGACCCTGA CACTTGGGGG GCAAAATTGT	360
	TIGICITETC GACCONITIT COCNICANIC COCNCCACE TECCCOCACA CITECCOCNCC	420
	OCAAAAAAGG CINTICCOCA CCNAGAINAA CCCCIOGGAA ANCCCCAAGG IGNCANNAAT	480
30	THACHUGAAG THINCUTHACU NUTUCACUNA ATOUGAAAAA TTGUGGANNA ANGOOCCANU	540
	CCAACACACA AANITTICIT GGAAAAAAA AGGOGAGCC CACCACGAGG GANINANITT	€00
	INTCCCCCC NATCC	615
35	(2) INFORMATION FOR SEQ ID NO:169:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 604 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1065UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:	
50	GATCTUTTCC CITCGATCAT OCCTCAGTTG GGFTCTGAGT CCATCGATGC GTTGACGCAG	60
	TTGCCCACAC AGTTGCAGAA CGCACAGGCT GCAGCTCCAG CAACCGAGGG CCATGAGGCA	120
	GOCGAGAGA AGGACAACGA CATCCCAGAG TTGATTGAGG GCCAGTCTTT CGACGCGGAT	180
<i>5</i> 5	GITGAATAAG TOCOCTIGTOC GAOGACTIGTG TICTCOCCOC CCATCTCAGA ATTIGTICTAT	240

	TICTOCAGOG AATATACATA TATIGAGIOC ACATATOGAT ATTATGTATA TATATGTACA	300
	TACACTATAC COGCCCCGTC TIAGTCGGAC CACATAAACC TACGGGTCGG CGCCCCTATA	360
5	TOGITITIACA ATAAACOOOC COINCTTOCG GONVINCTIC GANAATCICN TIGOGOOCC	420
	ONCONVOONT TANNAGGING TTCTINCCOGG TINGGAAGTNA AAAAGONNNN GTTONGTTON	480
	NAGNETOCCC 6666G-YAANC CINICCCCONG GNOGATTTTC NCCCAAACCG NAGAANACNN	540
10	ONITIOCNOCA ACTITICCCCCT GOGAGAAAAA AANOCNATIGN NGAAGNAAAA TITOCCCCCTIG	600
	CCCN	604
	(2) INFORMATION FOR SEQ ID NO:170:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 653 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1066RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:	
	GAITOCTGAGG CCTCACTAAG CCATTCAATC GGTACTAGCG ACGGGGGGTG TGTACAAAGG	60
30	GCAGGGACGT AATCAACGCA AGCTGATGAC TTGCGCTTAC TAGGAAITCC TOGTTGAAGA	120
	SCANTANTIG CANTOCTOTA TOCOCASCAC GACGGAGTIT CACAAGATTA COCAGACCTC	180
	TOGGCCAAGG TTATACTOGC TGGCTCCGTC AGTGTAGCGC GCGTGCGGCC CAGAACGTCT	240
35	AAGOCATCA CAGACCTGTT AFTOCCTCAA ACTITICATOG OCTIGAAACC GATAGTCCCT	300
	CTAAGAAGIG CGCAACCAGC AAATGCTAGC AGCACTATIT AGTAGGTTAA GGTCTCGTTC	360
	GITATOSCAA TTAASCAGAC AAATCACTOC ACCAACTAAG AACGSCCATG CACCACCACC	420
40	CACAAAATCA AGAAAGAGCT CTCAATCTGT CAATCCTTAT TGTGTCTGGA CCTGGTGAGT	480
	TICCCOSTGT TGAGTCAAAT TAAGCCGCAG GCTCCACTCC TGGTGGTGCC CTTCCGTCAA	540
	TICCTITIAG TITCACCTT GCGAACATAC TCCCCCCAGA ACCCAAAGAC TITGATITCT	600
45	CGTAAGGTGC CGAGTGGGTC ATAAGAAAAC ACCACCCGAT CCCTAATCGG CAT	653
	(2) INFORMATION FOR SEQ ID NO:171:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENTH: 669 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
5.5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1066UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:	
5	GATCTOGAGG ACCTATATAT ACCATTTCOC TOCACCTTTC TTTTTGTOCC TCATGTTTTA	€0
	TAAGTAGACG ATCTCTGATT ATTATCCCGA CGTCGTTAAA GTCCCATCCG AGCACACTGT	120
	TTOCAATGAT GOCCATCOCC CACCAGACCA GTCAGAAGTA GATATCTGAA TTOCATGTGA	180
10	OCCATACTAG GGTGACCTGT GTTGGCGGCC AGCTTGCAGG AGGAGAAAA AAAAAAGATT	240
	GCAGCACCIG AGITICOCCTI ATGGICACCC ACTACACTAC ICOGICACCC ICTIACCACC	300
	TTAACTACAG TTGATOGGAC GOGAAACOGT GCTTTCTGGT AGATATOGCC GCAACCGAAA	360
15	TATATAGCCT AGAGCAGACA TGATATCAGA TGGTGGATGC ACGTGACGCC GTAGACATGT	420
	AATAACGATA TOGAGTACAT TTOGTOOCAG ATOOCTOOOC CTATOOCOCA GATGTGTOGT	480
	AATTGCCACA TCCCCCTAAG TCACCCCCTA ACAAGAGTTT GTCCCCATTG GAGTGCCATT	540
20	COSTACOGAA TOTCACOTAG TGATCTGAAA ACTGATATOC TATGTGAAGT OCAAACTATG	600
	GGAAGTCTGG CTGGGGTTAR GAAGAAGATG TCRACTGCAA GGCAACGGAA CGTCCGARCA	660
	ATGCTTTGA	669
25	(2) INFORMATION FOR SEQ ID NO:172:	
<i>30</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 652 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1067RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:	
40	GATOCCCTAA CTITOGTTCT TGATTAATGA AAACGICCTT GGCAAATGCT TTGGCAGTAG	60
	TTAGTCTTCA ATAAATCCAA GAATTCACC TCTGACAATT GAATACTGAT GCCCCCGACC	120
	GTCCCTATTA ATCAUTACGA TOGTCCTAGA AACCAACAAA ATAGAACCAA ACGTCCTATT	180
45	CCATTATICC ATGCTAATAT ATTCGAGCTT GCGCCTGCTT TGAACACTCT AATTTTTTCA	240
	AAGTAAAAGT CCTGGTTCCC CTAGAGTACA AGTACCCTAG GTTAGCCAGA AGGAAAGGTT	300
	COGITIGATO COGTACACGA AGAAAATOOG ACGGGCCAAC CAAACCCAAA GTICAACTAC	360
50	GAGCTITTIA ACTGCAACAA CTITAATATA COCTATTOGA GCTGGAATTA CCGCGGCTGC	420
	TOSCACCAGA CTTGCCCTCC AATTGTTCCT CGTTAAGGTA TITACATTGT ACTCATTCCA	480
	ATTACAAGAC CCGTATGGGC CCTGTATGGT TATTTATTGT CACTACCTCC CTGAATTAGG	540
55	ATTOGGTAAT TTGCGCGCCT GCTGCCTTCC TTGGATGTGG TAGCCGTTTC TCAGGCTCCC	600

	TCTCCGGAAT CGAACCITAT TCCCCGTTAC CCGTTGAAAC CATGGTAGGC CA	652
	(2) INFORMATION FOR SEQ ID NO:173:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 669 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1067UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:	
	CATCOGGIAG TCAGGGCCTT GGTCAGACGC GGCAAGTGTG CTTGTGGTCT GTCCTCGGGG	60
20	OCTIOCTOCT GOOGACOGAC TOCTTOCOGIG CTCTGTCGTA GACGOCCTTG GTAGACCATC	120
	TCTGGTCGTC GCTTGCTACA ATTAACGATC AACTTAGAAC TGGTACGGAC AAGGGGAATC	180
	TGACTGTCTA ATTAAAACAT AGCATTGCGA TGGTCAGAAA GTGATGTTGA CGCAATGTGA	240
25	TTTCTGCCCA GTGCTCTGAA TGTCAAAGTG AAGAAATTCA ACCAAGCGCG GGTAAACGCC	300
	COGNETANCE ATTENCECTE TRANSFIRMON ARATECCTOR TOATCHAIT AGRICACCCC	360
	ATGAATGGAT TAACGAGATT CCCACTGTCC CTATCTACTA TCTAGCGAAA CCACAGCCAA	420
30	COCAACCOC TICCCACAAT CACCOCCCAA ACAACACCIC TICACCTICA CICIACITIC	480
	ACATTOTOAA GAGACATAGA AGOTOTAGAA TAAGTOOGAG CTTOGGCCCC AGTGAAATAC	540
	CACTACCITT ATAGTITCIT TACTITATICA ATTAAGCGGA GCTGGAATIC ATTITCCACC	600
35	TTCTAGCATT TAAAGTCCTA TACGGGCTGA TCCGGGTTGA ARACATTGTC AGGTGGGGGAG	660
	TITGGCTGG	669
	(2) INFORMATION FOR SEQ ID NO:174:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 596 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1068RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:	
	GATCCACCNC TNNCCCATTC AATCCGTACN ACTCCACCCC CCCNVIGTNN AANCCCCNCCC	60
55	GACCTAATCA ACGANAGCTG ATGACTAGAC GCTTACTAGG AATNCGTCCT TCAAGANCAA	120

	TGATTTOCTC TGINTCTATC COCAGTCATT ACNONCTANC AGACATGATC CTCCATGATC	180
	TGTCGGTGCT GTGTGGTATN CCGCAGGACN CCGNCNCTGT ACCGCGCGTG CGGCCCAGAA	240
5	NYICTANDOG CCTCCCAGAC NTGTTATINGC CTCTAACTTN CATCOCNICN ANACCGANAN	3 0 0
	TOCTNOTARG ANGTIGOGICNA CORGONNITIG CHINOCONGGINO TRATITIRACTIRG GITTRAGGITCT	360
	CGITCGITAT CNCCNITANI CAGACAAATC ACTCCANONN CTAANAACGG CNNTOCCCCN	420
10	NUNCONGAA NYINNYGAAA CANCTOTOAT CTGTCAATOC TTATOGTGTC TOGACOOGCT	480
	GACTITICCCG TGTTGAATCT AANTAANCCG CAGGCTCNAC TCCTNNTGGT GCCTTCCGTC	540
	NATICCITTA AGITICAACC CIGOGACATA NICCCOCAGA ACICANAGAC INIGAT	596
15	(2) INFORMATION FOR SEQ ID NO:175:	
2 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 641 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: LNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1068UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:	
30	GATCIGGAGG ACCTATATAT ACCATTTCGC TGCACCTTTC TTTTTGTGCC TGATGTTTTA	60
	TAAGTAGACG ATCTCTGATT ATTATCOCGA GGTCGTTAAA GTCCCATGCG ACCACACTGT	120
	TTOCAATGAT OCCCATOOCC CACCAGACCA GTCAGAAGTA GATATCTGAA TTOCATGTGA	180
35	GOCATACTAG GGTGACCTGT GTTGGOGGOC AGCTTGCAGG AGGAGGAAAA AAAAAAGATT	240
	SCASCACCIG ACTITICOCGI ATGGICACCC ACTACACIAC TOGGICAGOC TOTTIACCAGO	300
	TTAACTACAG TTCATCOGAC GOGAAACOGT GCTTTCTOGT AGATATOGCC GCAACOGAAA	360
40	TATATAGCCT AGAGCAGACA TGATATCAGA TGGTGGATGC ACGTGAGGGC GTAGACATGT	420
	AATAACCATA TOGAGTACAT TTOGTOCCAG ATGGCTGOGG CTATGGCGCA GATGTGGGT	480
.=	AGTTOSCACA TCCCCCTAAG TCACCCCCTA RCAACARGTT TGTCCCCATT CCACTCCCAT	540
15	TCCGTACCGA ATGTCACGTA GTGATCTGAA AAGTGATATG CTATGTGAAG TGCAAAGTAT	600
	GOGAAGTCTG OCTGOOGTTA AGAAGARGAT GTCACTGCAA G	641
50	(2) INFORMATION FOR SEQ ID NO:176:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 654 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5.5	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIG:	INAL	SOURCE	Ξ:
	(A)	ORG	:MRIN	PAG1069RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:	
10	GATICIACCCC GETICOCETIC GCATICACCGA GCTICCCCETTG CCGATICAGCA GCCCGGTICCC	60
	TAGGGACCCG CCCATGGCTA TCATGGACAC ATGAGGTGCC TGCAGGTCCT TCTTGAGCCG	120
	CATCCCCTCC TOCTTOCCAT CCTACTTCCA CTCTACCCAC TCCCCCTCCT CCTCTGTCCT	180
	CCTGTGGGTA TOCCCCAGAC COCCGCCCTC ACCAGCCGCG CCCAGCTTGG CGCCTTTCAA	240
15	CTCGTCCAGC GTGGACGCCT CTGATGCCTG TGCGAACTTC TCTTCCGCCA TAAGTGCGGA	300
	CCTGTTATCT ATCCTACTCA ACCTCCCCCC GTATACCCTT CCTATATATA CTTACCCTCC	360
	GACGCCCTAT TOCGGACACA GCTATATATT GGCCCGCCCT CTCGCGCCCT GCTTGGGCAG	420
20	COCACTGACC CCACCCTGAT AGTGCCGTTG CACTTCTGCT GGGCCGCCTC AGCCCGTTCA	480
	COCTOCGACT CTGACATOGC CCTCCGCGAG CCCCATTAAT CACCCGACTG CCCTGCATGC	540
	COCACTAAAC CTCCCCTCGC GOCGCAGGGC GCCCTTATCG CCTCCGTGAT GACGTACGTA	600
25	TGTTTATCAA AGATCCGGAG AMCTGTTCCA GGCTCCTACG TTGCGATAAG AGGC	654
	(2) INFORMATION FOR SEQ ID NO:177:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 708 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1069UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:	
	GATCHTICIG COCHTATCAG GGATGGCACC ACCGGTCTIC ACCTCGITTG ACTTGTACCC	60
	ACAGIGCICG CAGACCGIGG ACATGAIGAT GACCICTITG AAGIGIGGGA IGTIGACCGG	120
45	CTTCATATGC GTGTCACATG GGTGAACACA TGATGGGCAC GTGGCAGTGA AGGTCTGCAC	180
	CTOSITIGIOS AAGITICTOGA TATOOGEAGO GTOAGATAAG AGACOGGOOT GTOCOGOTTIG	240
	CGATTIGTIG CGCTCGCGCT GCGACAGCTC CGCGCGCTTC TCTTGACGCC GTTGCTCCAA	300
50	TIGGICGOSC CTAATGATGC CCACCTGGAC GITTITGCTCA TCTGAACGCA GGTACTCGGT	360
	TITIGGACCAT TITIGGCGCAG CITICGCCTGG CITIGTATICG ATCCAGGAAT TGCCAGCAGG	420
	GICGICCAGC GIAAAAGICA GCGGIAGAGI GCCCGGCICG CACGACAGCG CAGCGCGCAC	480

540

600

CTTGGCAATG AACTGCGCAA TCTGATCGTA CAGGTTCTCG TCCACTTCCT TCCGCGCCGC

CTGGTCGGCG TCCAAGTCCT CGATCATCTC GGTCAGCAGG CCCTCCACAG TCGTCAGCTG

55

	GCCGCGCTTG GGAAGAATCT CCAGGTCCAA TTCAACGAAG CGGGAAGCCG CAGTTTCGGC	660
5	CTIGATGACT GCCTGTCAAA ATCGGCCTTC TCCTCAACCT TCAGCTGA	708
	(2) INFORMATION FOR SEQ ID NO:178:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 703 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1070RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178;	
20	GATCCCGTAC ACGAAGAAAA TCGGACGGCC CAACCAAACC CAAAGTTCAA CTACGAGCTT	60
	TITIAACTOCA ACAACTITAA TATACGCTAT TOGAOCTOGA ATTACCOCOG CTOCTOOCAC	120
	CACACTIGOC CICCAATIGI TOCIOGITAA GGIATITACA TIGIACICAT TOCAATIACA	180
25	AGMCCCGTAT GGGCCCTGTA TCGTTATTTA TTGTCACTAC CTCCCTGAAT TAGGMTTGGG	240
	TAATTIGCGC GCCTGCTGCC TICCITIGGAT GIGGIAGCGG TITCICAGGC TCCCTCTCCG	300
	GAATOGAACC CITATICCCC GITACCOGIT GAAACCATGG TAGGCCACTA TCCTACCATC	360
30	GARAGITGAT ACCOCAGARA TITICARTGAR CCATCOCCAG CACAROCCCA TOCCATTOCA	420
	AAAGITATTA TGAATCATCA AAGAGTCOGA AGACATTGAT TITITTATCTA ATAAATACAT	480
	CICTICCAAA AGGICGAGAT TITAAGCATG TATTAGCICI AGAATTACCA CAGATATCCA	540
35	TGIAGIAAAG GAACTATCAA ATAAACGATA ACTGATTIAA TGAGCCATTC GCAGTTICAC	600
	TGIATAAATT GCTTATACTT AGACATGCAT GGCTTAATCT TIGAGACAAG CATATGACTA	660
	CTGGCAGGAT CAACCAGATA ACTATCITAA AGAACAACCC GAA	703
40	(2) INFORMATION FOR SEQ ID NO:179:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENSIH: 675 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1070UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:	
55	GATOCTITIAG TITCCTUDGAG TITGAGGCTA GAGGTGCCAG AAAAGTTACC ACAGGGATAA	60

	CIGGUIDE GCASICAASC GIRCATASCG ACATIGCTIT TIGATICITIC GAIGIGGGCT	120
	CTICCTATCA TACCGAAGCA GAATTCOGTA ACCGTTOGAT TGTTCACCCA CTAATACGGA	180
5	ACCTGACCTG GETTTAGACC GTCGTGAGAC AGETTAGTTT TACCCTACTG ATGAATGTTA	240
	TOOCAATAGT AATIGAACIT AGTACGAGAG GAACAGITCA TICGGATAAT TOGITTITIGC	300
	GOCTIGTICOGA COCCICATTIG CCCCCGAAGCT ACCATCOGCT GGATTATGGC TGAACGCCTC	360
10	TAAGICAGAA TOCATGCTAG AACGOGATGA TICTITITICT COCACATTAT AGATGGATAC	420
	GAATAAGGTG CTTTTAGCAT COCTGAACCA TAGCAGGCCG GCAACTGGTG TTCANACGGA	480
	AACCTCTCCC CCCCTCCCCC CCCATTCCAA TGTCATACTG CCCCACAGTA AATCATTTGT	540
15	ACACCACTTA RATGIACAAC ACCGTATTGT AACCAGTARA GTACCCTTGT TGTTACCATC	600
	TOCTGAGATT AAGOCTTOGT TOTCTGATTT GTTTTCTATT TOGAAGTCTG CAGGAGCAGG	660
	CTTTGAAATA RAGTT	67 5
20	(2) INFORMATION FOR SEQ ID NO:180:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 498 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1071RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:	
35	GATUTONOGO GGAAACNUAG CATTUACUGT TOTOCAAAAA GATTTGACTG GTAACATUAC	60
	CAAGCTTCGC AACAGACAAT TGTCGCACCC CGGTGAGTCT GCAACCCTGC AGGAGCTTGT	120
	GATTOCAÇÃO COTOCAÇÃOS OCASCAAÇÃO TOCTTOGGAA GOGOTOCTOT GOCTOACÇÃO	180
40	AGGCCTGCAA TTCACCGCGC AAGCTCTTAG AGAAACGCTA GACCATCCAG AGCTCGAATT	240
	GICTAAGACA TICACAGATG CGTATIGGAA GACGITGACG AAGCACCATG GTATGCTIGT	300
	ACGICCOGIT TICAAAGCIG GCCATGAAAG CITGCCCCTA CAGGAAGGAC TITITTTOCAG	360
45	AAACTAGGCA GCGACCAAGA GAAGGITGAC ACGCAACTIT AAGCAGTGGC TGGCTGCACT	420
	TGAAAAGATC GIAGAGATTC TGCTTCAAAT CCCTTGGGGG AAACGTGCAA AGGATTIATG	480
	AGTATTATTA TAGAAGCC	498
50	(2) INFORMATION FOR SEQ ID NO:181:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 625 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: INA (genomic)	
5	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1071UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:	
10	GATCGACAGC CTCGAAGAAG TAGCCTCCAC AGCTTCAAAC ACAGCGCACA GGTCTGCATA	60
	CATCACOCTE GIOCITIOCTE CACOCTIVAC COGAGAACTT TOTOCOCCTE GCACOCCCCT	120
	GOCAGACTOT GOCAGCACCC CCCCCGGCCC GGGCTTATCT GCAAGCTCGG GGAGGATGTT	180
15	CITCACCICG COGICCIGIT CATCOCCICC CCGICCCCCT ACGCACICGG CACACTCTAC	240
	CHICCATTIC TICACCCTCG CIGHICACGI CCCTCCATCT TCACCCCTCT TCACCCCACC	300
	GAAGAATOGG ACCAATGTGG CCTGCTTCTT TGGAGTAGAC ATTGGCCTGA AGTAAAAACCC	360
20	TACTGACCIG CCAAATAGCT CCACTITGGI CTCCCGACAG GAGCTTCCAIA AGANTGACAT	420
	TIDINIGINEN NAAGGOONIN NINTINGAAA GAGGAANCIN NIATCAAGGN CCINIVITINGC	480
	CCACNONIA NAACIAANAA MWWATIMW OCAATIMWW AAATIANOOT TMWWATIM	540
25	NCTINGNAAA TINNINGON TINNINATIC COMMOGNII TOMMIINOC NCNCNCCINN	600
	GGVITTIIN NAMMUINAAN NINCC	625
	(2) INFORMATION FOR SEQ ID NO:182:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 491 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: pag1072rp	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:	
	GAGCAACTAT TATTAGGCCC CCCCCACCCC ACTICTGCAGC ATTCGAAAGC CTTCCTAGCC	60
	TTTGTGCGAT GTCCCAAGGT ACAATTTTCT CGCAGNTGAA AATACGAAAG AAGCGCCAAG	120
45	AAGIGGCCTT CTTTGAATCC AACGCCGACG CCAATGATGT CGAGGCCGGC GAACATTTTA	180
	TAACAGAGET CGATAAGGGC GATAAGCGCC TCGGCCTGTT TTCTTCGATC GGCTTGATAT	240
	OCANTACANT OCTOOOGACA OCTATOTTIC TOOGTOCCOC GAAGATOTTC CAGTOCGACT	300
50	GOCTCAGTAT ACTITICOCCT AGGGTTATICG GTACTAGGAG CTTTAATTGC TCTAGCAGGT	360
	CITTATGITT ACATGGAATT TOGTAACTOC AATACCGCCG AACGGTGGCG AGAAGAACTA	420
	CCTTGAGTGC ATCTCCAATG AAACCGAACT TCTTCACTTA CAGTCAAGTG TACTCAGCAT	480
55	ATGATCATCT T	491

(2) INFORMATION FOR SEQ ID NO:183:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 726 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1072UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:	
	CATCOGCAGO TICOGCAAGO GOOGCTICIO CICOGIGIAC TOOTOGIGGI OGIOGIACIO	60
	COSCACCATC GACOCCICCE CCTCCTCCTC ATCCCCCCTC GCGTCCTTCT CCTCGTCCAC	120
20	COTOTOGGO AGAAGAGAGI COSCOTTOGO COCCOTOTOG TOGTOGTOGO GOTOGAGGAG	180
	ACCECCCCGA ACCECCTECT CETCCCCCGAC COCCCCGAEC TACCECTACT TCACCECCACC	240
25	CATCTCCCCC TCAATCCCCC GCATCAACAC CTCCCGCACG TACCGGTCCA TCATCTCCCC	300
20	ATAGIGGTAA GATTACCTAA TI'CATACGIG TAGATCATCC CATGCTTACC ATGITGAACC	360
	GICACCATGI AAATITICCAA TAATICTCTA GICTCICATI TGIAGANATI AGNANCITTIC	420
30	CITTATATTA ATNOTITITAC INAATAATIN ATNIANNITT INNITTGANC ANITOTOCAT	480
	ATTGIATTAA ANINATATAT AATATTATIN TCTACTAATC TAACAAATTA NINICINIAT	540
	TATATATTA NANANCATAT NATNATATTA AATTATTAT AATNATNOON TOOTOTTNIA	600
35	ATMITTAAAT MUMAMMINIT TMINCHIANN CIAATNNATT TITUGATATT TIMITINMIA	660
	MINIMINAAA AAATATININN TITATONANI ATCITOCATT TATNAATONN NITTTTATOA	720
	AACCCC	726
40	(2) INFORMATION FOR SEQ ID NO:184:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 641 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1073RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:	
55	GATCAATTAA TAAATOGTIT AACTAATAAA GITAATAATA AATCTATTAA TIATATAAAA	60
	CTACCIGATT TTATIGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120

ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA

	TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAALTG	240
5	GTARAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300
	ATCATTAATA TAATAACTCT TIVATTAGAG TOGUACCACA AGAATGCTGA AAGCATTAGG	360
	CONCRETAGACA TAMONACATA TOTOLOGICO ANITAAAATTA TOTOLOGICO ANATAATTA TOTOLOGICO ANATAATTA TOTOLOGICO	420
10	TATAATAAT AAADAAAAA ATTIOTAAAA TITAAATTAA TITAATAATAA	480
	GITATATITA AATAGATCAA AATITICAACA ATTITCCATITI CATITAGIAC TACCATCACC	540
	ATGACCAATT GITACATCAT TEAGTITATT AGGTTTACTA TEAACTITAG CTTTTACTAT	600
15	ACATOGIATI ATTOGIAATA TITATCCTTT ATTATTATCT T	641
	(2) INFORMATION FOR SEQ ID NO:185:	
20	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 662 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1073UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:	
30	GATCTEAATT TAAAATTITTA ATTAACTATT TATAATTIAG AAATATATAA TCTAGAGATA	60
	TATAATCITA AAATCATAGG TAAAAATACA TAAGATAGIA AGAATAAAAT TAGTAAAATA	120
	AATAGAAAAC CATAAGTTAA TIGATICATA AAGAAAAATG GAATTATTTG TOOCATCTTA	180
35	AUTTTATTA TITAATIGAT TATTATCTAT TTAACATAAA ACATTITAAA ATGITATAAA	240
	ATAAATAAGA AATTACTTAT AGAATATTTA TIAAATAGTA TTTAATTTAA TTTTAATATT	300
	AARITATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TTAATATTAA GTGATATATA	360
40	ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TTTCATAATA TITATTTTIA TTAGICTAGI AATATTTCTA TTTAATAGIC TACCCTTTAA	480
	TTOGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC	540
45	TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCN TTTTTTTATTA TTATTTAAAT	600
	TATTATTAAT TAGTAAATTA TATTTATTTA TITTATTAAC ATAATTITTT GNATAATAAT	660
50	AT	662
50	(2) INFORMATION FOR SEQ ID NO:186:	
<i>55</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 615 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	

(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1074RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:	
-	GATCTAAATA TATATAATTT AATTTATAAA GATTAATATA AACTTTTTTA TTATAATATT	60
	TAAGTATTAA ATTATTTAAA CIATTATTAT CATTATTTAA TAAATTAATT ATTIGATTAT	120
15	TAATACTTAT TATATAATTA TIATATAATT TACTTAATTC ATCATTATTA ATATTTATAT	180
10	AATTATAAAA ATAATATITA ATATGAATAC TATTTAGICT ATGTTCAAAT TITAAATTAG	240
	TTATTAAAAT AITATTAGAT AITATTATTT TCTTTAATAA AITATTAAAT AGATTATCAA	300
20	TAATTAATAT ATTATTTATT AATTTITTATT TAAAATAATA TATTTIATTA TTATAAACAT	360
20	TEACHTAIT TEACHTAITE AATTAITET TATEATAAT TOTTAAAT TEATAAATT	420
	TATGETGATT TATATTATTT AACTITTTAT AAGAATTATT ATTAAAATTA ATTITAACTT	480
25	TAATTICTTA TIATTAATIT TTATATTATT TAATAAATTA TATTCATTIT ATTIATTIAT	540
25	AAAATAATTA ATTAATTTAT TACKRITITA TAATTAATTT ATTAATTAAA TYAATTCATT	600
	TATTATAAAG AATGT	615
30	(2) INFORMATION FOR SEQ ID NO:187:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 663 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1074UP	
40		
	(xc.) SEQUENCE DESCRIPTION: SEQ ID NO:187:	
	GATCTIGATA CTAGAGCTTA TYTTACTICA GCTACTATAA TTATTCTTAT TCCTACTAGT	60
45	ATTAAAGTAT TTAGTTGATT ACTAACTATT TATOGTOGTT CATTAAGATT ACTAACACCA	120
	ATATTATATC TATTATCATT TTTATTTTTA TTTACTGTAG GIGGITTAAC TOGIGIAGIA	180
	TTAGCTAATC TATCATTAGA TGTAGCATTC CATGATACTT ATTATGTAGT ACTACATTIC	240
50	CATTATGTAT TAAGTITAGE TOCTGTATTC TCTATGTTTG CTGGTTATTA TTATTGAAGT	300
	CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATTCAATT CTGATTAATT	360
	TICITAGGIC TIAATATTAT TITCTTCCCT AIGCATTICT TAGGIATIAA TOGTATACCA	420
55	AGAAGAATTC CTGATTATCC TGATCTATTC CTACGITGAA ATTTAGTATC TTCATTTOGT	480

5	TCTATAATAA CTATTATATC ATTAATGITA TTCCTTTATA TTATTTATGA TCAATTAATA	540
	AATOGITTAA CIAATAAAGI TAATAATAAA TOTATTAATI ATATAAAACI ACCIGATIIT	600
	ATTGAATCAA ATAATATTIT CITAATGAAT ACTACTAAAT CATCATCTAT TGAGITTATA	660
	TTA	663
10	(2) INFORMATION FOR SEQ ID NO:188:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 639 base pairs (B) TYPE: nucleic acid (C) SIRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1075RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:	
	GATCTATCTA ATTACAGTAA AGCTGCAAAG GGTCTTTTCG TCTTTCTACA AATACTTAGC	60
25	ATCTICACTA AGATTICAAT TICACTIAGA TIAAAGGAGA GACAGITGIT GTATCATPAC	120
	GICATTCATG CAGGACCATA ATTAGTGCAC AATGAATTTC GCTACATTAT AACCCTCATA	180
30	ATAAGCCTCC TATTTAATAA AATTTATTAT TATTATCTTT ATTAAAATAT TAATTTTTAT	240
30	ATTITATCAT GGAGCAGAGT TCACACTTTA TACTITTAACT TACGITTCTG CAAAGTGTTG	300
	TGTTTTAGT AAACAGITGI ACAACITIGI TCTTATTATT AATTATTATT TTAATTAATA	360
35	TOTOTTTATT GACTAACGIC AGAGCTATTT TTGCCGAGTT CCTTTCCTTT AATTATCTAA	420
	TICACCITCA TATACTCTAC TAACATACCT GAGTCGGTCT ACATTACGGT ATTITATACA	480
	TARATATITC TIGAACITAA TARATIITATA AAGACATTAT TIAAGITAAT TIATATATITA	540
40	GATTATTCT ATCATATTAT ATTTTTTAAT ATATTACTTA AGAACCCCTT TTATTGTTAA	600
	ACCITATGCT TTAGGTGATA AGGATTATAC CITATTTTC	639
	(2) INFORMATION FOR SEQ ID NO:189:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 663 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1075UP	
55	(xi) SECUENTE DESCRIPTION SEC ID NO 189	

	GATCCAGITA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGTIAA	60
	CAATAAATT CAATAATTTA TTIAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
5	TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTTG	180
	TECCAGCAGO TOCOGTAAGA CAANOOGGT TAGOGTTAAT CGTAATGOOT TANAGGGTTC	240
	GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300
10	GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA	360
	THANTIGACA TIGAGGAACG AAGGCTAAAG TAGCAAATCG GATTCGATAC CCGAGTAGTT	420
	TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA	480
15	AATTAAAGTA TICCOCCIGA TGACTACGTT AGCAATAATA AAAATCAAAA CAATAGACGG	540
	THACAGACTT AAGCAGTOGA ACATGITATT TAATTCCGAT AATCCTCCGA TAAATCTTAC	600
	CATTITUGA ATATITAATT ATAATAATTT ATAATTAATT ACAGOGGITA CATAGITGIC	660
20	TTC	663
	(2) INFORMATION FOR SEQ ID NO:190:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 650 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1076RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:	
	GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GTACAATAGA TOCTOGIGIT	60
	ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT	120
40	ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCTTT AAAAATAAAA	180
	TAACCATGCA TIGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA	240
	TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA	300
45	TAATGAAACA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TOCTCATAAT	360
	CATAGTACAA TATCATITCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA	420
	GCACCICAAT GIGACATITG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA	480
50	GITAAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TTTATAAGAA	540
	CCATAATATA AACCTTTACC AATATGAATA TACATACCAA TAAAGAAGAA TGAAGCACCA	600
	TTAAGATGCA TATATCTAAT TAATCAACCT AGFTGFTCAT CTCTCATAAT	650

5	(A) LENGTH: 663 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1075UP	
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:191:	
15	GATUTAGAAT TATTAAGICA ACTATTAACT AATAICTATA ATAATAATOG TTTATCATTA	60
	AAATCATTAA AGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA	120
	TAATAATA TITAATAATA TAATATATT TAATAATAA TAATAAATA	180
20	AAAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATTCTT	240
	AATAATATAT TATTAGGTAA ATATTIAGTA OGIAGIAATA TCCAATTARR GOGIAGACTA	300
	TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT	360
25	TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT	420
	ATTAATAAAC TTAATAATCI ATTTATTAAT AAAAATOGIA TATTTAATAT TAAAATTAAA	480
	TTAAATACTA TITAATAAAT AITCTATAAG TAATITCITA TITATITTAT AACATTITAA	540
30	AATGTTTTAT GITAAATAGA TAATAATCAA TTAAATAATA AAAATTAAGA TOOCACAAAT	600
	ANTOCATTITE COTTENIGAA TOAATTAACT TATOGITING TATITEATITT ACTAATTITA	660
	TCT	663
35	(2) INFORMATION FOR SEQ ID NO:192:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 642 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1077RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:	
50	GAUCCAGITA CITAGIAGAA TGATAAAATT AATAAATAIT AITTAITAAT ATTIGGITAA	60
50	CAATAAATT CAATAATTA TITAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
	TATAATGAGA TATATATTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTIG	180
£.£	TOCCAGCAGC TOCCGTAAGA CAAAGGGGGT TACCGTTAAT CGTAATGGCT TAAAGGGTTC	240
55	GIAGAATGAT TATTITAAAAT AATAATTAGA ATTAATAAAA ATTAATTITAAG AATTATTICAA	300

(i) SEQUENCE CHARACTERISTICS:

	GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA	360
5	TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTCGATAC COGAGTAGTT	420
	TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA	480
	AATTAAAGTA TICCCCCTGA TGACTACGTT ACCAATAATA AAAATCAAAA CAATAGACGG	540
10	TTACAGACTT AAGCAGTOGA ACATGTTATT TAATTCGATA ACCCTCGATA AATCTTACCA	600
	THITHIGAAT ATTTAATTAT AATAATTTAT AATTAATTAC AG	642
	(2) INFORMATION FOR SEQ ID NO:193:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 658 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1077UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:	
	GATCCGTGIA TTTTTTATTT ACATTATTTA ATTAAAAATA ATGATTTAAA TAAATATTTT	60
30	TTATAAAAA TAATTAGIOC ATTGITACAT GTTCATTAAA GAATGATTAT TATCAAAACC	120
	ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTCAC TTAATTAAGA ATTAGGAACT	180
	TTATCTATTA GICTOGGCIG TTTCCCTTTT GATTATTAAC CITTATCGCTA ATAATCIGAA	240
35	ATATTIAATT TTAGATTAAT AATATATTCT GAGATTTAAT ATTTTTAATA AAATAAATAA	300
	TTATICOCIA AATAATATTA ATAACIATAC CATATATATC TAATATITAA ATAATCATAC	360
	TAACATATGT TIOGTAGAAA ACCAGCTATT TOCAAATCAG AITTGACTTT CICTACTTAC	420
40	CATTATTCAT CAGATAATAT TOCTACATTA ACCTGTTCAA TOGTTTTTAT ATTITATTAT	480
	ATTITAAATA TAATAAATAT ATAITTITAAT CATTIGATAA TAGTAAGATC ATCTOCTTTC	540
	GOSTITANTIA ATATTAACTA AMITITAATIT ATITTAATTA ATITITAACAT TOTTAAATAT	600
45	TTATATTATT TTTAATATCA TITTTTATTT TAATATTATG CTAATATTAA TTACITGC	658
	(2) INFORMATION FOR SEQ ID NO:194:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 445 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
5 5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1078I1	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194;	
5	GATCTAGTTC GTTAACTTCC GCAAAACACC TGTCAAGCGC TTCAACAAAC GTCTGGATCA	60
J	GATCCAAGAT GOCCAGTTCT GACTCCTGGT CGTCGACAAT GAAAGTAAAA TAGAGTGTTG	120
	CATAGITCIT GIAGATTATT TOGATATCIT COITAATOGI TICACIACCA CICGATAGIA	180
10	GCGAGGGCG CGTAATTAAG AATGAAGACT GAATTGAACT GTTGCCCTGC CTGATCAGCT	240
	CGTAAACCTG CTCCAGTAGT ACCTTCTGCT TCGGGAGATC GACAGGAGTA TAGTACTTTA	300
	CAAGCCTAGG TTGGCACTTC TTGTTAACTT CATGTGTTAG TAGGATAATT TAAGTACTGC	360
15	COUTOCOCOS TOOCAAADOG GITCACCCAT ATCAGGACOG CONCONNICA TOONCNGTCC	420
	CCACCACGGN TACNOGCCNC NCCCA	4 4 5
	(2) INFORMATION FOR SEQ ID NO:195:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 443 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG107812	
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:	
	GATCHAATAT TCAATHOOCA AACTCTTGAG AGTGTCTTGG AGGAAATTAT TCAAGGGGT	60
35	ATGGTAATTG AAACGAACGT GAAGAAAATT GTGGAGACGG TCGACGAGCT CAATAGAACT	120
	TCTAACCAGG AAGCCAGGIT TGOGAATIGGA CTAGGAAACG CTTTTCAGGC CATCACCATG	180
	OGTGGCTTTT CAAATTGGGG TGCGCGGCAG TGAATATTAG CACACACTGT CTTGAAACCC	240
40	CATAATAAAT GAAATAAATA CTCCTTGCTA GTGTCTAAGT ACGAAACAAC GCCAAGGCTT	300
	TTGGATCATC TATGTACGCA TTCAGTTCGG CAGCACTCAC CATGGGCACC AACTCTTCTT	360
	ACTIGOTATI TOCTIGIGICT TOATTITOCGO TICOGOCTICCO TGATOGICTO AAAGCTCCTO	420
4 5	CCTAATCCTC TGTAATTCTC CTG	443
	(2) INFORMATION FOR SEQ ID NO: 196:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 451 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(V1) ORIGINAL SOURCE: (A) ORGANISM: PAG1078RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:	
5	GATCAGGATG GOGATGAGAT ACTACCTTGA AGCAGCAGOC TTGACCTCAG CTAACTCCGC	60
5	AAATTOCTTT CATTTTTCGA AAGCAGATTA TAATTOCTTC TAAGCCATTC AATTOCTTTA	120
	CITTICCGIT AATCAATOCT CTATTTTACC ATCATTCGAA GTAAGAGTAT GTCGATATGT	180
10	CTGACCTAAG CTACAGATTA TCTAATCACA TAGITATGTA CGAACCAATA AGATTATCGA	240
	ATTICGITICA AAAACTCAGG GGAACGGCAC AGGGTTGCTT GGGCCTATTA GATGCTTTGG	300
	CCATAGCATA TCACGAAGIG ACCTCACAGT TTTTAAGTAA CCGGAATAGT CTGTAGATAT	360
15	GGIATTGIGA AAAGITTATT NOCIGGITTC ACCCCCTGGG AATCINGENG CTGGNCTGGG	420
	TICTIAGGIG GOGAATCOGG NCCCCCCNNT C	451
	(2) INFORMATION FOR SEQ ID NO:197:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 480 base pairs	
	(B) TYPE: mucleic acid (C) STRANDEONESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1078UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:	
	GATCTCCTTC CTTTCTGGTG TCTTGCCAAG CCCTTATTTG TTGACCAAAG TATTCTTCAC	60
35	CONTROLLE TACTOTETTO TOATAAATIT COOCOGIAGG ACACCTOTOG GOTTTOTOTT	120
-	GOOGATCTAT GAGGGCTTTG CAATCATCTT CACCGCCGCT AAAGTTTTCA CACCATTTTT	180
	GTATGAGCAG CTACTTCAGT AAGCCCCCGT ATTAGGATTG TTAAAAGAAG TAGGATCGAT	240
40	ACCCTICAAT TOCAGATGAT CGTTGCGGTG GGCTATTAAT TTGTTAGCCA CCTAATACTG	300
	AAATTTACAT ATTATTOCAC TAGITAATTA ATATTTATGA TOCAATGGGA ATCTATATCG	350
	GITCTCCGTT CCATCTTCTC GTAATTAGAT CACGTCGGAT ATNGTNGCCC CGTACCGAGG	420
45	ACCICACA TICICONITAT CITTATCCIC CCCACAANIN ATACACICC NAANATAGA	480
	(2) INFORMATION FOR SEQ ID NO:198:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 703 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55		

(V1) ORIGINAL SOURCE:

	(A) ORGANISM: PAGLC79RP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:	
	GATCOCTCAT TATTITIOGT COGACCCIOG COCCICTICT COTTCTICTC AAATACCTIC	60
10	ARATTITICGT CTATATAGGT CTOCAGCTCT TCCTTCTTCG AACATTCCGC CTTGTGAAGC	120
	TOSTIGAAAT ACTOCAGOOC CICTOCACTC ATOCGATICA CCATIGAATT GCOCTCITGT	180
	ATCTCTTGCT OGAACTGTTC TIGTTTOCGA ATCGCCTTTT GCCGCAGTTG AGCTTGCAAA	240
15	CTOSTIGIAT CAGACTOGIC CACTICATOT TOCACGIOCA GIOGATOCAT COCTOCAGOT	300
	AGTETAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGGGT GTTAGGGGGC TCACCTTCTG	360
	CGACTGTTCA AAGATGTGCG TTTCCAGCAA GAAAAGAGAC AACCGGAAGT ATAAGTACAG	420
20	CACOCGAGCC TAATTTTIGTC AGCTTOCGCA TTTAGCTCAG TTGGGAGAGC GCCAGACTGA	480
	AGAGAAACTT COGTCAATCG TAATCTOGAA GTCCTGTGTT CGATCCACAG AAITCCCATA	540
	TITITITOCTO ACGICACCCA CCOOGTANGA ACTOGCATTG CCTACCTAAT GGCCAGCAGT	600
25	GGAAAGCOCT CTTGTGATAT ATATATATCA AGTAACACAT CTATGTAACC TTTTGACACA	660
	GICCCAAGGI GAATCITGCC TCGCATCTGC CTCATCTGAR TCC	703
	(2) INFORMATION FOR SEQ ID NO:199:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 673 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1079UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:	
	GATCAGCGAG CTAGGTACCC GGACGAACAT GCCGTTGCGC AGCTTCCCAT ACTTCAGCGA	60
	COURTIGITY ACCOCAGAGO TICOGROCITY GAATAGOGAC TOCACCICITY COTICAGCAG	120
45	ATCGCCCTCT TTCAGAAAGC TGCGCATCTG CAGCTCATCG CTCTCAGACT TCCGCCGCAG	180
	CACGCCGCCG GGCAGGTTCA CAGAACCCAG CATGAGCACT GCGTGCTGCT TTCCCGCCAAT	240
	ATCCACCTTC CATCGTTTGT TOCCGACCTC CACGATCCTG CCGACAATGT GGTCGCCCGT	300
50	CTCTGGCGTG TACCGCCCGC GCCAAGGAAT CACCGACAGG AGTGGGTTCA CCCTGGAAAC	360
	GGTGCCCGCC ACCGACGAGT ACGTTTTGTT CTCCAGGAAG TATGTGCCGT GGCCTCGCAT	420

CCACACAGGA TCATCTGTAA TCAGCTCTCC TGGCGTCATA ATCACCGACG AATCCGCTCC

TICCATCTCC ACCTCCAAAT CAAACTCTTC TTCCTCATCG TCCAGGTACT GOCTCCGATG

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480

540

	GAALIGAAAL CUALGUGUT TGEGGATUGT TATTALUTUG CICATTALIG CIGAGALGAC	600
	ACCITICARA ACTICAGAGG CICOCTAGOC CAGOCGAAAC ACTGITGARG ATACOCTITG	660
5	TTACTICITG AAG	673
	(2) INFORMATION FOR SEQ ID NO:200:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 441 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1080UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:	
	GATCC990CA CGCATGTATT CCACTATGTA COCTATATCG CGGCCTCGCC TCCCGTGCCGCC	60
	GCACCOCCTT ACACCTCAAA GCCGCAGCCT TTCATGCAGC CCTTGTACTT TTGCACCAGT	120
2 5	TOOTIGGCACT TGACCGCATC CACGCCGTTG AACAGCACAC AGGTGTGTGT CGGTTCCTTC	180
	TOGGGCTTGC ACACACAGCA TGGCTTTGGC TTGTCGGTAC TACTACCTTG TGAAACACCT	240
	GOCACAGAAG AGGATTCAGG CATGATTAAT GCTACAGTTC TTGGAGATCT TCCTAACACCG	300
30	CCCCCTCCTT GOOGITTTIC TCACTTTATT TTTGCTTCAA CCCCCAAAAA TTGTTGTCGA	360
	ATTACAATAT ACAGAGGCGC AGTAACCCCT TTAGTGGCTT TTTGGCTTCT TGGGCTGGAA	420
	ANTINGACCE CECAACIVINE C	441
35	(2) INFORMATION FOR SEQ ID NO:201:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 644 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1081RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:	
50	GATCTTTCGC AGTGACTAGT GCATGCGGCT ATTTAAAAAG TATCGAGTTA CCCTTGGAAA	60
	TITCACCATT TATACTACTC ACOCACCOC TACAAAGOCA AGGCTTTCAA GCTACTACCA	120
	CACATATICA COCCCATAAA ICACCOCAAG CICGATIGAG CGAIGITTIG CGITGIGITT	180
55	ACAGGAGCCA GCGCGGTGGC ATGCGTTTTT GCGTATGGGA TGGTGGACCG ATATCTCTCC	240

	TICAAGCIGC ACAGGCATAC GCACCCGITT GIGITGGIAA CACTITICGC AAATATGACA	300
	CTGTTGCTCT CGATCACATA CCTGCTTCCA CTCGATGTGT TTTACTCAAA CCAGACAAGC	360
5	GGGCGGGAAG ACGAGCGGCC AGAGCTGCCG AACCTCGCGT TGTTCTGCGC GGTGATCTAC	420
	TOOOCCEAST TIGICATATE CHOSTHOSTS TICCCOSTOC TGATTTCGTA CGTGGATCTC	480
	AAGTACTTGT ATCCCCCCA GCCACAGGAG CCCCCCCCCC	540
10	CGANCOCCC TTATATOCAA TCTCAAGTTC TATOCTCTTT GTCTACTGGG OGTGATCTGC	600
	NOOCTOGTAT ATCTCAAGAC GACGACCGAT COCOGCGTC AGAC	644
15	(2) INFORMATION FOR SEQ ID NO:202:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 669 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1081UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:	
	CATCCAAGAC GAGCTGCGCC AGGGGAGAAA ACCCCCCCAC ATATGTCCAG CGATACGCTC	60
30	AGCATGGAAA ACCCAACCGT GGACTTGGGC TCGTAGTTGT GCTTGGCCTG TGCGATATAC	120
	TICAGCACAG ACATGATGAT TITTATAAAG TACAGCACAT GGCAGTAGAA CAGTGTCGAC	180
	TGATTGTTCA ACCCTGTTTG CGTAATGCTA ACCACATATT GCACTGTGCC AATGCAAAAA	240
35	ACCOCCATGA ACAACTGCAT CATCTTCCGG TGCGCTGTGC TCATCCTATT CGCCGGCTCT	300
	CCGGTGAAGC CCCATAGTCT GGTGCCCCCAT AGCACCTGCG ACGCCAGCAG TGCGTTAACA	360
	ACCCACCTAT GCATGGCATA CCAGTAGTCC GACCACCCTA CCGACGGCCT CACCGCGCTG	420
40	GACGIGICGC CITCATICTG CCAGAGCACG TCTGCACAAC CAGCGAGAGT ACTAGCGCIG	480
	TATACCCGAT GCAATTAAAC ACCACGTAGC CTTTCGACAA TGCTCTTGCG CTCTGCCGCT	540
46	TOCAGTIGAT COATAGIGGO GCATACATOG ACACOGACCA ACATGTOGOG TACAAGTATO	600
45	CGASCAACIG TCTCTTCCTC ATTCCASCCT CGTTCCAAGT CCTTCTACGC CGGTCTTCTG	660
	GCGTCAGAT	669
50	(2) INFORMATION FOR SEQ ID NO:203:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 654 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1082RP

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5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:	
	GATOCAGGAG CAAACTATTA TTAGGCGCCC CCCACCCCAG TCTGCAGGAT TCGAAAGCCT	60
10	TOCTAGOCTT TOTOCGATGT COCAAGGTAC AATTITTCTOG CAGCTGAAAA TACGAAAGAA	120
	GCGCCAAGAA GTGGCCTTCT TTGAATCCAA CGCCGACGCC AATGATGTGG AGGCGGGCGA	180
	ACATTITATA ACAGAGCTCG ATAAGGGGCGA TAAGCGGCTC GGCCTGTTTT CTTCGATCGG	240
15	CITICATIVIOC AATAVAATOC TOGOGACAGE TATCITTIGIC GITICCOGGA ANATCITICCA	300
	GTTGACTOOC TCAGIATACT TTGCOCTAGG GTTATGGGTA CIAGGAGCTT TAATTGCTCT	360
	ACCACCICIT TATGITTACA TOGAATTIGG AACTGCAATA CCCCCGAACG GTGGCCACAA	420
20	CAACTACCTT CACTICATCT TCAAGAAACC CAAATTCTTC ATTACCTCAA TCTACTCACC	480
	ATATGICATC TTTTTAGGCT GOOCCOCAGG TAACTCTGTG ATGCCAGCTG CAATGITCCT	540
	TEATECTECA AACSTEGAAG CAACACCTTG CCCTTGAACC CCCTCTTGGA GTTGCGGTCA	600
25	THICTICIE CHICCHIETC AACTOTOTOA GIGICAAAGC TEGGITEITA CITC	654
	(2) INFORMATION FOR SEQ ID NO: 204:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 680 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1082UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:	
40	GATCCGCAGC TICCGCCAAGC GCCGCTICIC CICCGIGIAC ICCICGICGI CGICGIACIC	60
	COGCACCATE GACOCCIOCG GETCETOCIC ATCCGCCGIC GCGICCITET CETCGTCCAC	120
	CETICTICOSEC ASCAECEAGT CETICCTTICEC CCCCGTICTICE TCETICGTCSC GCTICCAGCAG	180
45	TOCOCCOCA ACCOCCTOCT CCTCCCCCAC COCCCCACC TACCCCTACT TCACCCCCCC	240
	CATCTCCCCC TCAATCCCCC GGATCACCAC CTCCCCCACG TACCCCTCCA TGATCTCCCC	300
	ATAGTOGTAG ATTICCGACT CCTTCGTGTT GTACATCCGC GCGTTCCACG TGATCCGCAC	360
50	CAAGTOGITC ACCAACTOOT GOOCCOGCTT GTAGTOGITG ACCTTCTTTT TCACOGTOCC	420
	GAGGCTGAGC COCTTCTTGA TGATCCGGTA GTAGTCGGGA TAATCCTTCC TCAGCGGCAA	480

540

600

AGTIGTAGAAA ATCOOCAAAA TCTCAATACC ATTTTCCTCC TTTAAGTCAA ACACGCCATC

CAACAAAACT TIGABCTGGT CCCGTABCAA CATCGITAGC CCTCGCCACC TGAAAAGCTG

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	Market Market Heldered	960
5	ICACAGOCTT GCTTCAAGTT	580
3	(2) INFORMATION FOR SEQ ID NO:205:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 613 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1083RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:	
20	GATCATCAAT TICTITTIGG CIGITTICIT ATTIACAGCC TCTATTICIG ACCGAACATG	60
	CGACGCCACA GCAGTCCTAA TGAGCTCATC TGTTAGTTCG GTTGCAACCG CGTTACGCAG	120
	TICATICCCI TCTATICCTI TGCAGCCAGA ATCTCIAGCT TCATCITCAG COCIAGCTIC	180
25	ACTITICACITA AACCIGITIG GITAAAATGA AAAGIATITI CCTCTTTIAG	240
	CTOOGAATTG CCAGCAAATG GITTTCTGTG CGATGACTCA AACGGTACAT CTTTTTTTAGT	300
	TTPTGPTTCC TCTAAAATAT GCGGTGAGGT TGTAGAGCCG ACACTAGACA TAAATGGTGC	360
30	CGTAAACTGT TTCGTGGACT GCAGATCAGA CTGTTGCTGT GOCTTGAACT GCATGCTAGA	420
	TITCACTICA CITCCAGCGC GGGATTGGGT AGTGGGTTCG GTAGICITAT AATCTCCACT	480
	ATCGAAGITG AAAGITTTAG ATMINITOCTG GTGITCTCOG TGCAAGGAAG ACCCCTGCTC	540
<i>35</i>	AATGATGCTT TCCGAATATG TGGGTAGATT TGAATCATTG CTCCCTAGNA GCAGCATCAT	600
	CCTCCGAAAG AGA	613
	(2) INFORMATION FOR SEQ ID NO: 206:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 656 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1083UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:	
	GATCCTCAGC GCTGCGGAGC AGGAGGAGCG CGAGGAGGAG CCGGAGGCGC TTGTGGGGCA	60
55	AACCGTGAGC CBCAGCGCA CCGCCCAC GAAGCGGCC TITTGCCGATG AGCAGCACA	120

CAADOOCGAA GAGGCGGCGA COOCCGCCTC GGAGGACGAG GAGGCCCCA AGAAGGCGCG	180
GAAGTAGCGT AGATAGAAGG ATATAACTGT ACAGTACCAT GCAAGACGAA TCTGAGGCCG	240
GCGGACGCGC GCTGGCGCGG CGCCGCGGTA GCTGCGGAGG GCAGAAAAAA TCGCCGTCGA	300
CANTICTORS GICATONICS COOCCAGAGG ACAAGATOOC TOOCAAGAAG ATTOCOGGTIG	360
TOCTADOCOC GACGOOCTICC GTOCCOCACC GGTTTATCCT GCTGTTOGCG GACCACCCTG	420
ACTITICACCI GAAGGIGCTT GOOGCATCOC COCCATCOCC TOOCAAGCOG TATOCOCACG	480
COSTGANTIG GAAGCAGACC GAGCIGATIOC COGCOSTITIOC CGAAGACATIC GTIGGTIGAGCG	540
ACTOCAMOSC TGAAGCATTT TOCOGCTOCG ACCTTGTGTT CTCTGGGCTC GATGCGCACT	600
ACOCAGOCCC CATCCAAGCG GGAATTTGCC GACGCCSGAC TGGCTGTTGT CTCGAA	656
(2) INFORMATION FOR SEQ ID NO: 207:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 453 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1200RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207: GATCOCTCAT TATTTTTGGT COGRAGCCTGG GCCCTCTTCT GCTTCTTCTC ARATACCTTC	60
	60 120
GATCOCTCAT TATTITITGET COGRACOCTOG GCCCCCTTCT GCTTCTTCTC ARATACCTTC	
GATCOCTCAT TATTITITGET COGRECCIOG GCCCICITCT GCTTCTTCIC ARATACCTTC ARATTITICGT CTATATAGGT CTGCAGCTCT TCCTTCTTCG ARCATTCCGC CTTGTGAAGC	120
GATCOCTCAT TATTITITGET COGASCCTOG GCCCICITCT GCTTCTTCIC AAATACCTTC AAATTITICGT CTATATAGGT CTOCAGCTCT TCCTTCTTCG AACAITICCGC CTTGTGAAGC TOGTTGAAAT ACIGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT	120 180
GATCOCTCAT TATTTTTGGT COGAGCCTGG GCCCTCTTCT GCTTCTTCTC AAATACCTTC AAATTTTCGT CTATATAGGT CTGCAGCTCT TCCTTCTTCG AACATTCCGC CTTGTGAAGC TGGTTGAAAT ACTGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT ATCTCTTGCT GGAACTGTTC TTGTTTGCGA ATGGCGTTTT GCCGCAGTTG AGCTTGCAAA	120 180 240
GATCOCTCAT TATTITICGT COGAGCCTOG GCCCICITCT OCTICTICIC AAATACCTTC AAATTITICGT CTATATAGGT CTOCAGCTCT TCCTTCTTCG AACATTCCGC CTTGTGAAGC TGGTTGAAAT ACTGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCCCTCTTGT ATCTCTTGCT GGAACTGTTC TTGTTTGCGA ATGGCGTTTT GCCGCAGTTG AGCTTGCAAA CTGGTTGTAT CAGACTGGTC CACTTCATCT TCCACGTCCA GTGGATCCAT CCCTGCAGCT	120 180 240 300
GATCOCTCAT TATTITITGET COGASCCTOG GCCCICITCT OCTICITICIC AAATACCTTC AAATTITCGT CTATATAGGT CTGCAGCTCT TCCTTCTTCG AACATTCCGC CTTGTGAAGC TGGTTGAAAT ACTGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT ATCTCTTGCT GGAACTGTTC TTGTTTGCGA ATGGCGTTTT GCCGCAGTTG AGCTTGCAAA CTGGTTGTAT CAGACTGGTC CACTTCATCT TCCACGTCCA GTGGATCCAT CCCTGCAGCT AGTCTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGCGT GTTACCGCGC TCACCTTCTG	120 180 240 300 360
GATCOCICAT TATTITICET COGAGOCTOG GCCCICITCT GCTTCTICIC AAATACCTTC AAATTITCGT CTATATAGGT CTGCAGCTCT TCCTTCTTCG AACATTCCGC CTTGTGAAGC TCGTTGAAAT ACTGCAGGCC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT ATCTCTTGCT GGAACTGTTC TTGTTTGCGA ATGGCGTTTT GCCGCAGTTG AGCTTGCAAA CTGGTTGTAT CAGACTGGTC CACTTCATCT TCCACGTCCA GTGGATCCAT CCCTGCAGCT AGTCTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGCGT GTTACCGCCC TCACCTTCTG CGACTGTTCA AAGATGTGCG TTTCCAGCAA GAAAAGAGAC AACCGGAAGT ATAAGTACAG	120 180 240 300 360 420
GATCOCICAT TATTITICET COGAGCCIGG GCCCICITCT GCTTCTICIC AAATACCITC AAATTITCGT CIATATAGGT CTGCAGCICT TCCTTCTICG AACATTCCGC CTIGIGAAGC TCGTTGAAAT ACTGCAGGCC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT ATCTCTTGCT CGAACTGTTC TTGTTTGCGA ATGGCGTTTT GCCGCAGTTG AGCTTGCAAA CTGGTTGTAT CAGACTCGTC CACTTCATCT TCCACGTCCA GTGGATCCAT CCCTGCAGCT AGTCTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGCGT GTTACCGCCC TCACCTTCTG CGACTGTTCA AAGATGTGCG TTTCCAGCAA GAAAAGAGAC AACCGGAAGT ATAAGTACAG CACGCCACCC TAATTTTGTC AGCTTGCGGA TTT	120 180 240 300 360 420
GATCOCICAT TATTITICET COGASCCIOG GCCCICITCT OCTICITICA AAATACCITIC AAATTITICGT CIMIATAGGT CIGCAGCICT TCCTICITICG AACATTCCGC CITGIGAAGC TOGTIGAAAT ACTGCAGGCC CICTOCACTC ATGCGATICA CCATIGAATT GCCCTCTIGT ATCTCTTOCT GGAACTGTTC TTGTTTOCGA ATGCGTTTT GCCGCAGTTG AGCTTGCAAA CIGGITGTAT CAGACTCGTC CACTICATCT TCCACGTCCA GTGCATCCAT CCCTGCAGCT AGTCTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGCGT GTTACCGCGC TCACCTTCTG CGACTGTTCA AAGATGTGCG TTTCCAGCAA GAAAAGAGAC AACCGGAAGT ATAAGTACAG CACGCGAGCC TAATTTTGTC AGCTTGCGGA TTT (2) INFORMATION FOR SEQ ID NO: 208: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 590 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	120 180 240 300 360 420

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:	
	GATCAGCGAG CTAGGTACCC GGACGAACAT GCCGTTGSGC AGCTTCCCAT ACTTCAGGGA	60
5	COGNETICITY ACCOCAGASC TICOGNOCTIC GAATAGOGAC TECACCTICTIC CETTICASCAG	120
	ATCCCCCTCT TTCACAAACC TCCCCATCTC CACCTCATCC CTCTCACACT TCCCCCCCAC	180
	CACGCCCCC GOCAGGTTCA CAGAACCCAG CATGAGCACT GYGTGCTGCT TTCCGYCAAT	240
10	ATCCACCTIC CATCGYTIGT TOOCGACCTC CACGATCCTG COCACAATGT OGTOGCCOGT	300
	CICIOSOGIG TACCOCCOC OCCANOGAAT CACCOACAGG AGTOGGITCA COCTGGAAAC	360
	GGTGYCCGCC ACCCACGAGT ACGTTTTGTT CTCCAGGAAG TATGTGCCGT GGCCTCGCAT	4 20
15	CCACACAGGA TCATCTGTAA TCAGCTCTCC TGGCGTCATA ATCACCGACG AATCCGCTCC	480
	TICCATCICC ACCICCAAAT CAAACTCITC TICCTCATCG TCCAGGIACT GGCICCGATG	540
	GAACIGAAAC CCACOCCOCT TOCOGATOGT TTTTACCTOG CTCATTACTG	590
20	(2) INFORMATION FOR SEQ ID NO:209:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: LNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1201RP	
30	(1) 5-3-1-1-1 1-2-2-2-2	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:	
35	GATCTTCGAG ATGAACCCAA TATGGAACAC GOGCTTCGCC AGCTCGATGT GCCCGAAGTG	60
	GCCCGGGCAG TCGTTCATGC CCTCGCCACA CGTCTGACAC TTGAAGTTCC CGTCGATGCA	120
	COCCAGOOGC COGROCATICA COCCROCAC CITICOCCCCC ATCROCATCT CGROCATCGR	180
40	CTCTGGAAAC TCAATCTTGG CCACCGAAAT CGCCGGCACC TCCTCGGGCG AGAACAGCCC	240
	AAACIGCACC TCCTTGATGG TCCCCAGAGG CCCCCTCGAA TACCGAAAAGT CCACCATCGC	300
	TGTGTCGTAC TACCGCTCCC GGAGATACAC CCGTTTGCAA GTTCGTGTGT GCACCTGACG	360
45	CCCAGCOSCC ACTOSCAATO CTOSTITACS COGACOSCIT TGITTOSCIC CCTISCOSCA	420
	ACAACGAAGC TCTGTTATAT GTGCCCGCTC GAGACCCTAA GCCTGCTCCT GTCGAACACA	480
	COCTCACOCC CAGAAACTCG TGTCTTTACC TTGCAGCTCT GGAATTGGTN COCGCCAAAC	540
50	CNECTIATIG CITICOCCAA CNOCTATOCT COCTOTINATO TOACCTOCAA TNCACCANAA	6 C O
	ACNGACCCCC CACCTACCCC NCAACTCTGG TTATTGGGATT TTGCCGGGAA TAAACNCANT	660
	GTINCCAATC CHINCACCCC CAACHGITGT NICCONCTIGHT CNGINCNCIN TIACHCNINA	720
55	COCTOCNACN CCAATTITTT TINCCOGFIG COCT	754

	(2) INFORMATION FOR SEQ ID NO:210:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 643 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1201UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:	
	GATOCTCOGA TTAGOCTOGT CTTAAAACTC AACCAAGCTG CTCTGAAACA AACAACAGGT	60
	ACCACTACTG TETTETTCCT CTCCCCTTGT TGACCGTCCC CCAACTACTA TGTCGTTACG	120
20	TGTGTTTTT COOGAAACTT COCACCGTCT CAGAATCAGA COCTGTGAGA TTCTTCTGTC	180
	GAATATOGOT CTGGAOGATIC GOTTACGTGC GCCCCGCCAG TGCTCTTAAC CGGCGCCGTA	240
	GOCCCCGGCC CTGGCCCGTIA CCAACAAGCA TGGCAGGAGA CACAGAGTAC TACAAGCAGG	300
25	COGTICGAGGA GTIACOCCOCCO CTICAAGCAGG ACACCCCACCC CGAGGAGTOG GACAGCOCAC	360
	TOGOGCAGAC GGGCTGCTIAA GTOGAGAATIA TGGCGCTGCA GCTGTGCCAC GCGGAGACCG	420
	GOCACTOCCO GOCGTOCCOC GCCGACATOC COCCGTTCAA GOCGTOCTOC GCCGCCAACATOC	480
30	CAACCGCGAG CGCGTGACGC ACCGTGGACG GTGAGCTGCG GGCTGTAAAT AGGTGTATCT	540
	GGAGGGTIGT CACGITIGACA CTGGACACGT TACGAANCAT TIVICNGGNIN GGCGNCCGGA	600
	ATGOCCANCC CONATCINAN NACCCAAACN GOOGTATGAT NIN	643
35	(2) INFORMATION FOR SEQ ID NO:211:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 735 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1202RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:	
5 0	GATOGAAAAC OCTOCCACCG AAACCTTGAC ACTGAACOGA TTTGAGTATT CTCTTOCATT	60
	TICCAAGOCG AATACCAGCT TGTCCCAGGC TGCCGATCCA ACCTTCCCCT CCTTCAGGGC	120
	CIGCTIGIAC CIGICGICIA ICTOCACCIG ACGIACCACC ICIGIGATCA CCATGACGAC	180
5 5	OCCAGOCCA GACCTAAAAC CTTTCAGAAA GOCCTTTGAG ATTGCATTGT CGATGAAACC	240

	GAGCCTGAAG ATGCCCATGG CGAACACCAG GACCCCTGAT ATGCATCCGA TAACCGCAAC	300
	GGTCATCAAC GGTTCAAGCG ACTTGTGCGC CCATGCATCG CAGCTCTGGC CCACCACAAG	360
5	GGACGCAACC GTCTGCGGCC CTACAACCAT CGTCGGGACG CTGCCGAAGA CTGCATATAT	420
	CASTGGGGGG ATCACCAGTG CGTACAGCCC TGCGTATGGT GACACATGTG CCATAGTGGT	480
	CASCGARATE OCCASCOSTA TETEGRATICA CETUROCETE ASCCCASCAR SCATGICCTT	540
10	COCATTITOCC CAGAATACTIC TOOCAGCCAG CGTATAATOG OCCGTAGTAA GACNCATAAA	600
	ATTINITICC INCCIACOGT IGICNVITTA INGNCIGIAC COCNIACGAC ITGICANAAG	660
	CAGNINOCCC CCGCCCGAG ACTICCANCC CNICCCTACI CCCAATITIGG ACCANGACCC	720
15	GETTCCTGGT GCTTN	735
	(2) INFORMATION FOR SEQ ID NO: 212:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 777 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPCLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1202UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:	
	GATCGCCCCC GCCCCCCAGG ACTACGTCGA CTTTCTCTCG CTCACACACG TACTGGACGA	60
	CCCGCAGCAG CCCGAAGCGG ACTGCGTICGA GCACAGCTAC ACGCCCGATC CGCTGCAGCT	120
35	COCCUTICIAC OCOCACOCCC ANTGAGAGCT CATCOCTCCC GCOCAGTIGOG ATTITITITISC	180
	CGCCCCCCC CASCCCTCCC CCTGCCCGTC ACCGAAGCCC CAGCGATGAC AGCCAGCGTC	240
	CAGGATATOG TOSTOCCCAC COCCGGGGAC AGCOCCGGGG GCCGCGACGG GCCCCCAAC	300
⇒ 2	CACCOGNICA COCTOCCCGN COCCCTOGAC ASCOCCACOG GOGAGGNOCT CONGCCAAG	360
	GCCACCGCCA AGACCCCCCTT GCCCAAGGCC CAGACAGAAG AGCAGTACTG CGAGCAGCTG	420
	CACCAGTACT TOGASCOTIGA COCCOGTOCC GAGTOCACGG ACGAGGGCTG GCTGGACCGC	480
45	COGCUCCOCC COGCOCCCCC COCCACCAAG CAGGAGCCCC AGCGCCTCGC CCGCCGTCTA	540
	CCAACGCCIC TACTICCICG GCCGCCGTCG CGAANCCGCC GCCNVICGCCC GCCACTGCTG	600
	TATACGITCC CIVENTCH396 CNCCINCCNA TINGCGCCG AANINCTCNA NCTCINNNCT	660
50	NAINCINNON CACCOMININ COCTIAATTI TIONITIININ NAITINICIT TICCOCTOCC	720
	NCTGTTACCC TCNCTNONIC CATACTINATE CONTITUGTG NACTINICITIC CATACTO	777
	(2) INFORMATION FOR SEQ ID NO:213:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 756 base pairs	

(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1203RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:	
	GATCAAACAG CTGCAGTTGT TGAAAAGGTT GCTTGAATCC AAACCAAGGA AGGACGTATT	60
	TTOGTTTCTA GOCCTOGATA ACTAATCTCT TCTCCACTCT ACCTGGGGAT AACACCTGCA	120
15	OGACOTGAAC TAACAAGTIG ACTACTATAC AOCAAAATAA CTOGAACAAG TTATACAGAA	180
	TITTGTAAAT ATATTATAOC AGCCCTATTA CTATAATTCC ATCATTTGTT AACOCTTTAG	240
	CCTTCGITCT CAGACICGIC GICALTITICT TCATGATAGT TGATATITIT GOGFIGCCIT	300
20	GACCITITOC TIACIGOCCC IGCATIGACS CICCIACICT TIGGCCIGTA GICACCIGCA	360
	GACCITOGIC TATCITCGIC CICCCITICCC TCATCCACAA CTITICCCCTT CTTCTTAGIT	420
	TRACATCAGO CICATCATOS COCITOCOCT TOTICAATIC TOTICOTOTG COCTTOGOCA	480
25	TETTEAATTE GOEGGATTAG AGAAGOOGA TACTTTGGCC CITATATTTA CIGTCAGTET	540
	TICAACAIGC IGGICIGATA TATAGCICAT GAACGCGITT CITTGCGCCT CTICCCATAT	600
	TOCCGAATOG CTGATAAAGT TCAGAAGCCA GATTAGCTCC CAGGTAGACT GGTAGATTCC	660
30	ACCOCCETTE ETTTTACCTC AAANATNATC AATTCECAAC CNECTAGANA TAAININIGA	720
	ACATATOCTC COTOTINOCAT COCANTOCCAT CICCCC	756
	(2) INFORMATION FOR SEQ ID NO:214:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 781 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pag1203UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:	
	GATCATTOOC TOOCTOCTOG GOCAGACCAT CTCGGAATGC GACACTGTGT CGATGTCTGT	60
50	GCTGCGGAAG ATCTTCAACA AGTTTCTGAC ACACCATTTT GGCCCGCTGC GCTCCCTGCA	120
	GOCCTCCGCG CCCCACCCCG CCTTTCATTT TTCTCTCACG ATCTGCCACT CCTACAGTAA	180
	COGACTOGGG COGCAATTCA CGAAGTTCTA CTCCGAGATC CTGTACCGGA TTACGAACCC	240
55	TOGETEGGEC GOCTICAGGEG AGACCOCCCC CÉTOCAGTEG ACACTTGACT CÓGAGTTÓAA	300

	GACICITUTE AAACTGCATA AACTTACGGC CAACATATGG GAGCATGTGC COGAACTGCT	360
	GOCCICCOTC GICOGATTITG TOCATCAGGA GITATOCTCA GACAATGIGC COCTGCGAAT	420
5	TREBURCHACE CEACHTETIAG GIGATITICITI ACCCCCACCC TCCCCTCCCA ACTICGICAC	480
	GATOCATACG GACACATATA ATOCCTOGAT GTCGAAGATA OCOGACATAG ACOCCACBGT	540
	GAGGCGCGAA TGGGTGAAAG CCATACCTAA GATACTGGAT AACAGTCTGA TTTGGCAACA	600
10	GATATOTGCA AAGOCTCAAC AAGACACTAA TOGATACOGA CGATGTOGTT AGACTATOCA	660
	OCTIVAÇA A GOCTIÇA A ACTA CAÇTICO COACGATTOTI GOGANATOTIC A A A A ATTOCAC	720
	TINTICCVAA TIGITGOGOC TACOCAAANA AAACNAANCI TAGGAACTIT TCATTIGTAC	780
15	С	781
	(2) INFORMATION FOR SEQ ID NO: 215:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 765 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
25	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1204RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:	
	CATCCCCTTC CCTACCTCCT CACCCCCCAT CTCCTCACCG TATACCCCCT CCCACCCAAC	60
	TAGGAAGCCG CGCACCGGT CCCACTGGAT CCATGGCAAG TAGGTCTTGA GCGCATCCTT	120
35	CTCCATCGAA AAGTGAGCGT CGTCGTCTGG CCAGACACCG ACCCATAGCT TGAAAGCCAGC	180
	ACOGTCCGCA GCAGGACCCA AGAACTGCAA CGTGTTGCAG TCAGAGGTAG AGTAGACTTT	240
	CACCELLELCC GLELAGESCC CCAACECCLC CAACLCGLCC ACCLACACCCL CACLCHACLL	300
40	CCASCIACCE TOSTSCITICT TCACACCTAS STITGAAGSCC AAATOSCCCA TAGCGTGTAC	360
	AGACGAGGCA CCAAGCAGAG CTGCGGAAAC AGTGGCAGAG AAACGCATAG CTAAGGAATT	420
_	CATGCTGAGT TAGTCTGGCT AAAGTGGCTT GTACTGCAGA AACGACAGAG AGGGACAAAAT	480
45	ATATOTTAAT ACCAGOTCAG COCCATCTOC COGAGGAAAA AGAAATGTOC COCGTGTTCC	540
	COCCACCTIC CITAATITAG AAGCATIATC TATCACGIGA ATATCACGIG AAACACGITA	600
50	ACCUTACACA GACCUATURA COGUESCUCE GAACACEUTA GCACUGAGUT AUGUACUTAC	660
50	GTGGCCACGC ACCATGCAGC TGTCCTCCAT GCAATATAAC CCCCCGGCCC CCCCCAGTCA	720
	ACCOCCATCA AAAGTINCTON CCCCGAGNINC CCTCAAATIGT CCNTG	765
	(2) INFORMATION FOR SEO ID NO:216:	
55	(2) INCOMPLICE FOR SING ID NO. 220.	

5	(A) LENGTH: 776 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1024UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:	60
15	GATCAGGAAG CAATAGGTAC TCAATTGCGG AAGATTCAGA GACAGCAAAG GTCAAGTGCA	60
	GTTCAGCAAC ATCGAATCCA CACAAGTTAT GTCGTACAGA GGCCATAACT ACAACGCAAT	120
	GOCACCOGG GGCAGACOT TCTCCAACAG TCCATATACG AGCAATATGG GGTCCACGGG	180
20	COCTOCOCO COCACCTCAG ACCTOTTOCA GAAGTICGAG CGATTICCGA ACCOCATAGA	240
	GGACGTGACG GACCACCCCC TGGTGCAGCG GTTCGTGCCG TACACACCGC TGATTGCGCG	300
	GTTTITIATT GTOGOCACGT TCTACGAAGA CTCGATCCGG AFTCTGTCGC AATGGCCGGA	360
25	SCARGIGICG TITICTATOCT ACTACOSCG CIACCOCCGA GITTITCGIAG TGCIGITITIT	420
	CATOCTOCTC OCCCTOCTCA TGATGGTGGG GCCCACGATG ATCCTGCTGC GCAAGCAGCA	480
	OCTOTATOCG ACTOCCATOC TATOCOCOTIC TATCATCTCC CACCATTTICT GTACOCOCTIC	540
30	TTCTCCGGCA CTCCTTCGTG TTTGCCGGAAT TTCAGCGTAA TCGGCGGTTG CTGATTACTT	600
	COGTEACTICC ATCCGTGCAG AAGCGCATCA CATTCGGCAT GCTGCCGGAG CTAACAGCAG	660
	GAADOCOCAC CAAGOCTACA TOCTOCTTOC GOCCGCATAT CATAGTCTTA GITTGTGACT	720
35	TTACCTCCCC AAACTGGTGA CGNITCCTCN CCTCGCGNAC GGTNCTCCCC TCGGTN	776
	(2) INFORMATION FOR SEQ ID NO:217:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs	
40	(B) TYPE: nucleic acid	
10	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1205RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:	
50	GATCOCACTI CAACCCATIC AAGAAGACC ACOCCAGTCC GGAGGAGGAG AACCGICACG	60
	TOCOCCACAT COCCAACCTC CTCCCCCCACC CAAACCCCCT CCCCCTACCA TCCCCCAACC	120
	ACCCTCTAAT CAAGATTITT GETCCTACGT CGATTCTGGG CCGTACGGTC GTTGTCCACG	180
55	CCCCCAACCA CGACTTACCC CCCCCCCCAA ACGAGGACTC CCTAAAGACG GCCAATGCCG	240

	OCCCCAGACC TECTTECESC CTGAITESCA TTECCAACTG ACCTESCIEC TECCESOGIEC	300
	COCHADOTICT OCCHAGGITTOC CAACTAGAAG CTCTGATGAC TATGTTAGCA GAATAAACGT	360
5	TTTATOGTTC OCTOTOTTOG COCTOTATOT TACAATTOCA OCAATTAGAA GTCTOCTCTC	420
	OCCCCCACG GCACGCTCGG CAGCCAGTAG CTTGGTAGGA TGTTTGCGGC CGCCAGCAAC	480
	AAGOOGAGGA AGGOTTOCGA AGGOTTOTAG CACCTTGGAC ATGTTACTOT GGTTGGTACT	540
10	OCCTOOCCAC GITACTACOC TITOCICCACC ACCTOCACAA TCTCOCACCG GITCCCGTCTC	600
	GTCTCTGCCC CONAATTCAG CCAGONCCCG ATTTCTGCNC ACTTTGGTTG ATCCCNTAON	660
• •	ATGAAAINIT CONCCCAAAG AGOCTIGOOGI TATTITOTINAN ATGACATOGG TITOCOCCGAA	720
15	AAGIGICIAA ACATCOCTIGI COCCCCN	747
	(2) INFORMATION FOR SEQ ID NO:218:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 777 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1205UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:	
	GATCITCAGG TTCCGCGACA TGATTATCAG CGAGATGGGG TGGCTGCGCC GGCGCCCCGG	60
	CTCCTGCACA CGCTGCGTGA ACTGCTCCCG CTCCGGCAGG TCCTCGGGCA GCACCGCAGA	120
35	GATCATCTTG TOCAGCAGGA TGTCAATGAA GTGCTCCTGC TCCTGTACCT GAGACACCGC	180
	GCGCAACTTG GCCGCGCCCT GCTCCTCCGT ATCCTCCTCG TCCGACATAC CGGCGCCATT	240
	GTCGCTGGTC TCCTCCTGCC AGAASCTGTC CGCGCTGCTC TCCAGCTGGT GCCGCAACGC	300
40	GAACTOGTOG AAGTOGTOGT CGATTGTTTT GOGCTGCTOG TCTTTOCCOG TCCGCAGOOG	360
	CTCCCATGTC CCGTCGAACA GTGACCACCC GATGTTOGTC ACCACCTCCC GGTTCGTGAC	420
	CCACGCCCC CCCTTTTCAT CGTCTGCCAC CCTCTCCTCT	480
45	CITGCGCGCC AGGAATTCCC CCAGCAGCGA ACGCCGCTTC TTGCTGCCAA TTGCAACGCT	540
	CTCAAGCOCC TIGGTCTATC GTCCTCCTTC ATCGGTCCTC CGCCCCACG TCATATAGAT	600
	TOCGOCTCOC GOTAGCACAC TOCCGAAGOC TOCCTTOGIT ATATOCCOUT AGAAGCAGIC	660
50	TOGOCGOTCA GITAGTOCIT TOGTGATGAT GACGTGTTCA OCATGACTOG GATATAGAAC	720
	AGICATCIAT CGATTGAGAA CATACCTATA TAGAAATGAT TTACTGIAAT ATATCGA	7 7 7
	(2) INFORMATION FOR SEQ ID NO:219:	
55	(i) SEQUENCE CHARACTERISTICS:	

	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pagl206RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:	
	GATCOCCTICC GICGICGICG OCTOCTICGIC CTCGTTGAAC TCCGTCCACA GCTTGAACOG	60
15	CCCCGCCGAC AGGICCACCT TCGCCACCGT CTCCGTCACC ACCTCGGTTC CCAACTTCAC	120
7.5	GCACTOCOCC TICATCCOCT CCATGACGIC GCTGCCCGTT ACCCCGTCGG GCAACCCGG	180
	GAAGUTCTICA ATICTOCGTCG TTIGTOGTCAG TTIGCCCGCCT GCAGCCACTIC CGTTCGCGAA	240
	CATOCOCTOS TACASOGTOS OCTTGATOTO COCGOGOGOT AGGTAAATGS COGCAGTGTG	300
20	TOCOCCACOG CCGCAGCCAA TGATCGTAAC TTTGTGATGC ACCATTCGTG TCTGCAAAGC	360
	TIGICOCAAC COGTATCTIG TIGCTGCTGC TAGCATCAAC TGTGCACCGC TAAGTITCGC	420
	TOSOGCTIOC TOGITTIATA OCTICTOSOCT TCACCATOGG TGAACCTTGA TOGCOGITTAC	480
25	TAITICOGAC COTTATGICO COACCIGACA AATICOGOTT COCCOGGIGOG CGACTGOOGT	540
	CAGTGGGGGG TGCAGTACAA GATACGCACC GCGGGCCTNT NGNNNTCNNC GGCCCTCTCN	600
	GNGGCCCGCC GNCCCTTCNC AGGATCIVITN CCTCANCTAN AACUNGGCCC GGNGNNVICT	660
30	TTITTTGIN CNOCNAACGA AGGCAAINNA AINITINNIN GGNCNINNGI INGAANIGIC	720
	CINCINGTOOG CATCOCINOCT TATINAACACII C	751
	(2) INFORMATION FOR SEQ ID NO:220:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 778 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1206UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:	
	GATCCOCTOC TOCTOCIACCA CCTOCTOCIAG GTAGGITGCT ACTOCIACOCG CGAGATATGG	60
50	GTCCTGGTCA ACATCCTACA GCTGACCTGC TTTAACGAGA CAACCAAGGA CAAGTACGAC	120
	COCCOCATCA TCAGTICOCC COCAACOGTT TOCACCCCC TGTCTOCAGA TAAGACCTIC	180
	OCTCAGGAGT TTAACTCCAA ATGTCTCAAC TYTACGACCT OGTGGCACCT CATGGCCCGC	240
55	CTAGACCACG CTGTTTTCAT GTGGTGTCTA GACATTATCG TGGCCGAGAA CTCACAACCC	300

	TTCAAAAGCA ACCOCATCAT CCGCGATAAG CTCAACGGCA AGGACTGCGA CTACTACCGT	360
5	GATCTACACG TIGHTGICAN CTATAGGATT ATCTGCGCCC TGACTCTTAC AGTGCTTCTC	420
-	AGCTATCATT TIGGCTTCAA TAATCTCTAC GACCICTCTT TIGTCGACCC AGCCTTCCAG	480
	ATAATAGGGC CCGAACAAGC GACTTGGGGG ACGTGCATGC AACCTTTATC AAGAAATGGC	540
10	ATCACAACTA TAAAAAGTTC TAGTTGCTCG ACTIGTAATC TCATCTCTAA ACATAATATT	600
,,,	CTTTTATAIG CTTGTATTAC TTANOCTCAA CATGATNACN TATGOCTOGA AGATTTOCNC	660
	CNIGGCCGIN AGAACNGATT TGTGTCAACT TNTATAAAAC TGACCCGTGC GCCCCTCCCG	720
15	TAACCCGANA TITICCTGAIN CNIGATCCTA TGANGATGCC GOCNCATINN CANIATIC	778
	(2) INFORMATION FOR SEQ ID NO:221:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 756 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI 207RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:	
30	GATCTGTTTC AAAAATTGGA AACGCTTACC ACCTCACCAA CACACCAGGA CTTTATTTCG	60
	TAGAAACAGO CGATCOGOCT GAACAACAGT CACTAGAAAC OGTOCACCAA GOCAGCTTOG	120
	CAACGAGCAC GCACCCTAGG GCTCAATGOG TTGATAGTAA AGCATGTACA CGAGCTTTGT	180
35	CTCCGAGAGA AGGAACGACG TCTTGCACTC GGACACGTAC GAGTCTGAGA TACACCACCA	240
	COGGTOCGTA GTGGTOCCAC GTAAAGCCTT CAGTTTGCCG GGACGGCCCT GGGGACGGC	300
	GAGTIACCTIC GTGGCAGCCG AAGATIACGCC CGATGAGCTIC GCAGAGCTIGG CTICCGGAGCT	360
40	GTCCTGCTCG GCTGACCCGT CGGGCTTGCA GACCGGTTCT TCCGTTAGTA GTGACTGTTG	420
	ATGGAAGCTC CCCAGTAACG GTCTTGAGCA AGCGGCCATC GGCCCAGGCG GAAGGCTTCC	480
	AGCTGGCGTA GGGCACAGGC ATTGGAGGGG CTGGCTGGCG GACGGCGTCC GACGAGATCA	540
45	CATCIGAGOG AAIGATATOT COCCOGTOCT TOGTOCTICC TAAGICAGIT TGTTGOCGAA	600
	CATGCGTTAT GCCCTGAGAA TOGTTGCCAT GTGCTTGATT CATGCGCCAA CAGCTTATAG	660
	CEAATIGCCAA ACCCCCACCA TITGTIINTCCC CNACACTIGCT CNTGAGACAC CCCCCCCGGA	720
50	ANNINAATOC GETTTIVITTIG TTAAAACCCN TNAAAA	756
	(2) INFORMATION FOR SEQ ID NO:222:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 771 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1207UP	
10	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:222:	
	CATCIDATEA COGATAACTO ACCOCITATA GAAACTTCCC CGAATCCTAC AACTGACTCC	60
	AACTOOCCAC ACGAGATATO TOTATTAGAA AAGAATATOA ACGATGTOAT GOGTTOACTA	120
15	AAGGGGTTG ACACGCACTC ATGTGAACAG ATCATTAACG AAATTCTTGT GGTTGATTAC	180
	CATCTTCCAT COCAACATAT ACCTOCTCTT ACAATACCAA ACAACTGTTT CAAGGAAACA	240
	GITGITTACC CATTITIOCG GCCACACCIT TITICGGGGIC TCCGGGAACC TATCTCCGGG	300
20	ATGITGITAT TTGGACCTCC AGGAACAGGT AAAACGATGA TTGCCAGGGC CGTTGCGACT	360
	GAATCGAATT CAACTITCTT TIGCATCAGT GCTTCCTCTT TGTTATCGAA ATACTITGGT	420
	GAGTOGGAAA AACTIGICAA GGCCITATTT TACCTAGCCA AACGGCTTTC CCCCTCAATT	480
25	ATATTCATTG ACGAAATCGA CTCTCTACTA ACTACOGTTC AGATAATGAG AACGAATCAT	540
	CCAGAAGATT AGACGAGCIC TIGGTOCAAT GICCTCCCTA ACGAGCOCCA CGGCTAGGAA	600
20	CAGAGAGGCG AAGAGGCCAG ACGCGTACTG TCTTGGCCGC AACCACTTAC CGTGGGCAAN	660
30	AANGANGCTG CNATAAACIT TTICACGGGI CIATNATCCC TTGCCGGAAT ACAACNAAAT	720
	GITCTITGAA AACTINIGOC CTCCAAAAAG AATTICGAAC INATTCNNCN T	771
35	(2) INFORMATION FOR SEQ ID NO:223:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 740 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1208RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:	
	GATCAATTAA TAAATOOTITT AACTAATAAA GITAATAATA AATCTATTAA TIATATAAAA	60
50	CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
	ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA	180
	TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTOSATAT AGTTTAATTG	240
55	GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300

	ATCATTAATA TAATAACTUT TTAATTAGAG TIGGTACCAC AAGAATGCTG AAAGCATTAG	360
	GGGTGTGTAC CTTAGCTCTC CTAATTAAAG TTTATAAAAT TATCCTTAAC TAATAAAAAT	420
5	TARATRARDA ARARATITT DIRABATITA ARTIRATIRA TARATRARIA AGITARITAA	480
	AATATGITTA TAITTAAATA GAITCAAATT TOCAACAATT COCATTCAIT TAGTACTACC	540
	ATCACCATGA ACAATTGITA CATCATTAGI TTATAGITTA CIATACTTAG CITACTAACA	600
10	TOGTATATOG TATAATANOC CTAATAAACC TTATANANTT TTTACCNAAC TTNCATTAAA	660
	AAAAGGOOGA NONNOTTTOG NOGACCCCTA COONTAAAAG GNGTAATGGT TCCCCCAATTG	710
	GTGGCCGAAA TAANTTGGCC	740
15	(2) INFORMATION FOR SEQ ID NO:224:	
حی	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 782 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) Original Source: (A) Organism: Pag1208UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:	
30	GATCTIAATI TAAAATITTA ATTAACTATI TATAATITAG AAATATATAA TCTAGACATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
	ANTAGAANAC CATAAGITAA TIGATICATA AAGAAAANIG GANITATITIG TOOCATCITA	180
3 5	ATTITATTA TITAANICAT TATTAICTAT TTAACATAAA ACATTITAAA ATGITATAAA	240
	ATAAATAACA AATTACTTAT AGAATATITA TTAAATAGIA TITAAATITAA TITTAATATT	300
	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGIYTA TIAATATTAA GIGATATATA	360
40	ATTTAATTTA TATAAATTAT TTAATTTACF TOOCCTGATA TATATAATTA TTAAATGITC	420
	CITICATAAT ATTIAITITT ATTAGICTAG TAATATTICT ATTIAATAGI CTACCCCITT	480
	AATIGGATAT TACTACCTAC TAAATATITA COCTAATAAT ATATTATIAA GAATACTIAA	540
45	TCCIPATRAT TIRTIATCCT ARGTIRTATA ARTIARITAR TCCTFTFTAT TRITATITAR	600
	ATTATTATTA ATTAGTAATT ATATTTATTA TTTTATTAAC ATAATTTTTG ATAATATATA	660
	TOCATATAAT GETATTIATT ATATACONIN ATGAATTAAT GANAACCOTA TATATGANAT	720
50	TAGITATAGI GACTIAATCC CNATCICAAT ATATATAATT ATTATAGAAN ANATACTITT	780
	TC	782
	(2) INFORMATION FOR SEQ ID NO:225:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs	

	(E) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1209RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:	
	GATCAGCCTA TGTAGCAACT GATCGGCGCT GGTCCGTGTC AAACGCCGAA AACACCCCAC	60
15	CAGATTACOC ACACACTOCO ATATTTTGAC CGACTOGAAC TITIGTGTACA CAAAGCTATT	120
	CASCITIGICA CIGGOCACOG ICAGOGOCAT GITGITCACO OGAGIOSCIA GOCOCOCACT	180
	OCTIGITICCCC TOCOCCAGCG ATGGCTCCTT AAGATCCTGC GITCOCATAT ATTGCGCAAA	240
20	CTTCGATAGG TCTCGACTGA GCGAATTACC GACATGGTCC AGTAATAACA ACACCCCAGG	300
	CCACCCCCC CACCTGTAAT TCACCGTTTT GACCAGCAGA AAGTGCAATT GTAAAAGAAT	3 60
	GIACCAGIAA TOCCAGIAAA ATGTGGAAAA GACCTGGTCG TTCTGAAGAT ACGAAATCAT	420
25	CACCICAAGA TICTICAGIC TICTCCGICC CCAACATCIT GCAAAAATCT GCNCNICGIC	480
20	SCHICTCHIC CACTOGRADOC GCAGGGCTTC CAAGGACACT CCHIGCAATT GAA	533
	(2) INFORMATION FOR SEQ ID NO:226:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 534 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1209UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:	
	CGAGGATCGI CGAACTIGAT TATFITCTIC TGGIACGACG ACAGCTCGIC CGCGITCCGC	60
	TITAACOCCA CCACCACCAC GIACTIGIIC GACCOCAGCC CCACIGIOCC GCICCCCIGC	120
45	TICATOSCCT CTACCOCCIA CICCACCTGG AACAGTCTCC CAGTCOCGGA AAACGTCACA	180
	GINTCACCGI CGIAGFIATT TCTGAACATC ACTAACTCAC ACNOCCCCAA TTGNICGTGC	240
	ACACCOCCCT CTTTACTOGT OCTAGTTAAC TOGACAGGAG CTGTGTTTGC CACCGGGCCG	300
50	CESCAACTAC CECECCIATE GECATTEGAT ACCCACATE GATAFICGE GAAACCEATA	360
	TAGATGATTIC CGTCTCCCCG ATTGATTGGA GOCTCGGTCG CATACTGGAG TCGTCCGANG	420
	TGTCGNATCT TCTACATAAC CGTTGNAGGN CAGGGGAGAG GTTTGNNGC GCAGTTGTCG	480
55	COGRETACIO TATTAGOCCA TOTOCCETCA ACACETATICT ACTOSTIGETE TTAT	534

	(2) ENFORMATION FOR SEQ ID NO:227:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 547 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1210RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:	
	GATCTAAATT TATCAGCCCA TGGACGGATG GATTTACGGC AGCGTGTCOC CGCAGCACGG	60
	GOCACGCCAG ACTGCGAGGT GOCAAATAAT TCACATAGCA ACCTGCATTA TAAACATCCC	120
20	AAGICATTAA ACTTACTAAA TATTGITGCG TAACCAAAAG CACCGIGTAT CATCATCTTC	180
	ATAGICTIAG CIGAACCIAC IGIOGCACCA GCCCITTACT ACGIATIGIA ICICCCTITT	240
	ACAATGCTTG CCCACTGCCA GTTTTCCGCA CGGGGGTTAG CATGAAGTCT TTGCCGCCTT	300
25	TETACCACGE CITGACGICT GACTICTACGE GCACCAACGA GGTTAGACGE AGTIGCACCCG	360
	GCACCGAGTC ATCCTCGCTC GCGTGTTCCC AGAGACAATT TGAGGTTCCA CGGAGCATCC	420
	ACGCCCATGC AATCCTGCCC GTAAAAGTTT GCACANTICA TCCCACACTT GGGGGGTINI	480
30	TATCACNOCA NOCTGATICTO GTACGNAAAA MITTICCNIN TITIOGTIGAGG AAATCAGGIT	540
	CCCAATA	547
	(2) INFORMATION FOR SEQ ID NO:228:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 600 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) CRIGINAL SOURCE: (A) ORGANISM: PAG1210UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:	
	GATCGAGAAG ATGCGGCGCC GCAACGAGGC CGCCACGCCC GAGGCGGGCC GCNACGAGCT	60
50	CCLCTCCCCC CCCCTCCCCL YCCCCCLCCY CCTCCCCCC CCCLLCCLCC	120
	CCCTGTCGCN GACCCGGCNC GGCCCCTGGC GGTGCCCTGC AACGAGCTTC CCCGATGAATA	180
	CTGCATCACC AAGACTGACT TCGACCGGCT CGCTAGCCAC GGCATCCCGG TCGAGGACGT	240
55	CCACGAGGAC AGCAAGGACT GGTACTTOCA GTGCCCCTGT GGAGTAGAGG AGGTTAGCCC	300

	GGGCCTAGAG AGCCCCGCGC TGCAGCAGGC CCTGGTCTGC TGCCGACCAAT GCCTCCGCGT	360
5	GOCAGCAGOT GOGACTOCCA GCACCCCGCA GCGATTGAGC TTGCTGGCCAN GCGGGCAAGA	420
3	CTCCTCACTA TITTIGCCCTC CIVIGCCCCCT TGGCCTGGCC CACGCGCCCG CGCCCTCACG	480
	GOCOGNICACE GOCOGNIAAAC COCTIACCAGA ACCAAANNAA CNACOCCINIC GOCOCCCNIC	540
10	GGIGAAGCGA ACCCTITTIN NCTCCTGTCT TCCCNCCCTG AAAGACCTAN TTCTCCTTCA	600
	(2) INFORMATION FOR SEQ ID NO:229:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 539 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1211RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:	
	GATCTCCTCC AGTANTOGCG TCAGAGCACA CTGGTAGCGG ACCCCTGCCA GGTAGCTCAT	60
	COGCAAAAAG ATAGCACGCG TATGTACCCA CCAGCGAGCC GGGTGATAAG GAAACTGGTA	120
<i>30</i>	COSCASCASC CATASCICIE SIGCOCTOS SITCACOCCO TOCCACITOT ATAAATICAS	180
	CACOGAAAGC CACACTITIAC COCAGTIACOG CGAGCCAATA GCACOCCCCA TOCOCCAGCAG	240
	GGTCTTCCGC GCCCGCTGCA TCACGATGTG TTCGCGCTCC ATCCCTAAGA GCCGCAGCAG	300
35	AACGIAGTIC AGCGCGGTGC CCATCGACAG TCGACTTGTC CTCCGAATGC AATCCCCACC	360
	COCCOTOGAC AGGTGTGCCG TGTTCACCAC GTTAGCGCAC TAGCTCCCGC CGCTGAGGCT	420
	CAGGAATACC ACCCCCCCCA CATGCATCGC CACCACATAC CCATATCATN ACATCNGGCC	480
40	CCCTGTTACA ACAGGAAANT GCCCNAACCT CCTCCTGCAG ANGGCCCAAA CCGCCCCCG	539
	(2) INFORMATION FOR SEQ ID NO: 230:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPCLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
50	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1211UP	
5 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:	
<i>55</i>	CATCTACATC ATGGGAGGCT AGGAAGAGCA AGGCACCGCG TGCATTTGTA GACTACACGC	60

	TATAATATOC AAATGGCCAA TACCTITIOCC CCGCATCCAA AGAAGGGCAC TGICAAGCAT	120
	ATOSTITATOS AGACGACCIT CAACCACTIG OCTOTAGOCA TOSTCAGOCA GATATITICOS	180
5	CACTAAACAA OGICTAGAAA ATGACTIGAC CTATGACGIG CCCCCCTIGA CTCATCTTAC	240
	TATOCTCAGG CCCGGCCCTC TTCTTGGCGA GCATGGCTCT AAACCCGTAA TAAGCCCTAC	300
	CAACCCTGAT ACAGGAAACA TOCTTACOCG CTGTTACACT TATAAGAAGA ATGTTATOCG	360
10	CACGCAATTT AATTGGCTTG COCCAGTTTA AGAAGTTGGG CCAACACTAA GTCACCCGAA	420
	CTATCCOCGA AGOCTACCTA TCATTTACCC TOGAACTGGA TIGITTOOCT ACTCANTCCC	480
	CAGGIVIGAAA ATTGCCCCIVA ATTGCCGCTC CAGAANCGCT ATCCAACGGA ACTACTGGAC	540
15	CAAATCTAAT TICCCCTATA ATGTGAATTA CACTGTNAAT TCAGAANTGA ACN	593
	(2) INFORMATION FOR SEQ ID NO:231:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 536 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1212RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:	
	GAGATCTCCC AGTACGTCTT CAAGCTGGGC TITGGCGGTC TAGGATAGAG CCGGCGGAAC	60
	TCAGGACTGG TCGAGACGGG ATGCTGGATC CCGAAGCTCT TCATAAGCAA CAACCGCGGT	120
35	TOCCOCCIGI ACTICATOCAA COCIOCCICA CCCAATICCIG CCACATICCA CCTGACATCA	180
	CCATTGCCCA CGATGCACCG AAGCGTTTCT GGAAGGAACA CGCAAACTAG CAAGAAGCCG	240
	ATGCCGGCCA TGATGCTAGT GAAACCAAAC AACCATCICC AACGGICATT ATGGAATAGG	300
40	ATCAAGCCAG CAATAATGOG CGCCCAAAAT CGGGCCCACN TTTAGGGCCC CAACATNAAT	360
	TACGCAATIG CCTIGCCGGG GITITTCGGN GGIGITGATT TCNCTTACCG TACGGGCCCC	420
	TGAGAAAAG AGAACTONGA GGAAATGCTG CNCCCCTNIT AAAAAAATAC NCCCATOGNG	480
45	CAGGINIGAAA GCANTTACNC TIGACTATAA ATCANCCCCC GANAANNITA NACTCG	536
	(2) INFORMATION FOR SEQ ID NO:232:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 586 base pairs (B) TYPE: nucleic acid (C) SIRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1212UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:	
5	CATCAGCAGI GICTICCCCC ACGICAACCG CTICACCGIC TTOCGIACCG TGCCCAGCGI	60
	COGCACGOCA TIGAAATGCCT GCACTGCCTG CCGCAGTCCA CAGTTGCGCA GCGATGCCAG	120
	ACACGAAAAC ATCCTCGTTA ATGCAGCTTG GGTCCTTCCG TCGTCACTGT GCGTCTCGAT	180
10	TAAGCCCAGG TTATCAGTAA CATCAAAATT TTACATAACT GCCACGTGAT ATACACGTGA	240
	TAAAGATCTA CACCCATGCC CCCTGATTGT GTAAAAAAGC AACTTTTGAA AAATTTTCTA	300
	COGFFCCATC CGATGAGATG AGCTFAGCCF AGTGCGAGTC CAATATCAGF GCACTAAGFF	360
15	TATCCAGTGA TACTIGITCT CGAGCTTTCA GCAACAGCAT CAGTTTACAA ATCGCACCAG	420
	CAGITATOCC TOGAAAGAAA TOCTACOGTC OGAACTOCCA TGATAGITTG ATACOGCCCT	480
	TACAGACCOC ACCGAAAATC CCACATCTCC NGCNGGCTTC AAATNINGTT CCGNGGTTCT	540
20	AAAGCITAGG GGVATICCCA TGCANGGGIT TATNAAATIT GANAAT	586
	(2) INFORMATION FOR SEQ ID NO:233:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1213RP	
35	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:233:	
	CATCHTHIT ACACACHTCA GIGICOCCAC CAACACOGIC GGAGGCCCTT CAGCTACHTC	60
	CAGAAGGTOG TAAAGAGTCT CCAGTAGCCC CAGGGTGCGC TCGTGGTCAT AACAGTCCAT	120
40	CTGAGGTAGC GTGTTAATAA CCGCTTTCAG CATGCTCGTA GAGGACTTCT TTACTAGGGC	180
	AGAACITATA AACTTAAATG TCTOGTCTAT GCATTCAGGG GTACGAAGAG CTGCCAGTGT	240
	COGNATORICA TOAGCOGNIC TOCTOGETTE ACTIVICATOR GANTOCCCC ATACTITANO	300
45	TNONGTICCC AAATTAACCC GGITTCCCNG GACCCTTTIN AACAAAAAGG AAAAAAAATT	360
	CCGTTTCCCC CCCNCTNCCC NINNIGOOCN AAAAATTTTT TNCCNCOOGN AAAATTTANC	420
	OCCCCONCIT AAGNOCCATT AAAAAAAAAN NNNNNTITT TITTTITINI NOGNGCCONN	480
50	NAAAAANNIN CCCCINITIN NAAAANNCNG NOGNIINNING MINIANANIN NAINN	535
	(2) INFORMATION FOR SEQ ID NO:234:	
5 <i>5</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 603 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1213UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:	
	GATEGECCAE TICACGAACT CEAGETOCGE AGGOOGAAAC GTEGTEGECA GETEGECTE	60
	GCGCGACGCC CCCACGTTCA CATACACGTA GAAGCGCCCG CCCTCCGCCGC CTGCCTGCTC	120
15	CCCCCCCTAC CGCCGCCCA GCGCGTGAGT CACCCGCTTC ACCTGGTACC CCAGCCCCG	180
	CAACCGCACG TICATCTCCG TIACGTATGT CCCCAGCTCT CCCCCGTCGC CGCCCAGCGC	240
	GCCCAGOCAC TGTGCCCAGCA CTTGCTCGTG CACCGCCCCC CGCGCCCGCA GGATGCACTG	300
20	CASCASCASC COCCENCIAT CENCECCECT CENCECCENT ATTOCHETCC TECCCCCCCC	360
	ATGCACGCAA ATCCGCTCTC GAATGCCTTT GGCCTGCCCC GGCTTGCGGT GTCTGGGGTT	420
	GATIGOCACG AATOCIGAAC CAAACIGACA CATITIGOCA AAACAAACGC CAAIGICICT	480
25	CGAACGAATT TONOGVICTO GITGAACTAA COGCOGCGCC CAGITGGGIG AAGCOGCTGC	540
	TOTTCCCACC TATCCGGTAG GGITCAGCCT TCCTGTGNIT CCACTANTGG NAAACNCCTG	600
	CTT	603
30	(2) INFORMATION FOR SEQ ID NO:235:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1214RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:	
45	GATOGITCAC GICAGOCAAT TOTGIGIOGI AGOCCACIAC ATIGIAGAGO TIATAGATIA	60
	AACCTCGAAT OCAATCATTG GOGEAAGCCA CAGCTTCTGT AGTCTGCCTA TAGCAGAACT	120
	TITCATCITC AACOCTATGT CITGAACOCG OCTITAACGA ACCCITCATC GAAGTACICG	180
50	GICTTICTAC CCCICCGCGG GAGCAGGATG TTAGCCGGAG CTICIGAATC AAACICTIGC	240
	ACTICAAACT CTIGICGIGG ACCGAACOCA ACTITAGCIG CGCCTICAGG TITTIGITTICT	300
	TTACTOCCAG AACTIGIGGS COGICATOGT ACCAMITITIC TOCCATCIGG GITAAGTICC	360
55	TICCATATON ATTGACACTG CACGCCCCAA CATTONAATT TOCANANOCC CTACCCCCCC	420

	NAMES OF THE CONTROL	480
	CTCCATTIGI CCCNAACNAA CAATINAAIT CCCCTGTTCC TICCCNA	527
5	(2) INFORMATION FOR SEQ ID NO:236:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 597 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
15	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1214UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:	
20	GATCAAGACC TGACGGCTTC CTAAAATCGC TAAGTTTAGT ACATAAATTG CGGCAAGAAT	60
	TACCCAAATC ACCTOCTGTG GAGATACGAG GCAAGCTGAG CGGGTGGATG TGCCCATTCC	120
	ACACCAGIAA CICTIIGGIG IGIGGCIGIC AIGGIACIGC ICGCIACCGC CGIGIICACG	180
25	GCCTTGTCTA ACGGGAAGCG ATGCCGGTAA ACCCAAATCA TGTAACACCC AGCGATAAGT	240
23	CCACGAGCAG ATOCTICAGAG OCTICGACCAG AACGACGTICG CATGGGTGAT GCTACAGATG	300
	OCTATOCGIG IGACAGGICG AAGCAACTGI GITCTGCITC AAGTAATAGC CAAACITGGC	360
30	GOGGTAGAGA ATGACACTOC GGTGTCTGTG CATATGTTGG CACTATGCAA GGTTACAGAT	420
	TOSCAAGOTG COOGAATGIT GGCCCAAATT CGAACAACCA GCCAGCTATT GGTATGGAAT	480
	TATATACAAC TIOGINGGGG AGGAATICCG GIGAAAAACG GCGCACCAGG NAACTITACT	540
35	GCAACGGCAA NCGGCENAATT TCCCCCCCCNC CCCGGGTTTT TGCAACCGGC CCCTVITG	597
	(2) INFORMATION FOR SEQ ID NO:237:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1215RP	
	(xi) SPQUENCE DESCRIPTION: SPQ ID NO:237:	
50	GATCAGAGCA AAGTGATTCA AAGCGATTTT GGACGACGGG TAAGCTGCCA GCGCAGGATG	60
	OCCCATCTGA CTGAGCCCCG AGGTTACGGC AATGAAAGCG CCCTGCGACT TACGTAGCAG	120
	TOGAAGOOCC TTGCTGGCCA GATTCACGAC GCTAAACAGA TTAATCTCGA ATAGGCGTCT	180
55	CCATTCCTTG ATGICCGCCT CCGCGATGCG TTGTTGGTAC GAGACACCCG CGTTCGCTAC	240

	GACAGUGTUT AGCOGCOCAT ACTOCGAGGA CACCTTATOG ATCAGGGCCT GCACCACAGG	300
	CICGICAGIG ACGICICOGA CAACATAGIC GAATTICTIG CCAIGICICG CCTICAGCIC	3 6 0
5	CTGCAATTTG GTTTCCGCCC GTGCAACCCC TACTACAACC ACGTCGGGGG TTGAGCACAA	4 20
	TUTGTUAACG GITGCUGUGU CAATGCCACG CGATGCACCT GTCACAATTA TAACCTTCAT	480
	TCTTGCTTGG TACTTTATCT TCAATGGGCC ACGAACGCTC CCGCTGTTAG TITATATATG	540
10	ACTICACOGO CIGITOGOCAC AGCICACTAG CACACTACOC TICACATOTO ACACCAGTIC	600
	GAGAATGAAT GOCACAGTIC CATTIGTAAT CATGATTATC AATACAATAT GIGTIGTAAT	660
46	TATTICATTIC TAATATOCAT AATATAGATG GITATGATTT GTAATACAGT AAATATACOG	720
15	TAAATATAAA GIATITIAAG GAATATTTAT AATT	754
	(2) INFORMATION FOR SEQ ID NO:238:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 776 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1215UP	
3 <i>0</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:	
	GATCGCCCGG GGCCTACGTC ACTGCAGATT GGCGCAAGCC AGGAACAAGA CGGACACTAA	60
	GICATTCTGT TTATGTAGAT TGGGTGCGCA GCAGCGCACG CGGCGCCGCT CATCTAGCCG	120
35	TACCOCACCA ACCOCCOCAC GCATGCOGGC CCCGGCGCCT AAACCACCAC CGTCGTGCCC	180
	GGTGCCAATG GACCGCGG TCATCCACCC CGCTCAGCCG GAATGTAGAC CAAAAAAAGA	240
40	GIGIGGITCC AGCICTCAAA TIGGGCTGGT CICAAGGGGT CGCCGCCCCG CAATCGCCTA	300
••	TATAAACOGA CAGCOGAGAC AGTCOGTIGCA CTGTOGAGGA CAGOCACACC GATGGTGAGG	360
	GITATCATTG TGACAGGCGC GTCGCCGCCGC ATCCGTGAGG CAACCGTTGA AAAGTTGTGC	420
4 5	ACASCCCCG ACCITICIOGI GCIGGGACTI CCGCCCCCCC AAAAGACTIC AAGGICCTGA	480
	AAGAGAGATA TOOCAGTAAA TTOGACTACG TTOCTOGAGA CGTCACCGAT GAAAGCGTOG	540
	TGCAGGCGGT GCTCGACAAG GTGTCCTCGG ATTATGGGCG GCTAGACGCC ATCATAGCGA	600
50	ACGCAGGCT CTCGCGCTTC GAACGCATCG CCCGAGGCAGA CATCCAGCAG TGGAAGCCCA	660
	CGITTGAGAT CAATTGTTTA GCCCGGTAAG CCTGGTGAGC AAGGCGCTCC GATGCTAANG	720
	AATCCCAGGG TTACGGTGAN TGTGGTTACC TCNNGANTCA ACNAGGTAGN TANCCG	776
55	(2) INFORMATION FOR SEQ ID NO: 239:	
	(i) SEQUENCE CHARACTERISTICS:	

5	(A) LENGTH: 546 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1216RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:	
	CATCAAGTOT TITATCACTA CAAATGAGCA 6000TTAAAT TTOCAGAATC GTITACAGCT	60
15	COCTACOCTT CCAACCAAAT TIGGCCTTTT TGAGCTAGCG GAGGAACAGT TCGCTCACGC	120
	CAACCCCCC ATCCCCCCTA CAGACCCCCG CGAGCTTTAC ATGTATTACA AATCTCTCAG	180
	COOCHTCTAT TOCTTAGOCA AAATGCCGAC CTGCTTAATA GATACTCTGC GIGCCTTIAA	240
20	TAACGAGCCG CACTOGTOCC TOOGTAACAC ACTACTGCCT GCGCTCTATC OGAACACATA	300
	TCCACTGGCT CCGCCGCAAT AATGCAGAAG AAGAGGTCCA TAGATGAGCT GAACCAGCCA	360
	GCGCCANCAG AATGTACTCC CACTTATGCG AACTCCNANA NTGGAAGGCC CTGCATACAT	420
25	TICCOGICCC ACCNACTICT OCCUTCCTIC OCTIACCACT CTIGICAACC GAAINGIOCG	480
	GCATGCCTIG CCCAAAAACC CCTGGAAATC CATAAATACC TCNCGGGGGT TANCTGCGCT	540
	cccccc	546
30	(2) INFORMATION FOR SEQ ID NO:240:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216UP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:240:	
45	CATCIGIGAA TATATECTIE COCICCATIC GIPTECCACI CCTATACACA COCCICACOC	60
	COUTACOCAC COCAACTOTT CGAGTTGTCA COCCAAGTAG COTGATOATA TACAGGTGAT	120
	GCATGOCTOC TGTATACCTT CCCACACTGC AAGCCCCTGA GTTGCTCAGG TGTTACTGCG	180
50	CCAGATOGIC ACATOCCITC OGAGTATATA GICTOCOCTT TGAGCCACTT AAAAGGGCT	240
	COCCOCCIAG CCCCOCCCOC TOCTCACCIC ATTCCCATCI CCCCCCAACC GAAACCIAAC	300
<i></i>	ACCOCCUTET AACCTCCTCC TCATCCCTCA GCACCCCCCT CTCCCAATGT ACTTCCCATA	360
55	TOTTATTTTA COTTTATGIT ACCTATOGAG GGTCGCTCAG GGTTATGCCC GCGGTGCTGC	420

	CONSCIENCE AND CONTAINED CONTAINED CONTAINED	480
5	AAGCTIATAT CICCUTGCCT GATCCCCCAT NATGCATUTG AAGTICACCA NAGGACAAGA	54C
	AACANACNCA AAAAACNAAA TOGITAAGTA AAATIGATIII OGIGITOOCN OCT	593
	(2) INFORMATION FOR SEQ ID NO:241:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 592 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY, linear	
	(11) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1217UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:	
	GATCTOGTTT CTGGGGATTT TTATTGGGTT GGAAGAGGAC CTTGGGGCCTA CACCACTGAA	60
	GETGTGCGAG TTCTCCAGTT GAGGCCTATT GAAGTGCATA TCTGATGATA GAGCGCTCAA	120
25	ATGITCTGAT CCTGACATCG AATAGAGCGC ATTITTCTGT ATCGTAGCCG CTGGGTTCTC	180
	COGICOGATA TOTTICATET TICCACTOCT CITUTOCATO ATGIACACCA TATTICATOT	240
	AATCOGTIGA ATACCATGAG GAAGIGGACT CATTIGATIG GCTGGTGGCT GCGGATGTGT	300
30	TACCATTGOC GTAGAGGTTA GAAAATTGGT GAGTTTGCCA AAGGAAGAGC TGGCTGGCTA	360
	GCAGAATGAT GGACTGGCGT TCAAGCGCCA TGTTTCNTCC TTTCGAGGTT AAAAATTAGG	420
	AAGGGGACAA GGACTCCCCT GAATCCTACT ANCCCCTTCT AAAACTTGGC AATATTGGTC	480
35	CCCTGAACAG ATGCNCCCNC CACATCCCCC TATTAAATTT TTTAACAACC ATATTTGTGG	540
	ANACCINCAA NIIGAACIIG CONGONAANN GATICOOCIN CCICCOCAGA IN	592
	(2) INFORMATION FOR SEQ ID NO: 242:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 558 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1218RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:	
	GATCHTTGTG GGCCACGACG ACCACGGGAG TACCGCCCGT GGCTTGGACG TACCACTGAA	60
	AAATGITCTG CATGAATCCC ACCTTGATAA TACCCATGGA CCACTGGAAG TTCTGCCACC	120
55	ACCICACICAC GATGOGTICOC ACACGACCCA CTCCCATCAT ACACCTICATC CCCAAATTITT	180

	GCAAGTACGA GAAAAGAGAG ATCGAGTITCG AAGCGATGTG COCCOCAGTG GTTGAGTGCC	240
5	CCATCACAGA CACAAACCCG GAAGTCCAGG ACACCCACAC CAGCTATCGC GGCGAATCGG	300
	CCACGAATOC ATACTICGIC TOCACCGTCT TOCCGTOCCG ACAGCACCCG CCCTOCAACA	360
	CAGGCCCATT GGATGCTCCG TACTGGTGTT TCAGCTTTCC GCNAAGGCCT TTACACCATC	420
10	CGTGCTTCCC AGTTCCCNCG AAAATATACC CCNCCTTGGT ATCTTCCCNT GAAAAATCAC	480
	COCCGAAATT TCCCACTTGA ANCCTCTTTC ATTCCCCCCC CNTGCCCTCC CCCACANCCC	540
	GANATICACA ACTANTINO	558
15	(2) INFORMATION FOR SEQ ID NO:243:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 604 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1218UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:	
	GATOCACAGT TECCOCACTG AACTEACTAT COCTCAGCAA COGCAGGTICA TOGTCAAGCG	60
30	THE FRACATE ASSETTEACE COSTAGRICA TRATSCOTOS GARGGATOCE TROSTAGAST	120
	AACAACCAAA AAGGCATGTT GGATCAGCTG CATAAGCTAG TAAAAAAAGAG CAGACGCCGC	180
	CTGAGGCACT AAAGGCAACG ACCCGGCGAT ATATGATAAA TAGAGAATAT AGAATGITGC	240
35	CACTAGOCCA AGATGACCTG CATTGAGATC CAGCGACAAA GTGCCAGGAA TTAAGGGATC	300
	TTCAACATTC CTGATCATAT GAGAAGAGCA ATACAGGGIT AAAACGGCGG CGTTTAAAAT	360
	TTCACAGACT CAATCAAATG TTTCACAATA CCTGGTTTGG ACAAGTOOGA GACATCCCCC	420
40	TRACTGATCT GOCTOCCCCA GOCAAGGATT TTGCGCCATA TACGGGCCAT ATTTTGCCTG	480
	ACCATTCTTT TOCATTCCTC CCCGAACCAC AAANACCTTA GOGGCACNAA CGGCCCCATT	540
	CCCNANNGAA AAAAAAAATA GGTGCTTTGN ATNACCCGNA CCCCCCCCCC CCCCINITTIC	600
45	CONC	604
	(2) INFORMATION FOR SEQ ID NO:244:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 550 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SCHROE:	

(A) ORGANISM: PAG1219RP

5	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:244:	
	GATOCTGATA TIGIACOGGO TOATAAATAC TITOGATATO TITOGGACAAT GTATOGTACO	60
	CGATACUTTI CAGCACATIGG ATCAGTATAT CATGCTTCTT CCTAAATGCA GCAACAGTAT	120
10	TGAGGACTIC CTICAGACTG TCCGTCTGAG TATCTATCTT CATAAAGATG AACTTITCGG	180
	ACCICITOCT CATCAGCICT CIGATGAGIG ACGITGAATT CTTTTAATAG CGCTTCCCAC	240
	TOGETTGATA ATCTTGATAC AGTOGECCAT AGTCCTCCCT GGAAAGAAAT GAAGTCGGAA	300
15	GAAATCAGIT TIGGCAGCAC TCTCTCAGIT TCTGATTCAA CTCCCGITAG ATATTTCCTC	360
	CCACAAATGT TTACGGCCCT ACAGTTGGTT TCTTTTGANA CCTTCACTTC CNTCCNAAGC	420
	CATGAAAATG ANICCATCNC CNCCCCCCCA CITTGINAAA NITCCCATTC GCAAATINCN	480
20	CASTIGAATI OCCOCANOOS GSIGITOCOCC GOSTTOCCOC NAAAAAANAC NSAGOOGOST	540
	TTTAAAAAAN	550
	(2) INFORMATION FOR SEQ ID NO:245:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 598 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
3 0	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1219UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:	
	GATCOCOCCE CTGCCCCCCC CGTCCCAGGTG CCCCCCCTCTTTTCCCCAAA	60
40	TCCCAGCOGT GGGCGGGTPT CGAGCTGCTT GACCTTCCGC GGCATGTCAA AGTGCGGCGT	120
	TAGTITICGTC CTGTAGOCGA ACTGTAGCGG CGATOCGACC GTCTCOCCGA CGGTGGGGAG	180
	CAGGCCCTCG GCCAGCAGCT GGGGAGCAAA GAACTTGAAC GCATTTGACA CGGTTGGCTG	240
45	TITIGASCIOC ASCITOCIOGI CATACGICAG GAACIGATAC TOSCAACCOG ASCACITICCC	300
	GAAGTACTTG CAGTTGATGA GGTCGTCGTG GCGCATTTCA GCAGACGTCT GCACCTCCAG	360
	CAGAGACOCT TOGOCGTAGT GOGGTGTGTC TTGTGCACTT GGATGGTGAC CACGTCGCCC	420
50	TECCCACCC AAATTECCAC CCACCACTAC TETTTCCTTE TITTCCTATCC TCCCCCCTG	480
	TOCAACAANA COCATOCOTO COCATOCACT TTACNICOAC ACATOACTITI CATOAGONOC	540
	GETTERTOTT CTOCTOCATO GOCCCCCGAA TITINTTCAGA ATGATTACTO CTOCNONG	598
55	(2) INFORMATION FOR SEQ ID NO:246:	

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1220RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:	
15	GATCOCOCAG TTGTCOCCCT CAGCCAGCCG CTTTTTGGGC ACGCGCGGGA GCGTGTCCAT	60
,,,	GTACCCGTCG GGCACGCCCC CGTGGCCCTC GCCGATCAGC TGCAAGTGCT GCTGTAGCTC	120
	CTCCGGCATC AGTCTCACGA TCACATTTAG TAGCGCGGTG CTGTGCGCAT CTGCCTCCTG	180
20	CAACATOTCA GCCAGCTOCC TGCGAAGTTC GGACCGTGTC CCCTGGTGGT CTGTGACAGT	240
	TAGIATICIT GGCCGCAGIC GGICGCACAT TGGCATCACT TACTATTGTC GCTGGGCATT	300
	CACCTCCCIG GATCACTOGT CCTCCCCGTG GCGGTAAGGG GCAACAGACA GCCTTTTTTT	360
25	ATTITOCICT ATAATACOCT OCTCTATGTA OCGTATACTA TACAAGTCTT AACTAAGGTG	420
	AAGTGAGAAG TCATHATTHA GCTGCGTTTC GGCCGGTCAT GCAGCCGGCT ACCATATHAG	480
	CATOCCOCTE CCCTTCACCC CTTTGCACCT CCCCCAATTE TTCATGCCCA ACCACCTTAT	540
30	GGAGTTCAAC CTCACGGAGA GGTTTCCCGAG ATCGAAAATG TCACTTTCGG CAAATTGCGA	600
	CACACCGIAA TACTCOGCAA ACGAGITCTC GACACCGCTG AGCTCGTCGT CCACGITCGTC	660
	GACATAGGAC AGAAGAGGCT TOGTTOGGGC TGGCCGGCGCC GCGCGCGCAA CCGCAACNGC	720
35	CCCCCCANAG CTGGGGCCANG GCCGCCCC	747
	(2) INFORMATION FOR SEQ ID NO:247:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 777 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1220UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:	
50	GATOCAGAAT ACTOGICOCA CCACTICTIG AACCOCOGGI ACAGOCOGG GICCGIOCOG	60
	TOCAGOGOG COTTOTOCOC COOGTOGAAC AGOOGOGOGT COTOCTOGTA CAGGTAGOTT	120
	GECELCAGEL COCAGOGGC GCCEAACCAC CACGLCLGCE GCLLGCCCCC CGCGLCCCAC	180
55	GTCTCAAAGT AGCOGTAGTT GAGGTGCACG GTCGGCGCGT GCGGGTTCAC GGGGTGCATC	240

	ACCAGAGAAA TOCCOCAGOC GAAGAACCOC ACGCCOGOCOG CCGOCTGCOC GGTCACGGGG	300
	TOOGTIGGGGA GETGCAGETT TYTIGTIGCTICG GCCCGCATGG CACTGACGGC TGCCGGCGAC	360
5	AGCTCGCCGT GGACTACCGA GACGTTAACG CCGGCCTTTT CGAACGTGGT GCCGTGCTGC	420
	AGCACGCACG ACGTGCCGCC GCCACCCTCC TTGCGCTCCC AGGAGTCGGC CTTGAACTTG	480
	ACCUTICIOGA TOSCOTOGAA COCOGOCTOTA ATCTOGOGOT GOTTOCOGOG CACGAGOTOT	540
10	TOCATOCOCT COCCCATCTG GCGCCTCTGG GCGCATGCCA TTGCTGGGGC GCCGCAACAG	600
	GCGAAATNAN CNGTGCGCCC GCCGCCTTAT ATAAAAGCGT GGCACGGGTG TTTTGCCCAC	660
	GNCACCANGG GCTGCNAACG TOCGCGCCAA NANANCCAGG GTCCCGGCCA NAACACNTOG	720
15	GCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	777
	(2) INFORMATION FOR SEQ ID NO:248:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 537 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1221RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:	
	GATCHCICCT GITTGCCCTT CCAACCATCT TCCTCCCTAA CTCCTTCCCC GITTACGITT	60
	GAGGTTGCGG GCACGTATGC TANACCGAGG GCATTGCGGG GTTGAGGGGA AGAGGTTGAG	120
35	ATTATGAATG ATATATACTG TTATACCOOC TOCOGGTOGC TGTGCGCGTC ATCACGAGGG	180
	ACTTACAAGT TCAAAAGGTC TTCATCGATA TTTACCAACT TGTAATAACG CTCTTGTGAG	240
	TCTGAGTTGG AGGAGCOGGG CTGGTCGCCA TACTCCATCA AGGIGTTTAC CATTGCGGGT	300
40	GTATACCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCCT CCTTTAGGAA CATCAAAATG	360
	GTOGTIGTICC ACAANCNOGA AAACCTATCC TGTTAGTINNA GAAGGGTTGA GAACACCOCT	420
45	AATOCCTTAG GCACTCCACC ATGGTTTTAT CCGTACCCCA TTACCCAAAT TTCCCCCAAG	480
70	TOCCCTTINAA CTTTIGNOGAA CCCCCOCNAA ATNOOCGTTT TTAAAACCON AAAAANG	537
	(2) INFORMATION FOR SEQ ID NO:249:	
5 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 584 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: INA (genomic)	
J.J	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1221UP

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:	
	GATOGACOCT ATCAACGOCT TGCAGGCTGC TATGGAGGGC TATCAGGTCA CCACTATGGA	60
	CCAGTOCOCC AGCTACOCCC AGGTTTTTGT CACCACCACC COCTOCAGAN ACATCATCAA	120
10	GAAGGAGCAC TTCTTGGCCA TGCCTGAGGA CGCCATTGTG TGCAACATCG GCCACTTCGA	180
	CATCGACATC GACGTCGCCT GGCTAAAGGC CAACGCCGTC GANGCCGTCA ACATTAAGCC	240
	ACAAGICGAC COCTACITICC TITICCTCCOG CAGACACGIC ATCCTOCTIG CCGATOGITA	300
15	GACTAGTCAA CCTAAGCTGT GCCACTGGCC ACTCCTCCGT TIGTCATGTC TIGCTCTTTC	360
	TOCAROCAGT CTTTGGCACA GATGGTCTCN TTCAAGGGCA ATMAAAAGGC CTTCAAANAA	420
	ATTINITINIT TECCCAAAAA ACOOCCITCA AANOOCOTIT CATTETINIC CNAAAATTON	480
20	AAAGOCOCNC CCATTTCCCC CTAAATTTGG GTTFINNTTT AAAACATTCC CCCCCCCCCA	540
	TITCCOGGIT COCAAAAGGG INTITINGGGG NCCCTTAAAT NITA	584
	(2) INFORMATION FOR SEQ ID NO:250:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 535 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1222RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:	
	GATCGAATAA TAAAAGTOOC TAATACTTOG TAATAATATA ATAGAAAGGG AAATAGAAGA	60
40	GAAGTCAAAT GOGAAATAGT CAACGOCGTA CTAGGTGAGT GTTCAGTTGC ATGGAATCGT	120
	AGICAGAGAG GITTATCAAA AACOOCAGIC GICTGATGAT AOCAGIATCA CGAAGTOCTC	180
	ATGCGCCTG CATACAATGG CAGGCTCAGC GCAGGATCAA ATGGATAGCA GCGGGCGTAC	240
45	CCCCCAACCG ACTCAGTCCC TCCAGTCCCC CCCGTCGTAC TTCACCCCCT TCACGTTCTT	300
	GTAACGTTIG CCACAGACCT CGCACCGGTA AGGCTTGTCC TTCTCGAACC CATGCCCGTC	360
	TOGATAGOGC TOGITOGACT COGOGICCAT GATOCTAAAA GTGCCCGTCT GOGITTTCAT	420
50	GAASCTTTIG ATTCTGGIGG CCGIGGITTT AIGGIACTIG AGICCCGITT GATCCIGGIT	480
	AGICITATOG CAGCOCATGA GGGACNINTIG AAGGCTTINIC CCCINCCITIGT CONON	535
	(2) INFORMATION FOR SEQ ID NO:251:	
5 <i>5</i>	(i) SDQUENCE CHARACTERISTICS: (A) LENGTH: 581 base pairs	

	(B) TYPE: nucleic acid (C) SIRANDFINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original source: (A) Organism: Pag1222UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:	
	GATICTOSCTO AGACOGTICAC COACGTTGTC TGCAAGGGCC TCCGCCGCTT TANCTGCCTG	60
15	CCACGOCITE GABCACGCTA GCTGCACGCC AAACCCGCCC ACCTCCGACC ACTGCCCCTT	120
	GOBCAGCOCC CACTICOCAGT TOGTGCCCTG GATCAGCOGC ACAGCGAGCG CCATCTCACT	180
	GTACGTCACG TCGOCGCCCA ATTGGCGCAT CAGGCGCCGG AACGGCAGGT TCCCGACGGT	240
20	GGTCAGCOGA GAAACGATCT TCTTGTGATG CAGGTCCAGC GGCTTCTTCT CCTGTGCAAA	300
	GRAGOGIGIC TOGICARACT GGGCGRACAG CTCGCGCTGC CGGGCGCGCT TGTIGCTCAA	360
	TITOCTOCTOC COCTOCTOCA CCTGCGGCAC CTCTGCGACC GCCCCTCCGG GGCCGCGGGG	420
25	GCCCCCTGCA TCTCGTCGCC GGAACTCCTG CTGGATGCCG TCAAAATTCC ACNATTTCTC	480
25	CCTGCNCNGG AAGGGCCCCAA MFFTTCCCCCA ATNANCNCCA ATGAACCATT GWINCCCCCN	540
	TOSTINCAAA ACNAATTIIG CCCCCCCCCG AGATTNICCC A	581
	(2) INFORMATION FOR SEQ ID NO:252:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 544 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1223RP	
±0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:	
	CANCESTITI CACCICAATI CONTICIOST COCOCAGING GIGATECTEC TGATECTGAA	60
45	SCIGRAATIG CIGITICIOC IGAGCAAACT GCIGCIOCIG TIICATCCAG GGATICIOCG	120
	CASCAGCICA GICCGGITIG COCCUICTCI OCTIGIOGII CAACAAGIIG TIAIATAGCI	180
	GEFTCATACC TIGGGACGTC AGGAACTGAC TGACATTGGC GTCGCCCTGC GGGTGGTCTA	240
50	SCANACOGAG CATOSCCICT CICICCIGIA GAGTITICIT TOCCOCCAIC TCANACITICC	300
	TAGATTOCAT TATCAGCOCT TOTTOCTCAG CAATCTCAGC CGCCGACCTC GAAAGCAGCC	360
	TOOGTCAAAT ACTICTICCG CIGIATITCC CIGGICTITG GAATACGCTA GGATGGIAGT	420
55	ACCOGNITION COCCONGRAMA TRATTITIOS CANACONEGI TAAAAANICIN	480

	CCCGTANTIC CICCAACOGT CCTNVANNOG NCNTAAANAN ACNOGTCNGT AAATNATAGC	540
5	MACC	544
3	(2) INFORMATION FOR SEQ ID NO:253:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 608 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1223UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:	
20	GATCOCOCCC TIGAACATOG ACCITOGACAC GOCGAACTOG COCTOGACCC COCCCACCCC	60
	TOOGLOCTOG AGCICIGIGT GIGOCATOGT GOGCICTGIC TIGAGCTOGC GCACAACCGC	120
25	GECGGATATE OCCTGGACCC TACTGGCGGC GAGGACATET GGTAGCGCGG CCGCCTGCTC	180
25	GEACTIGACC ACGACAGIGG CGACGCGGAC CITGGIGGIC GGCGCCGIGA ACGCCGIGIT	240
	CALTIGUARAG TOGTICCGAGG GOGGGATGGT GOCGGGAGGG AGGGGTTTTG GTGAGGATGC	300
<i>30</i>	GTGTGCGCGG CGCGACGGCG AGCGAGATGA GCTGGCGCTG CAGCTCGGCA TCTGGATTGC	360
	OGICACETCC IGAATCIOCT COGIOGICAG IICTOCGIAG ICICCOGAAA AACAGGAAAA	420
	ATGGTTGGCG GCATNGTTCA ACATCCTTGG CNCCCTGGGT TAAAAATGGC CGAACTGGNN	480
35	GCCGATTTCC CCCGAGAACCC ATTITGTTAT CCCCCTTCCT TCTGCNINCC GATTTTTTTG	540
	CAAAANINAA AACCOCCCCT AAGAAGANNN CGGGGNVGCC CCNCGGGGGG TITTTTTTTC	600
	CNCCCCCA	608
40	(2) INFORMATION FOR SEQ ID NO:254:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 731 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1224RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:	
55	GATCAGTAAC AACCATAOCA GOOGCACCTA CGAAAGCATT CGATACATTT TTAATAAATT	60
00	CERCEGERS TREFRENCHT CHICKESTER CENTRACEC CHOCCESAG ARCHESTER	120

	AGCTICTTCCA AAGAGAAATT TGTGTAACTT CAGAGTCAGC AGCGGACTCA AAACAGCACC	180
	TCAACCAAGC GETTGACCGC ATAGETTCAT TCAAGCCCAA TAGTTTTTTGG AATAGATCAG	240
5	GGGGAAGAGT TOGAACATOC GTACOCOGTC TCCGTTTTAC TCCCCTAACT AGTTTTATCT	300
	CTACTITIGA AAGATAGTCG TAGTCOGGAA OCTCAACATT GTAAGTCAAC AAGCTAGGCA	360
	AAACTGTAGT CAAGATTGAG TTCCCCTCAG GGTTTTGACA ACAGAGTAGT TATTCTCTCA	420
10	CTCCCCAGGC AAGATGTACT GGTATAGAAA ATCCAGTTGA AGCCATAACC AGCTCGTTGT	480
	CACAGTOCAC CAGAAGATAG GANACATOAG GTTGAAGAAT TOOTOATOTA GGTTATOTGC	540
	TOCCITICCT GITCTECTTT GGACCAACOC ACAACCCNAA AACCAACOCN AAATCAAANA	600
15	CONSCITECT TECTTENTES SECONATES ANAGETTIT GASANSSTIN TESCHETISC	660
	COOCCAANT AAAAAAAAAGC CCCNCAGGNT CNACNATATT ANCANTCCCC NAAAAAGCCC	720
	TTCTCMICTA A	731
20	(2) INFORMATION FOR SEQ ID NO:255:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 762 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1224UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:	
35	GATCGGGTGC GGCACATGCC TCATCGGGCA GGTGGGGTTGG CGGAGGCATA AACCCACCCC	60
	TOGITGITOC AGIGAATAGG TATOGGTACA GOCTTOCCGG CCACGAATGT GCCGAGACGT	120
	THEASCISCE ASASSSACCE GACOSCACOS GIOGACIGIT GOCTIGOTIG GACOCTOCAS	180
40	OCTITACISADE COSCOCCTIC COSCASCACAT GATGICCADE TGTOCATTICG TCCASSTOCG	240
	CACTAACCAT GCCAAGGGCA TCCGGCCAAG GCGGATGGGG CTGGACGGGG CCAGGGGGGG	300
	ACGACTATCA CTAAGAAATC ATCGATTAAA ATATAAACTA CATAAAGTAA ACGCCCCACT	360
45	GAGTOCACTO TOAGCOCACT AGCAGOGAGT AGCOGTAGTT GAACCACTTG CNTGCGATCO	420
	GTGGCACGAA GCGGAAGTAA CCGGAACTCC GATAGTTCAG AACGAAGAAC CGAAAAAAGCC	480
	TTAAAATOOC TTCACNCCTA GSTCCCCCAA CNGGTCCTCC TGTTTGCAAT TAGGGTGGGC	540
50	GGAAACCCAA ACTGCCCANT TGTTNICCAA TTCCCCCCCAG GCCCCAATTT NAATTICCAA	600
	ACCNATONON ATOTOGOCTG NATOCOCCCC NITOCOCCCC TCAATGGCCC CGAACCTTTT	660
	MICHOCOCCC COCAAGGGCC CTIGNGNATT TITTITOCONG CCCNCCOGNT INTCITAAAA	720
	Medicecte ecompage climani illineem ecomecan intelliman	

	(2) INFORMATION FOR SEQ ID NO: 256:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 710 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1225RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:	
	GATCCTITTC TITCTICTIC CCTCCTCCGA CGATTCCCTT TITGAGCTTG CCCACTGCGC	60
	CCAACCCACC OCCTATGACA CTAGTACOGG COGACAGACC AGCOGATAAG CCCTTATTOG	120
20	CAAAATCCCC AACCTITGTC TOCACCTTGG TAACAGAGAC AGTGTACCTA GGAGAAAATT	180
	TCAACTTCAA GTAAACAATA OCACOGTCCT COCCGTTAGG ACCAGTTAGC TOGACTTCCA	240
	TICCOCTITIC ACTICICICOS TOCACCICAS CIACASCICAT COTICOCGTIC CCAATICACAT	300
25	CGICACTGTT TOCCOCCATCC CAGTOCATGA CCTTGATGCG CAGGTAGTTG TTAATCCCGGT	360
	TATICAACIG CAGGGAIGIG TICIGGIICC AAACAGGIIC AAGCGICIIC TICIGGGIIC	420
	ACCOMPANA TRANSPORT DESCRIPTION AND ANTICACAT ASSESTED ASSE	480
30	TIBOOGITICO GETCACCAGE TAGACCOTGA CTOCATTITAG AACCIOCAGT GITAGETCOC	540
	AGIGFIOGIA TCAGFFTGCT TGINGCATCT CNAACCCAAA AACGAACCAC AACCGTTANN	600
	TOCTTTICNG ACCOMAGOIT NITTACAANN AGGITTAAAT TACANITTON ATTINITTICN	560
35	TOGAANGAAC COCNAAGNET CONCOTETT TACTGANONI NATCOCNAAT	710
	(2) INFORMATION FOR SEQ ID NO:257:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 750 base pairs (B) TYPE: mucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1225UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:	
50	GATCCTACTG GAACCACCCA CICAGGAGCA GGITAAAAAA CCAGCCAAAG TAAAGACAGA	60
	GACAAACGTA AGCATCOCAA AGCAGACCCC TACTCCAAAG TCTAAGTCGG CTTCAGCTTC	120
	GTCTTCTAAA GTGCCTACAC CCCTGTCAAA GCAGGAGCCC GAAGCCCCGT CTACCATTTT	180
55	TODAY TO THE TOTAL TOTAL PROPERTY OF THE PROPE	240

	ATTIAGGAAA GCATCCAGIG ACTITIGACAA GCCCTTIGIG GCCGAGICGA ATGAAGITGC	300
	CGAGAAGCCG TCCGGGAAGG CCAAACGGCA AACTACTCCC GCTGCCAGCA AATTAAAGCC	360
5	COCTOCAAAC AAAATAAAGA COCCOOCOCT CGATGAAAGC GAATCTGATT TTGACCTTGA	420
	CCTCAGCGAC TCCCAGCCCG CCATCGCCCC TAGAAGTAGA GCCTCGCGAG CTGTCGCCAA	480
	AAAGCCAACC TACGTAGTTG ACCTTTCCGA TGACAGTTTT GTTGATOGAG ACCCCAGAG	540
10	ATGITGAGGA ACCGATACTG ACGAATCCTT CCAGCICTGA CTAGCACTCT AGCTCGCCCA	600
	TTGACAGINC NCTACCITAT GGAGGNITCC GAAATCCNIT GAATACCCCC CGITTTTTAC	660
	TAAAACCCCC NCTTTCCTTT TCACCCCCCA ACCCCCAGGG GACGAATACT TTTTTCTTTA	720
15	CTITICIATCA NECESTICGI CICCINCCONI	750
	(2) INFORMATION FOR SEQ ID NO:258:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 729 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
05	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1226RP	
3 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:	
	CATOGICCIC GCATGGCAGC ATCAGATGIC ATATCGCCGA AGCCITTICCA TATCGCCGCT	60
	ACCAACGATA CGACTTCCCC TCCTGCTTGC GCTGTTGGGG TCTGTGAGCG TGCTGCTATT	120
35	GCTGTCGCTG ACGCCACACA TGTGGCCTGG ATGGCCATCT CCGGCAGCAC GGGAGGTCCC	180
	GECTICACCA GAETCACAGE COCCESCTIC ACCAGAGITA CAGGOCCCGG CTICAACACA	240
	GCCACAGTCC CCAGCAGGGT CTAAGACGCT ACTGCAAGAC TTACTGCTAG ATAGCAAAAA	300
40	ACCOGAGGG GCCTCTACGC CACAGATGCA GTGCAAGCGC TACTTTGAGG GCACATATCT	360
	CCCCCACCCT TCCTCCCCAA ATACCCTCTT CCCCATCCCA GACGACTTTC TTACCCCTAC	420
45	GCAATACACA GCGAGGCTGT TGGAGCGGTG GCGCATATTT GCTGATTGTT TCGTTATTCA	480
45	CATTICCGAT TITCAAATAC NCTATCCAAA CAAAAAAAC TGCCCAANTT CCATCAGCGA	540
	ANTICCCCTT TCMINGGCAA AAAAAAAAAN NGAGGANATT TIGCCTNICC CCNGAATTIC	600
50	NCCCGGGAAA ATTTTTAAGG NGGNITTTTT GNAAANGGGC CCCACCAAAA NANAAAAGGN	660
<i>-</i>	GOCTITITIG GAAAACOOOC CCTTTICCCC GONGNGAACA AATTINVIININ GOGGACGCCC	720
	NGAATITIC	729
55	(2) INFORMATION FOR SEQ ID NO: 259:	
	(4) cross makes catable (marticipal)	

5	(A) LENSTH: 742 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1226UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:	
15	GATCOCTICA AATTICCAGC COTTGATATT CAAAGAGTOG TCACGITCCG AAAGATGGIC	60
13	CTICICITES TETETACETT TOGAGOSCOG COCTACCOGG COCTICOCCG TIGICICCAC	120
	GETECOGIEC TETECTATES GEACATECTS GATGITETTC TECAACOCAT TAGCAAATGA	180
20	GITTTIGIAG TOGIACITAG GAAGIFTATA ATTTAGOCTC AGITCIATAC TOCCOCTAAT	240
	ACTITICACCI GGAACAATCA TOGITATIGIG CICACCICIG GOGIGITICIC TAGOGIATIC	300
	COSCOGISCT TCASCATTIC CITICITICATE CATOSITICOS TATOCATOCT COCACTICATE	360
25	TACCCACTIC GUATCCACCT TCTCACCCTC CTGATGCGAT TCTGGACGCC GGGGTTTCAC	420
	CAGOCGITAG CAATGAAGIT GOCGITOCCG GITCAAAAAA AAANACOGGN GOGGOCNTOG	480
	TAANCCCONC CCITTAAGGG CGGCCCCATA TICNCNATNA CCNNNACCGC NCCCCCCATN	540
30	ACCCCCCAA AANAINITIG AAAAAATTGC CNIACCITIT IGNGGGAGCC CACNONCTTA	600
	NATAACCCAT TITTIGAAAN ANGCONNICT TITNITITAAC NOCNOGGITC NONANTATGC	660
	NEGOCCAAAA TIAAACCINC CCCCONAAAT CNAATCINITI TCCCCTCINAA NACAAAAAAT	720
35	ATTIMMITT NOOCOCO AT	742
	(2) INFORMATION FOR SEQ ID NO:260:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 744 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOROLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1227RP	
5 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:	60
	CATOCATCAA CAGACTGGAG AACAGAGAAA GGTGGTGCCC CTCGAACTCG AACAGTTTTT	120
	CCCOCTOGAT TITGATGAGA TATTACTCCG GGATACGATG CAGAGGAACG CAGCTATGGA	120
55	AGAGGAGGAC TACAGGGAGC TGGGGAAAAG AGATATTGAG GTGGGGTTCC AGAACACCGG	180
	CGICACGCIG GAIGACAGGC TOCAGICGIT GCCGGCCATA TCGCTCTTCG GGAGGIATGI	240

	ACCOGATATC GACCOGATGT COGAACCOCT TOCOGACCOCG GACAGCCACA TCATOGTGTT	300
	TOCOCCGAÇA AATGACOCCA TTACOCCGAT COCCAAGAAG COSTOGGAGT ATCCACGGAA	360
5	CATCGACAAG TIGGAGCAGG CAGGCGGGTC TGCGAGGGGAA ATCCACGAGG CCATCCAGGC	420
	GAATGIGAGA COCTITIGIOC TAACCCACGI COTTICCCAC ATCGACCICI CTAACGIOGI	480
	TODOGRAGAT TOCTOCADOC GTOTTTGACA AGOGRACTICA TOCCAAGAGO ATGCAGOGGA	540
10	TATTCTTTTG CGCCCAGGAT GCCAANDGTT TTACAGTIVIC NTCCAANANN GCCCGGACCT	600
	TOCCOTTNAG ANGITACCOC CCOCTCTAAC OGTTTATTTT OGTINICACN CCCCCTTOCN	660
	TOOGAATING AAAACCCTOC NOCTONOCCN NOCCAATNAN TONCTIGAAT CCCCONITING	720
15	GAACONION TINOCCCCAN CNCC	744
	(2) INFORMATION FOR SEQ ID NO:261:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 768 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1227UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261;	
	GATCATTIGC COGACCAAGA AATATTITCA CTCCTCGAAG ACCTGCCCAC TAAACTICGT	60
	GICTOGTTAG GTTCCCCTCC ASCTGATGTG CTAGATATCG AGGTGAGAGG TAASCTTATT	120
35	GAATACTICCA TIGAATACTICC ACTITIATTICC OGTICOGAAAA TAGAACATICC TACATOGACG	180
	ACTITICATICA CTICACCATICA TICAAACACGAA TICTICAAACCT CTICATTICOGA ATTAGTICCACG	240
	CAAGITAATA CCCAATOCIC GOCTITAGOC TCAAGOGAGA TATCOGTAAC AGCTCTATCT	300
40	ATTCTTCCCAG CACTIACGAG TETTTTACTAA ATTTTCCCATA CAGITCATCG TATTTCACAT	360
	AACCITAATG TITCATTOOC AACACAAGGC TIGCOGATGT GTAAAGIGOG COGCGTCTCT	420
	GCATTCAAGA CAGCATACAT GAACTITCAG TITTATACGC CGATCATGTT GATTICTAAT	480
45	AGGGCTAGTC CATGGCCCCT ACCTATAATA TACTACCATC CAGCCCNCCG AACCGNAACN	540
	NNATITITIA TITTAATNAA ATTITIGGGGG NATNOCACAC NNNOCCTANC NNGGANITCC	600
	AATGITTAIT TAANINAAAA ANCAGIIIGA AGGITAITCC NNONCCCCNC CCCACCNGNI	660
50	TOAAAACCAA ACNANACCGT GAACCINGIN NTCCCCCNCA AGGAGNOCCC CCCCGCTTCN	720
	AAAAACGGIN NCCITINCON CCCITGCNCA ANATTCCCCC CGCTGCCC	768
	(2) INFORMATION FOR SEQ ID NO: 262:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 738 base pairs	

	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1228RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:	
	GATCCATTIGG GCCCAACCAT GCTAATGAAG TICTTGCCTC CAAAACCCAC ATTGTGCACA	60
15	CCCTTGTACG ACTTGAAGIT CTTCACCTCT AAGCCAATCA GCCTCCCCAT CTTTTTGAGA	120
	CACTIGAAGCT CAGTICTAACT GCTCTCGATG TTGTTAGTGC GCTGTTAATA TGTCCAAACA	180
	AACCCCATCA TOSTTOTCAA GAACTOCOCC TTCOCATACA CCCTCAGCAC GTAGCCCAGC	240
20	OCCOCCOCCO COCCCAACAT CACTICAGATC COCAGGAACA COCCOCTICCA CAACACCACA	300
	AGAAATACCA AAATCGCCCC AAACCTTATG ATGTACACCA TCACCAGAGT CACCCCCTGA	360
	ACCCAGATOT GCCCGTGGCC CATCCCGACC ACCATCGACT GCCTGAATTA GTATATTCCG	420
25	TOCCACCTIGC TOTTTCATAC ATRICCACCCC AGGGCACACC AGGGGGTAAC AACCCCAAAG	480
2.5	CNCTCCCTAG GCAGCGCATG CAAAATATCC ACNCTCCGCA TGGCATCTGC CNNFTGGAAA	540
	GGGGNCCCCC NAAATTTGGG CCNAAANCCC TTAAAAACCNC CCTGTGNCCN CAANNACTTC	600
30	NAATTTCCCC NITNEGCCCC CCCCCCCCCC CAACGGCAIT TAAAAACAGGN GGCNGNEGGA	660
30	AAAACCCNCG AGGGENITIT TITINGCCCCT TICCGAAANA ANCCNCCCC CCNCGGAAAA	720
	AAATATTITT TITIMGGG	738
35	(2) INFORMATION FOR SEQ ID NO: 263:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 748 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1228UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:	
	GATCATOCCA TTCTTACOCT TTCCCCACAT GGACGCCCAA ATGAATTTCT GTGTATOCGA	60
50	GENTECTICAC GATCCAGCTG ANGCAGGACA CGACAGCGAT GTGACGCCTG GTTGTATGAC	120
	OCCIACIATI TCACCIGIGA ATACTIGITC TIGOCCCICT GIAGACATAA TCTIGITAAG	180
	GACAAAOCTC CTGCTGTCGG TGTGTATCAG GTCAAGTAAA GTAAOCCCCT TAAATGCCAA	240
55	THIGGAGATA COGAAGATTA AGCATOCCAA ATOGITAGOC GCCCTAAACT GCCATOGGTG	300

	ATGCTGGGAA CAGGTAAATA TGGCCTGAGG TGCTGTGTAC TTACCTGATA TAAAAGTATG	360
	CASTATOCOS GOCOCITOST ACGITICIOCT GIAGICIATO GGATOCIOSA TAGATOTIAS	420
5	TICATOGGIA AATOGITOGA GATAATTYIC GICCIGCGAG GCCIGIATAG TAGIITOCIG	480
	TGTTTGAATA TICATGAAAT GGTTGGGCTA GCTTTCAGCA GCTGCTTCTT TAGTTCTTGC	540
	TOATACTGAC TICTTCOCAG ATCTACNCCA COCONTIGGG GCTGACCCCA GCACACTTAT	600
10	GATTITITANA AGGAATOCOC GTAATOCAAN GOOCTINONI ACCONGTOCO AATNGITINGA	660
	TCAAAANGIC ANNOCCICNA TTICCNCTTT TCTCNCCAAA ACNCCCACNT TAATTGAANA	720
	NENCONITIC ACCOCGAGAG GIOCCONC	748
15	(2) INFORMATION FOR SEQ ID NO:264:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 653 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1229RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:	
30	GATOGTAÃCA ACAAGOCTAC TOTACTOCTT ACAATACOCT GITGTACATO TAAGTOGTGT	60
	ACAAATGATT TACTCTCGCG CAGTATGACA TTGCAATCCG CCCGGCACCCG CCCAGACCTT	120
	TOOGTOTGAA CACCAGITOC COGOCTOCTA TOGITCAGOG ATGOTAAAAG CACCITATTC	180
35	GTATCCATCT ATAATGIGCG AGAAAAAGAA TCATCOCGTT CTAOCATGGA TTCTGACTTA	240
	GAGGCGTTCA GCCATAATCC AGCGGATGGT AGCTTCGCGG CAATGCCCGG TCGCACAGCC	300
	GCAAAAACCA ATTATCCGAA TGAACTGTTC CTCTCGTACT AAGTTCAATT ACTATTGCGA	360
40	TAACATTCAT CAGTAGGGTA AAACTAACCT GTCTCACGAC GGTCTAAACC CAGCTCACGT	420
	TOCCTATTAG TGGGTGAACA ATOCAACGCT TACOGAATTC TGCTTCGGTA TGATAGAAGA	480
	OCCEACATOG AAGAATCAAA AAGCAATGIT OCCTATGAAC OCTTGACTGC CACAAGCCAG	540
45	TTATCCCTGT GGTACTTTCT GCACCTCTAG CCTCCACTCC CGAGAACTAA GATTCGATAG	600
	CACACTITICA TETTIETATE ACACTEAATE AATCACCACT TTACCTIETE TAC	653
	(2) INFORMATION FOR SEQ ID NO:265:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 528 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
<i>\$5</i>	(ii) MOLECULE TYPE: DNA (generaic)	

(vi)	ORIG	INAL	SOURCE	Ε:
	(A)	ORC	:MRIN	PAG1229UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:	
	GATCAGATAC CGTCGTAGTC TTGGCCATAA ACTATGCCGA CTAGGGATCG GGTGGTGTTT	60
10	TCTTATGACC CACTOGGCAC CTTACGAGAA ATCAAAGTCT TTGGGTTCTG GGGGGAGTAT	120
	GGTCGCAAGG CTGAAACTTA AAGGAATTGA CGGAAGGGCA CCACCAGGAG TGGAGCCTGC	180
	GOCTTAATTT GACTCAACAC GOOGGAAACT CACCAOGTCC AGACACAATA AGGATTGACA	240
15	CATTCACACC TCTTTCTTCA TTTTTGTCCGT CCTCGTCCAT CCCCCCTTCTT ACTTCGTCCA	300
	GIGATITGIC TOCTTAATTG CGATAACGAA CGAGACCTTA ACCTACTAAA TAGTOCTOCT	360
	AGCATTIGCT OGTTOCOCAC TICTTAGAGG GACTATCGGT TICAAGCCGA TGGAAGTTIG	420
20	AGRICANTARIC AGRICTIGIGA TIGOCCITAGA COTTICTOGGIC COCACOCCOG CTACACTIGAC	480
	GCACCCACCE ACTIVATACCIT TOCOCCACAC TCTGGIATCIT GIGAACIC	528
	(2) INFORMATION FOR SEQ ID NO: 266:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 756 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1230RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:	
	GATCCCGGTA GGCGTCTGGC GGCATAATGT CTGCCGTATA GGTGGACTCT GGCTGTATTG	60
40	TCCGCAGGGG AATGGCATGC TTCTTGTAGA AATACAACCG ATCATAGGGC GAGCTCATAT	120
	CCACCGTACG TCGCTGGGAC ACGTACTTTT TGACTGAGCC ATCATTCGCG CTGTTCATTG	180
	CGACTCTAAT CTGATTCAGA ACCCTGACCT CTAGTGCTAT AGCGCAGGGC GTACCTGTCT	240
45	CATCATOCCC TTTTCAATGC TCCAGCGTGC GCAGTGTTAC ATCCATCGTC GCGCACGATG	300
	TTTAAGCAGG ATGCTGAGCT AATATGTATC GGTATAGGCT ATTGGCAGTA GACCTGGGTA	360
	TATACOCCTA GATATOGACA AGATOCTOCG CCTAGACATC CAGAACTTAA CCAGOCTCOG	420
50	GTTAAAGCCA CCCAGATAAC ATTTGAACAT TAGAACAATT ACCACCOCGA ATGGAGOGGA	480
	ACCCAGTOGA AACCCCACGG CATOCAATAG TITOCCCCAA CNOOGAAANG GCAGAATGCA	540
	CCGCCCAATG CTGCCCCAAC GCCCACGGCC ACCCTGACCC CATTGACCTN GAAGCCCTGG	600

660

GECNAAACTG CATTTTACCC CCCCCCATIN GCAAAAANTG ACCGAATAAA ANNOCCCCCN

55

	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	720
	AAAANNANTG GOOGGOGGTT TCCCGNNYTTT AAAAGG	756
5	(2) INFORMATION FOR SEQ ID NO:267:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 784 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1220UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:	
20	GATCTTCCOC TCCACTTCCT TCCCCCCGAATC	60
	GTGTACTGAC GCGAACTTGT TGGATCTTCC GGAAGAACAC AAGGACGTAT CCGCGCCCAA	120
	GCACGOGAAA TCATAGGTOG GCATCCACTT TACATCACGG ACGGAATCTG AGCCTGAATT	180
25	GAAATTCAGG TOGCTGOGGT TCACCTTGTA AGAGTGOGAC COCAAGTCOC ACACCTTGAT	240
	GCAGCCGTCC TGGCCACCGC TGATAAGGAG ATGCGTCTGG CCCATGTTGA AGTCCACGCT	300
	CHICATOGAA COCCACIOCT COCACAGOGT COCTCATCAG COOCCAATCC TITIOCCCACG	360
30	COCCETTICAT ATCITACATIC CAAACCGAGG TOCACGTCCC GCATATGGGG ATGITAATTCT	420
	TOTOGTOGTG GAACCCCCC CTTGACGTCC CGAAATCCGT GCTAATCTTC CCCCATGTTC	480
	CCCCCCCAT CCTCCTCGAA GAACTTCGTC CCCCCCCCC AACCNICCCC NGITGTTCNT	540
35	GITATICCGI GCACCCIGCI GCICCCIGIA CCCICCGICN AACTIGITCA GCCCAAAIGG	600
	TOTTCCCCCN CCCCCNCAAC CATGCCCCCT ANCTTCTTTG ATTTTTTTCC AACCCTGCCA	660
	CCCCCGGTTG CCTGGAGGGG GGGTACCCCC CCCAAAAACCC CNGGCCCCCC CAATINTCCC	720
40	ACCCCCINCCC GAATTTGGTT TNCCTINNGCG NCCCCCINNGG GNCCINNAAAA CCTCCCCTAA	780
	ACNA	784
	(2) INFORMATION FOR SEQ ID NO: 268:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(11) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1231RP	
55	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:268:	

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CATCATCTCC GTGAAGGCCG ACAGAACCCT GGCGATGGAA ACATTGGAAT TGATGCATTA	60
ACCICAAACAC ATCOCTICATT TOCTICAAACT CAACACAAAG GGGACGAAGC TOCCCACACA	120
GICGCIGCAA ATCTITAGOC GAGITICIGAA AATTCAAAGI COGTAGITICI CGTATGITICA	180
AGCCAGATICC ATAAACTATC TICTCACTCG CCGCATGCAA AGTATCAAGG AATAGGCGAC	240
ANTOGETAAT GATTOOCTOG AGCTCACGCA GATATTGGCG CACTTCTGAT ATCCGTGGGT	300
TICTTOCATION ATGATICANA TICAATAAAAG GAAGAACCTT CCAAAGACCT ACACCCCCC	360
GGT/AGCCGTG TCATGAGAGC TGTTAGT/CG GCTTCAACAT CAGCAAGTTT CTCTATAGGG	420
CACGCAGGGT CGICAACATC ATTTATTAGA CACTCCCAGC ATTTGTTCIT GAAAAAAAAGT	480
NGTGCATGNA CAATNOCNOC COCCOCTTTT GAAANGOOGG AGAAAATTTC CCTNNAANAC	540
NAATNICING GINNAANIGC TINNAAANCC CCTINAATIA AACCCTINNN GOCNCAAAAA	600
AATINITITAA ANCCTITIINA ACINOCCOGGG AAACANAAAC COCCOCCCA AAAAAAAAACA	660
NGITTINICC NCCCCCCCC CCCCCCANNI TIINAAAACC TIINNAAAAT CCCCCCCCCC	720
CNAAAAANCC CNCNAATITI TITITIAANC C	751
(2) INFORMATION FOR SEQ ID NO:269:	
(A) LENGTH: 762 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1231UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:	
CATOGICAGO GIOCATOCAC TIGGOATITOC AAAOGGATGI GATOCCIGAG GOGAGOCTIG	60
CASCASOCSC SCTCCTTGTT TCACATCATA SOCTGTCGAG SCCSGACTGA TTCASCTCTC	120
AAGBOGAGCA COCTOCCAAC GOOCCAATAGG GGOOCCOCTOC TGGOCTGTGC ACGGGAATAC	180
CTCAGACACT GCGTTAAGAT ATATGTATTT AAGAGGGCAC CAGCTGGCTA TCAATTGCCC	240
TOTOTOCTOT TOTTOCAACA COAGGCAAGT ATCATGATGT CTGCTGCAGG AAAAATGTTC	300
AAGAACAACG GCCAGAAGGA TGAGCGGAAG AATGCGGGGCC AGAGAGAGAGAGA GCGCCAGTAC	360
AGGGTCGGCG ATGAGCAGGG CTTGGGCCGC CAACAGCAGG CTGACTTGGG CGCCCCAGTA	420
CCASCAGOCG CCACGCTCCC ACCAGTTCGA CCACACTTGG NGCTTCCCCNA CATTTGGGCC	480
CCCCACCAAT TGGGNCCCCA GCAAAATNGG CCCCNCNNCT TINATITTING GGGCGAATGG	540
GOCINAAACCT ATCCCCCAANT TCNOOCENAAC TCCCCCCCCA GNANGAGAAC NCATTITTOC	600
ATTGGAAAAC NCACCTINNN TITGNNAACG CCCCCCCNA AAAGCCANGG GACTGTINIT	660

5

	THINGAAAAC GNOCCCCTTT NIGHONONN ANAAATTTIT CTANAATTIG CONGGATTCC	720
5	TOCCTIGGOG CONTICONIT TITACCCTIT TAACCCCCCC CC	762
	(2) INFORMATION FOR SEQ ID NO: 270:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 746 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1232RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:	
	GATCHTATTA ATGAATTITT COCCACGAAG CTTGTCGAAT TTTGATTCTA TCCTTTGCAA	60
	GCACTCAACT TOOGCTGTGG TCATGCGAAA CTAACACGCC GOGAAACAGA TACTGCCCAA	120
25	COUTTAGCAC TOUCTOTTE COGEOCTACA AACAAGIGIC GAGCATTAGC GEGEGACITA	180
	TITAGOGITG GAATATACAA AAGTAAGOOG TACATGOOGA TATCTCTCTT GTGTTGCTCT	240
	CTCTTACCTA CATCTAGATG TATTCAGGGA ACTTCCCCGC GAGATTCAGG GCCAAGGCCG	300
30	TOCAGOCCET ANAGIGCTEC ACCOGNIGAC CHINOCATOG TROTEGRITET ATTENTOGET	360
	AACAAAAACC ACCITTCCCC AAANICNAAT AAITGNITCA ACAGGITGIT CCCCCCATTG	420
	AAAGGGATAN NOGITTAAAC OOGGANAAA CAANNAANGG GNIKENITITI TIGGGCANAA	480
35	ACCCCCCCC NAATINAACC GCGIGGGGCC CINCNCAAAA TINITITITI CCCCCCNIGG	540
	GGYCCCCCCC NAANAACCCC CGNUGITINNA ATATATCCCCN CTTTTINCCAG AAGNGANTCC	600
	CCCINIAACCC GVOORGAINT TITTGTONT TAAAAANNCC CCCCCCCCCC CCNEGGAGGE	660
40	NIVITICATION COCCANCATTY INVACCINAGEN GAGTTYTTTT TOCCTOCOGG GGGAAAAAAC	720
	ANIGITINIT TINNINCONA AAAAAA	746
	(2) INFORMATION FOR SEQ ID NO:271:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 777 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: INA (genamic)	
	(vi) Original source: (A) Organism: Pag1232UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:	

	GATUAGITTIG CUGTAATTGA TAUAAAAGGU AAUTGGTOUG TOOGGGAUGT TOOGAGGAT	50
	AAAAAGAAGT CCCCGCCGACT GCCCTTGTTA ACGAAGTTTA GCCCGACTAT TTTTCACCCA	120
5	GAGGAGIACT CCAATTGGAA TATGATAGAA TGGTCACATA TTCACACAAG ATTGCTTGTG	180
	ATGAATAGGT CAACTITCAT GGAAATTGAC TITIGTAGAGG GATGGCAGCA GGAAATTGTC	240
	CAAGCAAAGA CGTGGTCTAA CTTGCGGGAT TTTAAACGCC TTTGCGATGA GAGCAGTGTC	300
10	CTACTCACCT GCAAAGAGAT TATATTCCTA GACCACAAGC AGCAGGGAAC AAAGAGGGGC	360
	CTATCCTGGA AACACAATTG GGATAGCAAA GAITCATCTC TAAAGCTTGC TATACACAIT	420
	TOTGOCAGOC ATATGAAACA ATATTTACAT GCATTOCTAT TTOCACCATG ACTOCCTOCA	480
15	GIGCITATGE GEOCTECTIC COGGEOGGAA AACACTITICC ATTITECCAG COATCCCCCC	540
	OCTUMPTICITY THENCOMENT TACACHOCKS NEITHACOGA ANTIACCTCC COCNIGINOC	600
	NAGAAACCGA GITITNANAGA ACCACACCCC CITTCATTIC CCTANNIGIG CCCGCCCCCC	660
ro	CCAGGOCCAG AGTITIGOGN COCCCNITTI NIGNACCAIN TINCCCCNCC CCNCNAGOGI	720
	TOCCCACONT AAAANCOOTIG AAACOOCTIT TOCCCCCCAC ATTITINGGIN GOOGAIN	777
	(2) INFORMATION FOR SEQ ID NO:272:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 734 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
0	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1233RP	
5	(will consider promotestost, con 15 kg-277.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:	60
	GATCACAGIG CIGIGGOCAT TECTOCTOGT CGIGCTCTTC TCCCCCTCAA CCCCCGAAGT	60
0	AGACAAGCIG CCAGCAAGCA CIGAITGGIA CAGGAGCIIT TIGITCACGI TCITAAGCAG	120
	GTTCCCCGTC GAGTCCCCGT TGTTCAAAAC AGCGCCCGC TGCACGCTCG AGCTCGACTC CCCCCCCCGCC GACGACGCCG TGGAATACAC CTCTGATCCC GGGTCCCCAT CCCTCGTTCT	180
		240
5	COCAGICOCC CCOGAAGCAA AAAATTCCTC CACGGATGTA TTCCCGTGGT TGCCCAGCTG	300
	CGCACCGGGC GTACCCGCAG CGCTGTTGAC ATTGGACGTG ATATTCTCCA TCAGCAGCTG	360
	CGACCICATC CCCCCTCCCC CCCCTGTCTT CCTCCCATCT GIAACGTCGT CACACCCCGA	420
)	GETTIGITET GIUGICCACG AACGAGACGT TCAACCATGT GACGACCCAG GCCCGTTTGG	480
	CCTTCACCAC CANATTTOGG CCTTTCTOCT GGAACNCCAA CCCCGGGAAT TTCCCAACCT	540
	NIGATICCON AANIGCCCGG CONCONICCC AAAITANAAT CCCCAATIGN GNIIGAAAIN	600
ŝ	GNCNAAATNA AACCCCVITT TCCCCTNAIN CNAMCCCING GCCCINAANGA GCCGATGGGG	660

	CONTROL CONTROL AND THE CONTROL OF CONTROL O	720
	TETETINOCC MICN	734
5	(2) INFORMATION FOR SEQ ID NO: 273:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 761 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOSY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(V1) ORIGINAL SOURCE: (A) ORGANISM: PAG1233UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:	
20	GATCCAGCTT CCATATAAGC TOGIGTTIGC GGTCGCGACC TCTACAGAAG TGGTGATATA	60
	TGATACTGTT ACCACGAAAC CCATTGCAGT GGTGGGAAAT TTGCATTACA CCCCCCTAAC	120
	GEACCTCAGE TOGICTGACA GOGGCCACCT ACTOGTOGTG TCATCAACAG ACGGITTICTG	180
25	CTCCTATATC TCAATGGAGG ACAGCCTATT TGGGGAGCCA TACAGTTCOG AGGCACAGCG	240
	CACCCATTCT CTCATACCTT CGACTCCAAA AAGCAACATC TTCAGGAACA CCCTCCCGTC	300
	CAACCCGGTC AACGTAAAGC GGAAGCACTC TGTAGGCGGC CACAACGACT CACCCATAAA	360
30	OCCOCOCTOCC AAAAAANGIC GCOCCTTICC CCIGIGGTCG TCGATGACGG ATCTGCCCCG	420
	GCACACAACC GCCTACTCCT AGCAAAGATC TCAAGCCTCC GAAGGCGCAT CCAACCCGTC	480
	CITGITIANT GACAACAACG GCGGCACCTA GTATCCCCNC ACGCCATCCT ANAAGTITING	540
35	ATTOCNIVIAT ACTIVAAATAC AAACCOGANA ANCINITTIC TIGITINACAA ACTITITITIT	600
	CACCTOCATO ACACTATOCO GONGNOGICA TICTIGOCGA ATOCCOCCIO COCCITANAA	660
	CNECCNIACN TARACCITICS CNENICCATA TITACICATG ARTENDIOG ARMICNETOS	720
40	CCATCHNOCA NOTTITIOCGE AGINITOCCC TETETIGETOC C	761
	(2) INFORMATION FOR SEQ ID NO: 274:	
4 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 728 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1234RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:	
55	CATCACAGIG CIGIOGOCAT TOCTOCTCGI CGIGCICITG TGCCCCICAA GCGCCGAAGT	60

	AGACAAGCIG CCAGCAAGCA CIGATIGGIA CAGGAGCITT TIGIICACGI TCTTAAGCAG	120
	CTTCCCCCTC CACTCCCCCT TCTTCAAAAC ACCCCCCCC	180
5	COCCOCCOC GACGACOCCG TOGAATACAC CTCTGATCCC GGGTCGGCAT CCCTCGCTCT	240
	CGCAGTCCCC CCGCAAGCAA AAAATTCCTC CACGGATGTA TTCCCGTGGT TGCCCAGCTG	300
	COCACCOGGC GTACCCGCAG COCTGTTGAC ATTOGACGTG ATATTCTCCA TCAGCAGCTG	360
10	CGACCTGATG CCCCCTCGGG CGCCTGTCTT GCTCGCATCC TGTAACGTCG TCACACCCGA	420
	GITTTIGTTC TGICGGTCCC ACGAACGGAG ACGTCCAACC ATGTGTACAA CAAGACGITT	480
15	TTGCCCTTCA CACCCATTTG CNCTTTTCTG GINGAACGCC AACCCCGGAT TTGNCAACNG	540
15	CNATTICCONT ATMOCCCCCC CCCCNCCNNA AATANAACOC CAATGINGNN TGAAANGGNA	600
	NAAAANAACC CCCTTTTCCC CCTTTTCAAA CCCCCCCO AAAGCCCONT GNGTGNVTAA	660
20	ANCOCCOCC COCAATITAA TOCCITITAA TIGOCCCACC CCCCACCCTT TINITINATC	720
20	CCINNICI	728
	(2) INFORMATION FOR SEQ ID NO:275:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 782 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI234UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:	
	GATCCAGCIT CCATATAAGC TOGTGITTGC GGTCGCCACC TCTACAGAAG TGGTGATATA	60
	TGATACTGTT ACCACGAAAC CCATTGCAGT GGTGGGAAAT TTGCATTACA CCCCCCTAAC	120
10	GGACCTCAGC TOGTCTGACA GOOGCCACCT ACTOGTCGTG TCATCAACAG ACGGTTTCTG	180
	CTCCTATATC TCAATGGAGG ACAGCCTATT TGGCGAGGCA TACAGTTCOG AGGCACAGGG	240
	GACOGATTCT CTCATACCTT CGACTCCAAA AAGCAACATC TTCAGGAACA CCCTGOOGTC	300
15	CAACCCGGTC AACGTAAAGC GGAAGCACTC TGTAGGCGGC CACAACGACT CACCCATAAA	360
	SCOCCETECC AAAAAGIGIC GCCCCTTTCC CCTGTGGTCG TCAANAAGGN ATTTGGGCCC	420
	OGACCACNAA COCCTACTOC TTANCAAAAA ATTTTTCAAA NCCCCCAAAG GCGGTCCCAA	480
50	CCCGNCCCTT GTTTTTTGA AAAAAAANG GGGCNCCTCA TTTTTTNCCC CNCCCCCNCC	540
	CCAAAATTTT GGGGATCCCN NTNCONAAAA AACAACCCCC AAAANCCTTT TTCCGGTTAN	600
	NAAANNITNN CNVINGACCC CCNCCCCCCC TTCCCCCCCC TCATTIVINC NAATNOCTCC	660
55	NCCCCCTINA AAGNICCCNI CITAAAANCN CCCCCCCCC NTTTTTCCCC NWWAACCCCC	720

	GGGAAAATTC CONCNEGGAN NNNCNANITT TICTTGGICT CCCCCINITIT NITICCCTINA	780
_	Œ	782
5	(2) INFORMATION FOR SEQ ID NO: 276:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1235RP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:276:	
20	GATCCTTGAG AAGCCAGATA ACGACGAGGA CGAGGAGCCC AGTGACGATG ACGATGCCGA	60
	CGACTACGAC TCCGATTCTC CCCGCCCCCG CGACACCGCC ACCGAACTCA GAGACCCTCC	120
	TECCCCCCCC ACATTOCCTA CEGAACTECA CEGATOCAGC CTCCTCCCCC CCCCCTTCAC	180
25	CHATTOCTITG COCTCOSTCA TOGTOCACTA TOGCACACAC AACTACGGAC ACHACATTIGC	240
	CITCOCCAMO TICOGIOGIO TGIOGIOCOC CATCAGOGAC GAAACAGOGT ACATOGIOGA	300
	TGAAGCTGAG GTCTTGTCCA CACCGGGGGT TTTCATGTTG TTCTACGATA TGACTATGAC	360
30	GAGGCCACCG GOCAGTTCCG TGACCACTTG GOCTGCCTAC ACCACCCCAG TCCGTGCTGT	420
	CAGATGGGGA COCAAGAATA CGACTCATTG ACCGGGTCCA CCAAGACCTC GATTCAACGA	480
	NCCASCIGIT SCICCOCCA ATAAACITIG TITISSESCIG SCCSSCCATA ININCTCCAT	540
35	GCATGUTCAT GCCCCCACCG GACATGUTTG ATCCANATAC TUTTUGUTUN GUINCCCCT	600
	TICAGNEVIT COCCCNAAGO AAGATTOITA NUCTACTIGO CINGITGITO CONCCIGGIT	660
40	TOGNACCICA AATTCCINIT NINCONITINI GGCCCANCCC NINGGNAAACC CNCCCITITI	720
40	TTTCAAACCA GGNTINCCCT TTINCCN	747
	(2) INFORMATION FOR SEQ ID NO: 277:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 776 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1235UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:	

	GATCACACCC GIGITCITIT CAAAOGICAC CIGCAACTIC TIGITATICA AGAIGATAGI	60
	CICACIGICO TITGACACOC TAGCAGOSTA AAATACOGAC TOCTGOSOGT CAGOSTITIC	120
5	TOCASCOATG TIMICOCATT GCAAGGIGCC TATTGGGACC AAACTTTCCC CTCCTGTGTT	180
	CAAGGCCTCC AAAGCTCTCT CTATGAACCG ATCTGCTAGC TOCACGACCT TGTTAAGCAT	240
	TOSTATIOCT TCATATFIST ATACCATTIC TATACATGIC CCGGGAAGGA CATCGIGGAA	300
10	CTCCCATAAC AAGATATCTT CCCATAGAGC GTTAATATCA TTAACAGGGT ACGTGTACTT	360
	GITAGGCGCT AGTAGCGAAA CCTTTGTGGC AATCCACTCC AAATCATGGA TCTTAACCTC	420
	AGATAGTOTO ATCAACOGIT TAAOGTOTOC CTGTGTOGTA TACGTGCCTC CTATGCAAAT	480
15	CARACITACA ATCCCCCCAT CCARGITGCC CARTCROTTC CCANTGICTG NCTTCNCCAT	540
	AATATCACCG TAAAAAACCGI TIANGGAATC COCNACCCCC NACCIINGGG AANAACAITG	600
	CATTCCCCCT TAAAATTCAA COCANACCCC CCATTTGTTC CACCNCCCCC TGTTTCAACC	660
20	CONCCCCON CNOCOMPACCO NNAAAAANAA COGTTGOONA ANGITCATTN AAAGITTIGI	720
	TOCCOCCOCG TITEAAAANCC NAATTITNAN AAGCGTTCTT TITCCCGGGG GGGTTG	776
	(2) INFORMATION FOR SEQ ID NO:278:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 722 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1236RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:	
	GATCICCCTC COGTCGAAGT ACGICGACTG TTTGAGACTC TGCAGGTCGT CTTTTGATAG	60
40	CTTCGATGCC TTAGCTCCCA TGTCTACTAT AACGCTGTCC CGGGCCTCAG CTATGTGCGG	120
	OCTOCCIATO TIACIGOCIA ACICTIGGAA GOGIGAGAGG COATAAGOCA CGATOGOGGA	180
	OCTOCTCAAA TEATGICCIC IGAAAGCOGT GIGIGOGICC ACTITICCCAG ACCCAAGGCT	240
45	ATGCCOGGITTA CCTGACCTCC GGTCCGGGATG TGACGCTGGG AGGCGGTGCG ATGCCGGCCC	300
	TCATOGCTGT COGTCGCGAA GGACTATCTA CCAGGGACTT GGCTGCCTGC GCAATTTGCA	360
	CIGCAGCTIG CAGTGGAGGT CTTGGCGAAG CTCACGGGCA GCGGCAGGCA GTTACAGCCA	420
50	160CACADGC CAAGCCCCCC GAGITGACCG GAGITGGTTG CCAGATATTIG 66CCGTCCCAA	480
	ATTOTIGANTA GOCCTITIATA INAGANOCOC NOCGTIGAAC COCAAGNITI TITATGOGGA	540
	TEGTICGAAT TCNECCCCCT CCCTTAACCC CCCCCGAACC CCTNCCCCCG GCAAAANCAA	600
55	ATCCTNCCCC NGTTCNAAAA ANCCCAACNC NNAAAATTTT AAAAGAGACA AATCANNACA	660

	CCCGNGAAAA AGASCCCINI CITTICAGAA TICCCGGGGG GGGGNGIAAA TINAACCITT	720
	GA	722
5	(2) INFORMATION FOR SEQ ID NO:279:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENCTH: 789 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1236UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:	
20	GATCTICGIC COCTTOCOGT CAGGAAATIC AAGCOGGATG AGCICTIGTT TCAGTTIACC	60
	ATAAAAGAGC TGTTTTACAA GGTCGAATTG CTCGCCCTCT TCATCCAAGC TGAGCGGCGAC	120
	GCACGCACTC TCAATTTGGT AGAGGACGTT CCCAATGCAT TCCGTCACAT CTTGCTGTCT	180
25	GCCAATCTCC AATGTGTTTT CTAGCTGGTC GGAACTAATT TTCGCAACAT AGGTGGAAGT	240
20	TICACOCCOT TOSSOCTOTS GACTOCCCAC CATOGIGATA TOTITACCIG AGICATCATT	300
	CTCAACAGCC TGCCTATCCT CAAGCGGACC TGCCCTGGTG TTTTCACCCN TTGGGAGGAN	360
30	GAANICCAAT ANNOCCCCTT TCTGGGGTTC TTGGGAAAGNA TINGGANAAT TINVIGGCCC	420
	OGTINITACC NITTINGANA GAGACCCTIG GNITINICIVAN ACCIVAAATINI TOCCIVIOGOG	480
	CNOCCOCNOG AATINITITIN INTOCAAANI TICCNAAANN CONCITTINI OCITITICCOC	540
35	NITTINGGNEG NAGCOCCCCA GEGGGCOCCC CGAANIAATC NGGGGGTNTGG AAAAANAAAA	600
	NAATTICCCA NAGGGGINIT INTITTICCN ICNGAGAAGG GNOGITANAA AAACCCATTI	660
	THICCCCCCN NIAGANAACC CCHTTINCNC CGGGGGVICC NGCCGGGGG ATINHICCNG	720
40	GARCANTIGAN MACCICCCTT CCCCNCTATA MAAATMOCCC CGGGGGGGGG TITINATTTIC	780
 0	CCCINIAAN	789
	(2) INFORMATION FOR SEQ ID NO:280:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 676 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPCLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1237RP	
55	(xi) SPOURNCE DESCRIPTION: SPO ID NO:280:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

CATCCOOGTT GAAGACATTG TCAGGTGOOG AGTTTGOCTG GGGCGGCACA TCTGTTAAAC	60
GATAACOCAG ATGTCCTAAG OSOSACTCAT OGAGAACAGA AATCTCCAGT AGAACAAAAG	120
OGTAAAAGTC CCCTTGATTT TGATTTTCAG TGTGAATACA AACCATGAAA GTGTGOCCTA	180
TOGATOCTITI AGITICCTCGG AGITITGAGGC TAGAGGTGCC AGAAAAGITTA OCACAGGGAT	240
AACTIGOCTIG TOOCAGICAA GOGITICATAG OGACATIGCT TITTIGATTICT TOGATGICOG	300
CTCTTCCTAT CATACCGAAG CAGAATTCGG TAAGCGTTGG ATTGTTCACC CACTAATAGG	360
GAACGITGAG CTGGGTTTAG ACCGICCGTG ACACAGGITA GTTTTACCCT ACTGATGAAT	420
GITATCOCAA TAGTAATTGA ACTTAGTACG ACACGAACAG TTCATTCOGA TAATTGGITT	480
THEOGRAPHIC COGACCORGE ANTIGCORGEA ACTACCATOC GENEGATIAT GEORGAACGE	540
CTCTAAGTCA GAATCCATGC TAGAACGOGA TGATTCTTTT CTCGCACATT ATAGATGATA	600
CGAATAGTIG CTITTANCAT CGCTGAACCA TACAGCCGCA CTGTGTTCAA CGAAGTCTGG	660
CCCTTCCGCG ATTGCA	676
(2) INFORMATION FOR SEQ ID NO:281:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 709 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1237UP	
(xd) SEQUENCE DESCRIPTION: SEQ ID NO:281:	
GATCCCCTTAC ACGAAGAAAA TCCGGACCCCC CAACCAAACC CAAAGTTCAA CTTACGAGCTT	60
TITAACTOCA ACAACTITAA TATACOCTAT TOGAGCIOGA ATTACCGOGG CIGCTGGCAC	120
CAGACTIGOC CTOCAATTGT TOCTOGTTAA GGTATTTACA TTGTACTCAT TOCAATTACA	180
AGACCCGEAT GOSCCCTGTA TCGTTATTTA TIGTCACTAC CTCCCTGAAT TAGGATTGGG	240
TAATTTGCGC GCCTGCTGCC TTCCTTGCAT GTGGTAGCCG TTTCTCAGGC TCCCTCTCCG	300
GAATOGAACC CITATICCCC GITACCCGIT GAAACCATGG TAGGCCACTA TCCTACCATC	360
GAAAGTTGAT AGGGCAGAAA TTTGAATGAA CCATCGCCAG CACAAGGCCA TGCGATTCCG	420
AAAAGITATT ATGAATCATC AAAGAGTCCG AACACATTGA TTTTTTATCT AATAAATACA	480
TCTCTTCCAA AAGTCGAGAT TTTAAGCATG TATTAGCTCT AGAATTACCA CAGATATCCA	540
TGITAGITAA AGAACTATCA AATAAACGAT AACTGATTTA TGAGCCATTC CGCAGTTTCA	600
CIGIATAAAT TOCHTATACT TAGACATOCA TOCTTATCTT TGAGACCAGC ATATGACTAC	660
TOGCAGATTC AACCAGATAC TATCTTTAAG ACACCCGAAA TOCGCAACA	709

(2) INFORMATION FOR SEQ ID NO:282:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 820 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1238RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:	
	GATCACOOCA ATGAAAAACT ACOCAAACGT TACAGACTITT GAGTGGIACA TCGCCCTCCT	60
	THOOGATCHO HOCATAGHOT COCAGGACOT GCAAGACAAG ACCOTOGOGO AGAAACTGGG	120
20	TGAGCAAATT AGAAACATCA TGGTGAAGGT TCCTGACCTG CGGGATCGCA CTTTGCCGCA	180
	GATTIGTICCAG CTGGTGAAGA GCGAGGACAT CACGGCCCGG CTGCCCGGTG TTCTGAAGGA	240
	GTGCATCTIGG TGCCTGGGCG AGTATTCGTC GTTGCTCGAC AATAAGGATG AGTATATTCT	300
25	OCTATIOSCA GAAAATICGA AATTATATGA GOCTGAACTA CAGCAAACTI IGATCCCTGC	360
	CATTITICAAG ATTITATACICA ATTICCICTAA CCACTICCCIC CTCCCACACCACCAC	420
	AATGOGTTAC OGAGCGGATA ATCACCCCAC TAGAAGATCT AATAATCTOG AAGAACTTCG	480
30	AAGTOCAGGA GOOGTOTTOC GAGGCTOTOG AATTOTACCC TINITTICTOG ACNOCOCCTC	540
	CNAAATINVIC TGNATCCCTA NCNOCTGGCA NCTTACNAAT TCCTNOCCCA NTTCTNCAAC	600
	CCTTTGAATT NACCIKINNIN CCNTCGGGCC CCCAAAAAANC TCINNINIVAAA CTINTINITCN	660
35	ATGGGAACCC CCTTINCCCN AAANGAAGCC ANANNNIACC GNAAAACNCN CTTGAAGNGA	720
	TITOCCOGAG TTITGANAAC ATTICNNOCN AATTITOCGG GACGGCCAAA AAGGGTTTIN	780
	CAAATTANTI COUCOCCCA ACUCCAANCC COCCCINCNIA	820
40	(2) INFORMATION FOR SEQ ID NO:283:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 875 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(V1) ORIGINAL SOURCE: (A) ORGANISM: PAG1238UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:	
55	GATCAGAAAC GOODGCTGC AAGAATGGAT GOOGATGAGC ITCGAGGAGT IGAGGCAITCG	60

	CITATOCAAA AAAAGAAATT OCTCAGATCA CGIGACAAAG TITICGICATC TCTAAATGIC	120
5	GACCGTTGGG CGAAATGTGC CGTCCTCTGC TATAAAATAT AAACTAGTTT CTCTACCACT	180
3	AGACTGATTG GGAATATCTA AGCTTTCACT TGATAGCAGC AGGAGCACTT CATAATCCAG	240
	TACCTICTIT COCTTATCCA CACTAGTCAT CTCATCGAAA ATCTCACAGC CAGTGCAGAG	300
	AGCCGCCCCT CAATCCTTGA TATCCAAATA TGTCAATAAG GAAACCCTAA AATACATCCT	360
10	TACAACGCAC TICTICOCCCC CCGTIATCGAA CTITTGGTATT COCATITOCTG CGATTTATGA	420
	CTIGAAGAAG GACCCTGAGT TGATTTCCGG CCCCATGACG TTGGCGCTCG TGGTATACTC	480
15	AGGTATTTIC ATGCGTTACT CGATGGCCGT CACTCCCAAG AACTACCTCT TGTTTGGGTG	540
15	COCACTITAT AAACGAGICC COCCCAACTC OCACAGCGTT CCCGCTGGCT CAAGTITICAA	600
	TTACTICGGC GAGAGCCCTG CTGTCAAGGC ACCCGAGAGA CCCGCATAGG TGCGTTTGCG	660
20	TOGGCACACG THOCATTACA COGHOGACCA CHACATAGAA TAHTATTAAG COGACTAHOC	720
20	TACACGITTC TAGAGCTAGI CGAGATGCCT TIGGCTGATA CTGCTGCGIT GGCCCAGGCC	780
	GTATCTTOCT CCTCCTGCCT TTGCTGCGTT GCCCAGCTCC CANTIGNCCG TTCNCGATNN	840
25	TOCTIGTICTOC COTATOCAST GNOTAAATIGT CTCCC	875
20	(2) INFORMATION FOR SEQ ID NO:284:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 716 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1239RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:	
40	GATCAACTTA GAACTGGTAC GGACAAGGGG AATCTGACTG TCTAATTAAA ACATAGCATT	60
	GOCATOGICA GAAAGICATG TICACGCAAT GICATITICIG CCCAGIOCTC TCAATGICAA	120
	AGTGAAGAAA TICAACCAAG COCOOGTAAA COOCOOGAGT AACTATGACT CTCTTAAGGT	180
45	AGOCAAATOC CIOGICATOT AATTAGICAC OCOCATGAAT GCATTAAOGA CATTOOCACT	240
	GTCCCTATCT ACTATCTACC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGCGG	300
	GEARACARCA COCTOTTICAC CTTCACTOTA GITTICACATT GICARCACAC ATACACOCTG	360
50	TAGAATAAGT GGGAGCTICG GCGCCAGTGA AATACCACTA CCTTTATAGT TTCTTTACTT	420
	ATTICAATTAA GOOGAGCTOG AATTCATTIT CCACCTICTA GCATTIAAAG TCCTATACOG	480
	GCTGATCCGG GTTGAAGACA TTGTCAGGTG GGGAGTTTGG CTGGGGCGGC ACATCTGTTA	540
55	ልግልልግርነልግ ጉጥሞከልልጋልግ ልልጋልግርነውልግን ምንፈርፕሮርኒስል ምንርሞንውለን ግንፈናውለል	600

	AAGGGTAAAG TCCCCTTGAT TTGATTTCAG TGTCAATACA ACCATGAAGT GTCCCCTATC	660
	GATCCTTAGT TCCTCGAGTT TGAGCTAGAG TGCCAGAAAT TACACAGGAT ACTGCT	716
5	(2) INFORMATION FOR SEQ ID NO:285:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 793 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1239UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:	
20	GATCATCTIC GATCCCCTAA CTTTCGTTCT TGATTAATGA AAACGTCCTT GGCAAATGCT	60
20	TTCCCACTAG TTAGTCTTCA ATRAATCCAA GAATTTCACC TCTGACAATT GAATACTGAT	120
	GCCCCCGACC GTCCCTATTA ATCATTACGA TGGTCCTAGA AACCAACAAA ATAGAACCAA	180
25	ACGIOCTATI CCATTATICC ATGCTAATAT ATTCGAGCTT GCGCCTGCTT TGAACACTCT	240
23	AATTITITCA AAGTAAAAGT OCTOGITCOC CTAGAGTACA AGTACOCTAG GITAGOCAGA	300
	AGGAAAGGTT COGTTGGATC COGTACACGA AGAAAATOOG ACGGCCCAAC CAAACCCAAA	360
30	GITCAACTAC GAGCITTITIA ACTOCAACAA CTITAATATA COCTATIOGA GCTGGAATTA	420
	CCCCCCCCC TCCCACCACA CPTCCCCTCC AATTGTTCCT CGPTAACGTA TTTACATTGT	480
	ACTCATICCA ATTACAAGAC COGTATOGOC CCTGTATCGT TATTTATTGT CACTACCTCC	540
35	CTGAATTAGG ATTGGGTAAT TIGCGCCCCT GCTGCCTTCC TTGGATGTGG TAGCCGTTTC	600
	TCAGOCTOCC TCTCCGGAACT CGAACCCTTA TCCCCGTTAC CCGTTGAACC ATGGTAGCCA	660
	CTATCCTACC ATOGAAAGTT GATAGGGCAG AAATTTGAAT GAACCATOGC CAGCACAAGG	720
40	CCATCCCATC CGAAAGITTA TATGAATCAT CAGAGTCCCA GAACTTGATT TITTATCNATA	780
70	AINCNOTOTO CAA	793
	(2) INFORMATION FOR SEQ ID NO:286:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 836 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: INA (genamic)	
50	(vi) Original source: (A) Organism: Pag1240rp	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:	

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GATCTTAAAA TAAGATAGAA TOGTAATAAA TATCATTCAG GTACAATAGA TOCTGGTGTT

	ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT	120
5	ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCTTT AAAAATAAAA	180
	TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA	240
	TGIACATGIA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA	300
10	TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT	360
	CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA	420
	SCACCICAAT GIGACATITG TOCATATACT AAACAATAAC CIAAGAAAGC TGCIGCIATA	480
15	GITAAAATAA AGATAATAAC ACCAACTGIT CCATACAATA ACTCTAGGTG ATTTATAAGA	540
	ACCATAATAT AAACCITTAC CAATATGAAT ATACATACAA ATAAAGAAGA ATGAAGCACC	600
	ATTAAGAATG CATATATCTA ATTATCCACC TATTGTACTC TCTCANAATA GITCCTACCT	660
20	GATGANAAGC TATCCATATT ANAAGAATAT GCATACCTTA AAAATACCGT TANAATTGAA	720
	TACTAACATA ACCTATAANA CONAATICAC CATAATAATG AGAGGGTGAG CNGAACCATA	780
	CNIACNATAC TAATITAATT ATTGATTTCT TTCCCNITTT ATTATTAAAT TITAAT	836
25	(2) INFORMATION FOR SEQ ID NO:287:	
<i>o</i> 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 860 base pairs (B) TYPE: nucleic acid (C) STRANDEUNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1240UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:	
o	CATCHAGAAT TATTAAGTCA ACTATTAACT AATATCTATA ATAATAATGG TITATCATTA	60
	AAATCATTA AGATAATTAT TAAAAATTA CCATTAAATA ATGATAGATA ATTAAAAA	120
	TAGTAGATAAA TITAGTAATA ATTAGTCATT TAGTAGAGT AAATAAATAA TITOGATTAA	180
5	AAAAAAGATT TAATTAATTT ATATACITTA GATAATAAAT TAITAGATTT AAGIATICIT	240
	AATAATATAT TATTAGGTAA ATATTIAGTA GGTAGTAATA TCCAATTAAA GGGTAGACTA	300
	TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGIAC ATTTAATAAT	360
0	TATATATATC AATGAAGTAA AITAAATAAT TTATATAAT TAAATTATAT ATCACTTAAT	420
	ATTAATAAC TTAATAATCT ATTTATTAAA TAAAATGATA TATTAATAT TAAAATTAAA	480
	TTAAATACTA TTIRATAAAT ATCTRTAAGT AATTTCTTAT TTATTTTATA ACATTTTAAA	540
5	ATGITTTATG TITAAATAGA TAATAACAAT TAAATAATAA AAATTAAGAT GOCACAAATA	600

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	Meccariff certialsaa reastracif Alegimeet Afrianiffa ciartifale	טסט
5	CITCTATCIT ATGINITITA CCTAAGAATT TAANAATATA TACTCCTAAA TATATATICC	720
_	NAAATTATAA TAGITATTAA ATTITAATTA ATCCANIATG ATCCNTATTT ATAAATATAT	780
	ANGAANATTI TAATATATAT ATATGAATNI TATATOOON TGAACCATTG NAATNNATTA	840
10	TAGTITIACAC CCCCTANATC	860
70	(2) INFORMATION FOR SEQ ID NO:288:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 837 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1241RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:	
25	GATCTAAATA TATATAATTT AATTIMTAAA GATTAATATA AACTITITTIA TTATAATATT	60
	TAACTATTAA AIVATTIAAA CTAITATTAT CAITATTIAA TAAATTAATT AITTICATTAT	120
	TAATACTTAT TATATAATTA TTATATAATT TACTTAATTC ATCATTATTA ATATTTATAT	180
30	AATTATAAAA ATAATATITA ATATGAATAC TATTTAGTCT ATGITCAAAT TITAAATTAG	240
	TTATTAAAAT ATTATTAGAT ATTATTATTT TCTTTAATAA ATTATTAAAT AGATTATCAA	300
	TAATTAATAT ATTATTITAT AATTGTTTAT TAAAATA TATTTTATTA TTATAAACAT	360
35	TIPATITIATA TAAATATIGT AAATTATTAT TITITATTA ATATCTATIT TITAAAATAT	420
	TATGITGATT TATATTATTT AATCTTTTA TAAGAATTAT TATTAAAATT AATTTAACT	480
	TTAATTICTT ATTATTAATT TITATATTAT TTAATAAATT ATATTTCATT TTATTTATT	540
40	ATTENTIA TAATTAAT TATTELATA ATTENTE ATTENTE AATTEAAT	600
	AATATTATAA AGAATGTAGT TAAAAATACT TATFAAAAGGA TOOGAACCTA TATTATTGTT	660
	TATGAGACAA ATOCTITIAGO COATAAGOTA TATAGTITIGA CTATGATTIG AGANTIGOGT	720
45	NENOCCCCIA TOCUNICATO CUCIVIGUOCO CINCTAAANGA ATTUNITUMI TNANANAIGA	780
	AAAANTTATT TATCAAAGAA TEATAATTT TEAANAACGG GNANAACGAA AGACCCG	837
	(2) INFORMATION FOR SEQ ID NO:289:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 856 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) WOI DOUTE TWOE: TWO (menomic)	

	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1241UP
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:
	GATCHGIATA CTAGAGCTIA TITTACTICA GCIACIATAA T
10	ATTAAAGTAT TTAGTTGATT ACTAACTATT TATOGTOGTT C
	ATATTATATC TATTATCATT TTTATTTTTA TTTACTGTAG G
	TYROCTARIC TRICATTAGA TGTRGCATTIC CATGRIACTT A

TATTCTTAT TCCTACTAGT 60 CATTAAGATT ACTAACACCA 120 TOGTTTAAC TOGTGTAGTA 180 ATTATGTAGT ACTACATTIC 240 CATTATGTAT TAAGITTAGG TOCTGEATTC TCTATGTTTG CTGGTTATTA TTATTGAAGT 300 CCICTIGITT TAGGITTAAA TIATAATGAA AAATTATCAC AAATTCAATT CTGATTAATT 360 TICITAGGIC TEAATAITAT TITICITCCCT ATGCATTICT TAGGTATTAA TGGTATACCA 420 AGAAGAATTC CTGATTATCC TGATCIATTC CTAGGITGAA ATTTAGTATC TTCATTTGGT 480 TCTATAATAA CTATTATATC ATTAATGTTA TTCCTTTATA TTAITTATGA TCAATTAATA 540 AATGGTTTAA CTAATAAAGT TAATAATAAA TCTATTAATT ATATAAAACT ACCCTGATTT 600 TATIGAATCA AATAATATIT TCITAATGAA TACTACEAAA TCACATCTAT GATTTATATG 660 AATCACCACT CITAATCNAT CAATTAAACC CTCTAATCCA ACTITAAATA NNCITAATTA 720 TAAAITANNA ATAAATTTAG TOGAANAATT AATNGTAANC AATNTITINA NOGANITTAT 780 CTONVICCAA CCGAAACTAC TITTATCCTT AANNAAAACC TTTAATNAAT GGACCNCANA 840 NICHNAACHN GITTITC 856

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

(A) LEWGIH: 831 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genamic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1242RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GATCACGIGC TAAATGICCG GGTACATING TGCACCCGTA CACCGCATTA CGACATTACG 60
ACGCTTCTTG ACTAACCAGG TTATCACGIG TATATAGTTA CATACGAACG TCTGGTACAA 120
GGAAGAGCCG GCCGGAAGTC CACTTCACCC TTAAATTGCC ACATTTCATG AGCATTTACA 180
ACAGAAGCAC AGCTGTAAAC GTTTCTCGAA CTCGTGAAGT TTCATATTGT TCCTTAAGGG 240
CCCTTGATGT TGCAGTTCAA GCTAGTTCTG TTGGGAGCT CGTCGGTCGG TAAGTCGTCA 300

TITISSENCE COORDINGS GROOSING ANTOCITISE TECRNISTRY TRANSPING CONCROSS GREETINGS TRAISACTIT GRANDERS GRITICITISE CANASSING GREETINGS THE ANGENGS TRAISACTIT GRANDERS ATTICITISTRY CITICOTISTS GREETINGS TRAISACT ANGENGS ACCINGS ATTICITISTRY CITICOTISTS TOCCAACC CRESTONY TOCCHAST TINNOCAN COSCOSSIT NOCSCATTIN TOCCAACC CRESTONY TOCCHAST TRAISCOCC CRESTONY NOCSCATTIN TOCCAACC CRESTONY TOCCHAST NOCCHAST NOCCHOCC N (1) SEQUENCE CRARCTERISTICS: (A) INDIBITIE 878 base pairs (B) TYPE: INDIBITIE 878 base pairs (B) TYPE: INDIBITIE 878 base pairs (C) STRANBENESS: Single (D) TOFOLOSY. Linear (II) MOLECULE TYPE: INA (genomic) (VI) ORIGINAL SURCE: (A) GRENITSH: REGLETION: SEQ ID NO.291: CANCELOTE ATTICHASE ACCICACAN ANACCTAC ATCASTONS ACCICACAN CANCELOT ATCOCRATEA TITICCTOSC CREGORISM ACCICACAN ANACCTIC COTRACCCT CITICACACAT CRITICIPATE GROCACAGE ACCICACAN ANACCTIC COTRACCCT CITICACACAT CRITICIPATE GROCACAGE TRACTORICA ANACCTIC COTRACCCT COTRACCCT COTRIGURAL GRACOCACAGE TRACTORICA ANACCTIC TOCCACCCT COTRIGURAL GRACOCATIC ACCACTURED ACTOCCCT ANOCCTAC ACCACTCA CRITICIPATE GRACOCACT ACCACTURED ACTOCCCT ANOCCTAC COCCACTCACACAT TRACTORICA ACCACTURED ANTICIPAT TITICICACACAC COCCACACATAT TANCACATT ACCACTURE CANCENTET ACCACTCACT TOCCACCC CATCOCCAC ACCACTAT TANCACATT ACCACTURE CANCENTET ACCACTACT TOCCACACAC CATCOCCAC COTROCICA ACCACTURE CANCENTET ACCACTACT TOCCACACAC CATCOCCAC ACCACTACT CANCENTET TANCACACTURE ANTICIPATE TITICCACACAC CACCACTCAC CANCENTET TANCACACT TOCCACACAC TRACTORION TOCCACACAC CACCACACAC ANACACTIC TOCCACACA		ATTOTICATE OCTIONIONA GRATICOTTE GRATAGOTTE GRATAGOTE	200
CGAACCOCC CITEGICE TIATGACCIT GACACAGA GATICICIAE CANAGEACA CGACCOCC CITEGICE TIATGACCIT GACACAGA GATICICIAE CANAGEACA GACCOCCT GACCAAITA GAACCACTT GGIGACGAA ATTCIGGIAT CITCCCISTT 600 GECCAMACC CAGGIGANT TOCCCAAGGT TIANACAAA COGCOGGT NOCGCATIN TICCCCAAACC CAGGIGAN CITAAAACAG GCAATTCAN NOGGCCCC COGCATCOC 781 ANTITICATIC CAGGICCOC CAAGAACAC COTGGGGNT ACCCCTCCC N 832 (2) INFORMATION FOR SEQ ID NO:291: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 878 base pairs (B) TYPE: insclicic acid (C) STRANESTICS: (A) CHARACTERISTS: single (D) TOFOLOGY: linear (ii) MILECULE TYPE: INA (genomic) (vi) ORIGINAL SURGE: (A) ORGANISM: PRG1242UP (A) SEQUENCE DESCRIPTION: SEQ ID NO:291: GATCTIGGG ATTGCCAAGG ACAGACGAA AAACCCTACC ATCAGGGTG COGTCGAGAA CAACCACTC ATCCCAATCA ATTGCCTGGC GGACGGGAG ATTGAGGGAA CAACCACTC ATCCCAATCA ATTGCCTGGC GGACGGGAG ATTGAGGGAA GGAACGAAAG GTGAATGTTC AGAATTACTT GAACACTTAT GCACCAGG ATCAGGGAA AAAGATTC CATACCGCT CTGAGAAGAT COTTCTTATG GCACCAGGG ATCAGGGAA AAAGATTC CATACCGCT CTGAGAAGAT COTTCTTATG GCACCAGGG ATCAGGGAA AAAGATTC ATCCCCAACCC CTGAGAACAGA CAACCAGA CAACCAGG ATCAGGGAA AAACATTC CTGACCACCC CTGAGAACAGAT GCAGGGAGT TACAGGGAA AAACATTC CTGACTACCACCC CTGAGAACAGAT GCAGGGATG TCAGGGAGAA AAACATTC CACCACCCC CTGAGAACAGAT CGATCCTTATG GCACCAGGG TACAGGGAA AAACATTC CACCACCCC CTGAGAACACCC CCTTGGGAT GCAGCGATG TCAGGGAGAA AAACATTC CCGTTACT CCAACCCC CCTTGGGAT GCAGCGATG TCAGGGAGAA AAACATTC TTGGGAGTAT CCAACGCCAACGATGCA TAACCACTTC ACCAGGATGT AACAACTTT AATOTTCACT TTGGAGGTAT CCAACGCCAACGATACC CAGGAAGAATTT AATOTTCACT TTGGAAGGTAT CCAACGCCAA CAGGAAGAAT TAACCAATTCAT AATOTTCACC TATCCAACGC CACCCCC CATTGGAT GCAACAAATTT AATOTTCACC TATCCAACGC CACCCCCCAACGATACAC CAGGAACAATTT AATOTTCACC TATCCAACGC CACCCCCCAACGATACC CAGGAACAATTT AATOTTCACC TATCCAACGC CACCCCCCCCCCCCCCCCCACCCC CATTCCACCC CAGGAATTCACC CCTTCCCCC AGGACTTAC CACCCCCCCCCCCCCCCCCC		GCATTICTGT CCCGTACCAT CAAGCTGGCG GACCACGACG ACGCAATGAT CAATTIGAGA	420
GACCIGGGIT GAACGANITA AGACCAGIT GGIGACGACA ATTUTGGIAT CITCCUTGIT GCCCATAACT CATINECGA NEAGANCEG AACCANGGIG ATTGACKGA GAACACCAG TCCCCAAACC CAGGIGANT TCCCCAAGGI TINNOCAAA COGGCGGIT NCCGGATTIN TCCCKCAAACC CAGGIGANT TCCCCAAGGI TINNOCAAA COGGCGGIT NCCGGATTIN TCCCKCAACC CAGGIGANT TCCCCAAGGACAC CCTGGGGATT NCCGGCCCC CCGNICCCC ANITOCHT CAGACCCCC CAAAGAACAC CCTGGGGATT ACCCCCCCC N (2) INFORMATION FOR SEQ ID NO:291: (3) SEQUENCE GERACTERISTICS: (A) LENGTH: 878 base pairs (B) TYPE: Incleic acid (C) STRANBERISS: Single (D) TOTOLOGY. Linear (ii) MCLECULE TYPE: DA (genomic) (vi) ORIGINAL SOURCE: (A) CHGNILS: PAG1242UP (C) SEQUENCE DESCRIPTION: SEQ ID NO:291: GAACCACCTC ATCCCATTCA TTTCCCTGGG GAACGACG ATTTCCGAGAA 6 CAACCACCTC ATCCCATTCA TTTCCCTGGG GAACGACGA ATTCCGAGAA 6 GAACCAAGG GIGAATGITC AGAATTACTT GAACCACTTTA GCAACCAAGG ATCAACGAGA 18 GGAACCAAGG GIGAATGITC AGAATTACTT GAACCACTTTA GCAACCAAGG TCCAGGAGAA 30 ATACCAAGGIC CCTAACCGCT CTGAGAACCA CGTTCTTATG GCAACCAAGG TCCAGGAGAA 30 ATACCAAGGIC TCCGTTATCT TCCCAAACCC CTTGGGGGAT GCAGGAGG TCCAGGAGAA 30 ATACCAAGGIC TCCGTTATCT TCCCAAACCC CTTGGGGGAT GCAGGAGGG TCCAGGAGAA 30 ATACCAAGGIC TCCGTTATCT TCCCAAACCC CTTGGGGGAT GCAGGAGGG TCCAGGAGAA 30 ATACCAAGGIC TTGGGGAT CCCAACCCC CTTGGGGAT ACCAGGATT ACCAGGATT ACCAACGATT TCCAGGAGAT TCCGGGAGAACAAT TCCGCGAGAACAAT TTGGGAGATC TTGGAGGATT TCCAGGACGA ACAACGATT TCCAGGAACTA ACCAGGATT ACCAACGATT TCCAGGAGAT TCCAGGAGAATT TCCAGGAACTA TTGGAGAGAT TTGGAGAGATT TTGGAGAGAT TCCAGCACGC CAGGATTATC CAACCACCT CCCAACGAATTA TCAACCACT CAACAACAATT TAACCAACTTC TTGCAACCAC CACCACGATTAT TCAACCACT CCCAACGAATTA TCAACCACT CAACAACAATT TAACCAACTTC TTGCAACCAC CACCACCAC CAACGAATTA TCAACCACT ACCACGATTA ACCACTTCACC CACCACGATTAT TCAACCACTC CAACCACACTAT TCAACCACTC CAACGAATTA TCAACCACTTC CAACCACACTAT TCAACCACTC CAACGAATTA TCAACCACTC CAACGAATTA TCAACCACTC CAACAACAATT TCAACCACTCAC CACCACCACCAC CACCACTACC CACTCACCC CACCACCACAC AAAAAAATTCACC NAAACAATTAC CAACCCCCC CCCCCCCCCC	5	TOTOGGACAC COCOGGACAG GAGCOGTIACA AATCOCTOGC TOCGATGTAT TACAGGAATG	480
TOCCCAAACC CHOSSIGNT TOCCCAAGS TINNOCAAA COSCOSSIT NOOSACTIN 720 TOCCCAAACC CHOSSIGNT TOCCCAAGS TINNOCAAA COSCOSSIT NOOSACTIN 720 TOCCCAAACC CHOSSIGNT TOCCCAAGS TINNOCAAA COSCOSSIT NOOSACTIN 720 TOCCCAAACC CHOSSIGNT TOCCCAAGAACAC COTGSSINT ACCCCCCC CCCNICCCC 780 ANITOCHT CAACACCCC CAAGAACAC COTGSSINT ACCCCCCCC N 833 (2) INFORMATION FOR SEQ ID NO:291: (1) SEQUENCE GRAACTERISTICS: (A) LENGTH: 878 base pairs (B) TYPE: INcleic acid (C) STRANDENISS: Single (D) TOFOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) CREANISM: PRO1242UP (X1) SEQUENCE DESCRIPTION: SEQ ID NO:291: CATCTIGICA ATTGCCAAGS ACCACCAA AAACCTACC ATCAGGGTG COSTGAGAA 6 CAACCACTC ATCCCATTCA TITOCCTGSC GAACGGAG ATTGCCAAGA ACCACTGT 12 GAACCACTC ATCCCATTCA TITOCCTGSC GAACGGAG ATTGCCAAG ACCACTGT 12 GAACCACAG GTGAATGTTC AGAATTACTT CAACACTTTA GCAACCAGG ATCAGCGAA 18 GGAACCAAG GTGAATGTTC AGAATTACTT CAACACTTTA GCAACCAGG TATCTGAGAA 24 AAAGATTICG ATTCCTCCCA AGITCCAGCC TOTGGTGAT GCAACCAGG TATCTGAGAA 30 AATCAACGCT COTTATCT TOCCAACCCC COTTGGTGAT GCAACCAGG TATCTGAGGA 36 AATCAACGCT TOTGTATCT TOCCAACCCC COTTGGTGAT GCAACCAGT CATCTGAGGA 36 AATCAACGCT TOTGTATCT TOCCAACCCC COTTGGTGAT GCAACCAGT CAACACATTT 46 AATCTTCCCC TATCTTGAT ACCACCTCC CAACGACTAT TAAGGAATTT TAAGGA		CGAACOCCOC GITGGIGGIG TIAIGACGIT GACACAGGAG GATICICIAG CAAAGGCACA	540
TCCCCAAACC CMGGIGANT TCCCCMAGGI TINNOCAAA COGGCGGT NCCGGATTIN 72: TTCCMGGAT TGGGGAANN CTAAAACNG GCNATTCCNF NGGGCCCC CCGCNTCCCC 78: ANTITICENT CAACNCCCC CAAAGAACAC CCTGGGGTT ACCCCTCCC N 83: (2) INFORMATION FOR SPQ ID NO:291: (i) SEQUENCE GGRACTERISTICS: (A) LENGTH: 878 base pairs (B) TYPE: Inclicie acid (C) STRANDEIRESS: single (D) TOFOLOGY: linear (ii) MCLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) CHGNNISM: PAGL242UP (Xa) SEQUENCE DESCRIPTION: SPQ ID NO:291: GATCTIGIGG ATGGGAAGA AAACCCTAC ATCAGGGTG COGTGGAAA 6 CAAGCACCC ATCCCATTCA TITCCCTGGC CGAGGGGAG ATTTCCGAGA ACGGACGAA AAACCCTAC ATCAGGGTG CGAGGACGAA AAACCCTAC ATCAGGGTG CGAGGACGAA AAACCCTAC ATCAGGGTG CAAGCACGAA AAACCCTAC ATCAGGGTG CAAGCACGAA AAACCCTAC ATCAGGGTG CAAGCACGAA AAACCCTAC ATCAGGGTG ACGGACGAA AAACCCTAC ATCAGGGTG CAAACCAACG ATCAGGACGAA AAACCCTAC ATCAGGGTG CAAACCAACG ATCAGGACGAA AAACCCTAC ATCAGGGTG CAAACCAACG ATCAGGACGAA AAACCCTAC CATCAGGACGAA CAAACCAACG ATCAGGACGAA AAACCCTAC CAAACCAACG TAACCCCCAAACCAACG ATCACCCCAAACCAACG ATCACCCCAAACCAACG ATCACCCCAAACCAACCAACCAACCAACCAACCAACCAA		GAGCTGGGTT GAACGAATTA AGAGCAGGTT GGTGACGAGA ATTICTGGTAT CTTCCCTGTT	6 00
TICCNEGAT TOCOGGANN CHARACHE GONITION NEGOCOCC COCCNICOC 786 ANITICENT CAMBROCC CARACHARD COCCEGNITION 833 (2) DEFORMATION FOR SEQ ID NO.291: (1) SEQUENCE CHARACTERISTICS: (A) LINGTH: 878 base pairs (B) TYPE: Incleic acid (C) SERANDENESS: single (D) TOFOLOGY: linear (ii) MELECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PRO1242UP (A) SEQUENCE DESCRIPTION: SEQ ID NO.291: CARCHITICE ATTOCCASE ACGARACAA MARCHINC: ATCACHARG COCTCAGAA CARCACCTC ATCCCATTCA TYTCCCIGGC GEACHIGEAG ACTICOSAG ACGARACAAC CARCACCTC ATCCCATTCA TYTCCCIGGC GEACHIGEAG ACTICOSAG ACGARACAAC CARCACCTC COCCAACGCT CICAGAACAT COTICITIATE GEACACAACG ATCACCAAA ARACATICG ACTOCTCAA ASTICAGC TOTACTGAT GCAGACAAG TATCTCAGAA ARACATICG ACTOCTCAA ASTICAGCC TOTACTGAT GCAGACAAG TATCTCAGAA ARACATICG ACTOCTCAA ASTICAGCC COTIGEREAT GARACAGT TAGGACAGA ATCACACCT TOCGTTATCT TCCCAACGC COTIGEREAT GARACAGT TAGGACAGA ACTGTCCGT ANTOTIGATE ACGCATTCA CGAACGAAT TRACGAATTC GAACGAATTT COCTAGATCT TICGCACTT ACGAACTCC CATCGTCTA ACCAGTACAT ACTGTCCGT ACTCTTCATC CAACGCTCA CGGAACGAAT GTCCCTCAG CAACGAATTT ACTGTCCAC TATCTTCCACACG CAACGAATTT TRACGAATTC GTTCCAACGG ANTIGANITT TICGCACATT ACGACTCCC CAACGAATTT TRACGAATTC GTTCCAACGG ANTIGANITT TICCCAACGC CAACGAATTT TRACGAATTC GTTCCAACGG ANTIGANITT TICCCAACGC CAACGCCAC CONTITUANA ACACTITINA ATTCCAATTC CAACGCCTT ACGACTCAC CAACGAATTT TRACGAATTC GTTCCAACGG ANTIGANITT TICCCAACGC CACCCCCC CAACGAATTT TRACGAATTC GTTCCAACGG ANTIGANITT TICCCAACGC CACCCCCCC CAACGAATTT TRACGAATTC GTTCCAACGG ANTIGANITT TICCCAACGC CACCCCCCC CAACGAATTC CAACGAATTC TAACGAATTC CAACGAATTC TAACCAATTC TAACCAACACAA AAANNIGINT TOCCCCAACGAACAA AAANNIGINT TOCCCCAACGAACAA AAANNIGINT TOCCCCAACGAACAAA AAANNIGINT TOCCCCAACGAACAAA AAANNIGINT TOCCCCAACGAACAAA AAANNIGINT TOCCCCAACGAACAAA AAANNIGINT TOCCCCCAACGAACAAA AAANNIGINT TOCCCCCAACGAACAAA AAANNIGINT TOCCCCCAACGAACAAAA AAANNIGINT TOCCCCCAACGAACAAAA AAANNIGINT TOCCCCCAACGAACAAAA AAANNIGINT TOCCCCCAACGAACAAAAAAAAAAAAAAAAAAAAAAAAAA	10	GUCCATAATT GATTNOOGGA NGAGGANCOG AACCNAGGTG ATTGACNCGA GAACNCAGGC	660
15 ANITTOCNIT CAMANECCC CANASANCAC COTEGGRATI ACCORDICO N (2) DEFORMATION FOR SEQ ID NO:291: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 878 base pairs (B) TYPE: fincleic acid (C) STRANDENESS: single (D) TOPOLOGY: linear (ii) MELECULE TYPE: DA (genomic) 25 (vi) ORIGINAL SOURCE: (A) ORGANISM: PRO1242UP (AL) SEQUENCE DESCRIPTION: SEQ ID NO:291: CATCHIGGE ATTGGAAGS AGGACGAA AMACCUTACC ATCAGRATIG COGTOGAGAA (CAACACCTC ATCCCATTCA TYTCOCTIGG: GRACHIGGA ATTGGGAGA ACGGACAGA ATCAGRATIG COGTOGAGAA (CAACACCTC ATCCCATTCA TYTCOCTIGG: GRACHIGGA ATTGGGAGA ATCAGCAGA (CAACACCTC COTAACGCT CIGAGAACAT COTTCTIANG GRACACAACG ATCAGCGAA (AAGACTTC COTAACGCT CIGAGAACAT COTTCTIANG GRACACAACG ATCAGCGAA (AAGACTTC COTTAACGCT CIGAGAACAT GATCCTTTA GCAACCAACG TATCTGAGAA (AAGACTTC TCCGTTATCT TCCCAACCGC COTTGGTCAT GCAACCAACG TATCTGACGA (ACTGTCCGCT AATCTTGATG ACGCGATACGC COTTGGTCAT ACCAGTACAT (ACTGTCCGCT AATCTTGATG ACGCGATACCAC COGTAGACTAT TAACCAACTTC GAACGAATTT (ACGTAGAATCT TTGGCACGT ACGAACCACAC GTCCCTCTA ACCAGTACTT (AATCTTGAACTCT TCCCAACCCC COTTGGTCAT ACCAGTACATT (AATCTTGAACTCT TCCCAACCCC CAACCAATT TAACCAACTTC GTCCCAACGG (AATCACACTT TTGGCACGTT ACGAACTCCT CCAACGAATTT TAACCAACTTC GTCCCAACGG (AATCACACTT TTGGCACGTT ACGAACTCCT CCAACGAATTT TAACCAACTTC GTCCCAACGG (AATCACACTT TTGGCACGTT ACGAACTCCT CCAACGAATAT TAACCAACTTC GTCCCAACGG (AATCACACTT TTGCCAACGC GACATTTTGC CAACGAATTT TAACCAACTTC GTCCCAACGG (AATCACACTT TTGCCAACGC GACATTTTGCC CAATCCACTA AAAAANTGTTTAAC (ATCACACTTT TTTTTCCAAACG GACAATTTTTG GGGAACAAAA AAAANTGTTTTAAC (ATCACACTTT TTTTTTTTTTTTTTTTTTTTTTTTTTTT		TCCCCAAACC CNGGGTGANT TCCCCNAGGT TINNNCCAAA CCGGCCGGTT NCCGGATTIN	720
(2) INFORMATION FOR SEQ ID NO:291: (i) SEQUENCE CHRACTERISTICS: (A) LENTH: 878 base pairs (B) TYPE: nacleic acid (C) SERANDENESS: single (D) TOFOLOGY: linear (ii) MCLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PRG1242UP (x) SEQUENCE DESCRIPTION: SEQ ID NO:291: CATCHISTC ATTORDAGG ASSIGNMENT ACCURATED ACCURAGE GAAGGACTA ATOCCATICA THICGCIGGC GRACITEMS GOGGAAGGA ACCURAGE GAAGGACTA COCCATICA THICGCIGGC GRACITEMS GOGGAAGGA ATGAAGGAA GAAGGACTA GOTAACGGCT CIGAGAAGAT CONTITINIS GOGGAAGGA ATGAAGGAA AAAGATHICG ATTOCTCCA AGATTACTT GAACACTITA GAAGCAAGG TANCCGAAA AAAGATHICG ATTOCTCCAA AGATTCACCC COTTGGIGTA GAAGCAAGG TANCCGAGAA AAAGATHICG ATTOCTCCAA AGATTCACCC COTTGGIGTA GAAGCAAGT COAGAGAATTT GACGAAGTT TOCGAACGGC COTTGGIGTA ACCAGTACAT 42 GCTAGAATCT TIGGAGGAT CCAAGCATCC AGGAAGAAT GTOCTCATG CAAAGAATTT 46 AATGITUTAC TITGGAGGAT CCAAGCCTCA CGGAAAGAAT TAACCAATTC GTTCCAAGGG AAAGAATTT TITGGAAGATT TACGAACTCC CAAGCAATTT TAACCAATTC GTTCCAAGGG AAATTTCACCAACTCC CCAAGCAATTT TAACCAATTC GTTCCAAGGG AAATTTCACC CACTCCCGGA GOGATTTGCC CANCGATTT TACCAACACTTT ACCAACACTTT TACCAACACTTT TACCAACACTT TACCAACACTTT TACCAACACTTT TACCAACACTTT TACCAACACTT TACCAACACTT TACCAACACTT TACCAACACTT TACCAACACTT TACCAACACT TACCAACACTT TACCAACACT TACCAACACT TACCAACACT TACCAACACTT TACCAACACT TACCAACACT TACCAACACT TACCAACACT TACCAACACT TACCAACACTT TACCAACACT TAC		TICCNEGGAT TOXOGGAANIN CIAAAAACNGG GCNAITCCNI NGGGGCCCCC CCGCNTCCCCC	780
(i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 878 base pairs (B) TYPE: nucleic acid (C) STRADELINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) 25 (vi) ORIGINAL SOURCE: (A) ORGANISM: PRG1242UP (xc) SEQUENCE DESCRIPTION: SEQ ID NO:291: CATCHIGICG ATTGINANCE ACCACCARA NANCOCIACC ATCAGIGITE COGTICAGAA CAACCACTIC ATCCCATICA THICCCIGGO GEACHTCAGA ACTGIGITE COGTICAGAA GAAGCACTIC COTAACCGCT CIGAGAAGAT CGITCTIATG GEGOCACGGG ATGAGCGAA AAAGATTICG ATTCCIGGCA AGITCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGGAA AAAGATTICG ATTCCIGGCA AGITCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGA AAAGATTICG ATTCCIGGCA AGITCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGAA AAAGATTICG ATTCCIGGCA AGITCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGAA AATCCAGGGC TCCGGTATCT TCCCAACCGC CCTTGGTGGAT ACCAGTACAT ACTGICCGCT AATCTTGATG ACCCCATCGC ATATCCTCGC CAGTCGTCTA ACCAGTACT CGTAGAATCT TTGGAGGTAT CCAACCCCTCA CGGAAAGAAT GTCGCTCATG CAAAGAATTT 46 AATGTICAGT TTGGAGGTAT CCAACCCCTCA CGGAAAGAAT GTCGCTCATG CAAAGAATTT AATGTICAC TTCGCCAGTT ACCACCTCA CGGAAAGAAT GTCGCTCATG CAAAGAATTT 46 AATGTICATT TTGGAAGGG GGGATTTTGC CAACGATTT TAAGGATTC GTTCCAACGG AATTCAAACGT TTGCCAACGC CCCCCCCCAGA GGGATTTTCCC CATCCACCAACA AAAGATTTTAC CAACCCCCCCCCAA CGGATTTTCCC CATCCACCAACA AAAGATTTTAC CAACCCCCCCCCC AGITCATCCC CATCCACCAACAAAA AAAANTGTTT TCCCCCAACCAC TACCTTATCCCC AGAGATTTAC CACGCCCCCCC AGITCATACAC AAAANTGTTT TCCCCCAACCAC AAAGATTTAC CACCCCCCCCCC AGAGATTTCCC CACCCCAACCAACAAAAAAAAAA	15	ANTITICONIT CAACNOCCCC CAAACAACAC CCTGGGGGNIT ACCCCCCTCCC N	831
(Å) LENGTH: 878 base pairs (B) TYPE: mucleic acid (C) STRANDELNESS: single (D) TOFOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) 25 (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI242UP (xa) SEQUENCE DESCRIPTION: SEQ ID NO:291: CATCHIGUGE ATTGUARGE AGRACARA RARCECTRAC ATCAGNGTUGE COGTOGRAM CARCARACTO ATCOCRATICA TOTOCONGE GRACENGER AUTHOCRAGE AGGICACTRY GRACOCCTIC COTRACOCCT CUGAGAGEAT CONTOCTRIC GRACEAGGEA TRACEGRAM GRACARAGE GUGARITUTO AGRATUACTU CARCACTITIA GUARCACAGG TRACEGRAM ARACATUTOS ATTOCHOGRA AGTUCAGGO TOTGAICGAT GRACEAGGA TRACEGRAM ANACATUTOS ATTOCHOGRA AGTUCAGGO TOTGAICGAT GRACEAGGA TRACEGRAM ANACAGUTT TOGATATOT TOCCARCOCC COTTGGIGRAT GRACEAGGA GACAGGAGAA ANACAGGIC TOCGTTATOT TOCCARCOCC COTTGGIGRAT GRACEAGGAT COMPAGNATOT GOTTGAICGAT GOTAGARICT TUGGAGGIAT CUARGCOCTA COGRACAGAT GROCETCAIG CARAGAATTT GOTAGARICT TUGGAGGIAT CUARGCOCTA COGRACAGAT TRACGGARICAT GUARGAATTT ANTIGAANIT TUGGACGIAT ACCACTOCCOCA GOGRATICOC CONTURARAN ARANITITINA ANTICACANIT TUTCCARAGG GRAATITITG GOGRACAGAA ARAANITGINI TOCCCOGNINA TINCCITATUT INITIACAGGO COCCOCCOCC RISTITOCHOC GRICGARACC NANITATING TOCCITICOCCC AGRACATUTAC CHOGGOCANIN CAGGGGANIC CINCTITUTIN CITCOGGANIC AANAGAGGA ARAACCININ GCITITOCAC GONIGANAAA ARAATCONICO COCCCAGAGG		(2) INFORMATION FOR SEQ ID NO:291:	
(XI) ORIGINAL SOURCE: (A) ORGANISM: PAGI242UP (XI) SEQUENCE DESCRIPTION: SEQ ID NO:291: CATCTIGUE ATTORAGE AGGACAGA ANACOCTIAC ATCAGIGITG COGTOGAGA 6 CAAGGACTC ATCCCATTCA THTOGCTOCC GGACGIGGAG ATTHTOGAGG AGGIGACTGT 12 GAAGGACTC COTAACGCCT CIGAGAGGAT COTTCTIATE GGGCCAGGG ATGAGCGAA 18 GGAAGCAAG GIGAATGTC AGAATTACTT GAACACTTTA GCAAGCAGG TATCTGAGAA 24 AAAGATTTCG ATTCCTCGCA AGTTCCAGCC TCTGATCGAT GCAGACGATG TCAGGGAGAA 30 ATTACAAGGIC TCCGTTATCT TCCCAACCCC CCTTGGTGAT GATACTGTGT CGTTCTAGGG 36 ACTGTCCGCT AATCTTGATG ACGCGATCGC ATATCCTCCC CAGTCGTCTA ACCAGTACAT 42 GGTAGAATCT TTGGAGGTAT CCAAGGCTCA CGGAAAGAAT GTCCCTCATG CAAAGAATTT 48 AATGTTCTACT TTGGACGTAT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG 54 ANTICAANIT TTGTACTACC CACTCCCGGA GGGATTTGCC CANTGANAC AAAANTGTTTAA 66 ATTACACATTT TTTTCCAAAGG GAGAATTTTG GGCNACAAAA AAAANTGTNT TCCCCGCANAC TTCCTTTTTTTTTTTTACAACC CCCCCTCCCCC NGTTTTCCACC CNIGAANACC NAANTATAGC 77 AANAAAGGGA AANACCNGN GCTTTTGCCA GGNTGANAAA AAATCCNCC CCCCCAGAGG 86 AANAAAGGGA AANACCNGN GCTTTTGCCA GGNTGANAAA AAATCCNCC CCCCCAGAGG	20	(A) LENGTH: 878 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	
(A) CHGANISM: PAGI242UP (CALCULTIC ATTROCAGGA AGACCAGAA AAACCCTACC ATCAGGACAA ACCAGGA ATCAGGACAAA ACCAGGACAAAA ACCAGGACAAAA ACCAGGACAAA ACCAGGACAAAAAAAA		(ii) MOLECULE TYPE: DNA (genomic)	
CATCHIGICG ATTGREAAGG AGGACAGAA AAACGCTACC ATCAGRGITG COGICGAGAA CAACCACCIC ATCCCATICA TITCCCTGGC GGACGIGGAG ATTTCCGAG ACGTGACTGT 12 GAAGGCCTIC CCTAACGCCT CIGAGAAGAT CGITCTIATG GGGCCAGGG ATGAAGCGAA 18 GGAAGCAAAG GIGAATGITC AGAATTACTT GAACACTITA GCAAGCAAGG TATCTGAGAA AAAGATTICG ATTCCTCGCA AGTTCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGAA ATACAAGGIC TCCGTTATCT TCCCAACCGC CCTTGGTGAT GATACTGTGT CGITCTACGG ACTGTCCGCT AATCTTGATG ACGCGATCGC ATATCCTCCC CAGTCGTCTA AGCAGTACAT 42 GGTAGAATCT TTGGAGGTAT CCAACGCTCA CGGAAAGAAT GTCGCTCATG CAAAGAATTT 43 AATGTTCTAC TTCGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAACGG 54 ANTIGAANTT TTGTNCTACC CACTCCCGGA GGGATTTGCC CGNITTAAAN AAGNTTTINA 60 ATNCACANTT TTTCCAAAGG GAGAATTTTG GGGCAACAAA AAAANTGTNT TCCCCGANNA TNCCTTATTT NITAACNACC CCCCCTCCCC NGTTTCCACC GNIGAANACC NAANTATNAC 72 CCTTTCCCCC AGNGACTTTAC CNGGCCNIN CAGGGGANIC CNCITTITTIN CTCCCGGNIC AANAAAGGGA AANACCNINN GCTTTTGCCA GGNIGANAAA AAATCCNCC CCCCCAGAGG	25		
CAAGGAGCTC ATCCCATTCA TUTCGCTGGC GGACGTGGAG ATTTTCCGAGG ACGTGACTGT GAAGGCCTTC CCTAACGGCT CTGAGAAGAT CGTTCTTATG GGGCCACGCG ATGAAGCGAA GGAAGCAAAG GTGAATGTTC AGAATTACTT GAACACTTTA GCAAGCAAGG TATCTGAGAA AAAGATTTCG ATTCCTCGCA AGTTCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGAA ATACAAGGTC TCCGTTATCT TCCCAACCGC CCTTGGTGAT GATACTGTGT CGTTCTACGG ACTGTCCGCT AATCTTGATG ACGCCATCGC ATATCCTCGC CAGTCGTCTA ACCAGTACAT GGTAGAATCT TTGGAGGTAT CCAAGGCTCA CGGAAAGAAT GTCGCTCATG CAAAGAATTT AATGTTCTAC TTCGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG ATTCCAAATT TTGTACTACC CACTCCCGGA GGGATTTGCC CGNTTTAAAN AAGNTTTTNA ATTCCATATTT NITAACTACC CCCCCTCCCC NGTTTCCCCC CNTCAANACC NAANTATNAC TCCCTTTCCCCC MAGGATTTAC CNGGGCCNIN CAGGGGANIC CNCTTTTTIN CTCCGGANIC AANAAAGGGA AANACCTCNIN GCTTTTGCCCA GGNIGANAAA AAATCCNCCC CCCCCCAGAGG	30	(xa) SEQUENCE DESCRIPTION: SEQ ID NO:291:	
GAAGGOCTIC OCTAACGGCT CIGAGAAGAT CGITCTIATG GGGCCAGGG ATGAAGGGAA GGAAGCAAAG GIGAATGITC AGAATTACIT GAACACTITA GCAAGCAAGG TATCIGAGAA AAAGATTICG ATTOUTCGCA AGITCCAGCC TCIGATGGAT GCAGAGGATG TCAGGGAGAA ATACAAGGIC TCCGTTATCI TCCCAACCGC CCTIGGIGAT GATACTGIGT CGITCIACGG ACTGTCCGCT AATCTTGATG ACGCCATCGC ATATCCTCGC CAGTCGICTA AGCAGTACAT GGTAGAATCT TIGGAGGIAT CCAAGGCTCA CGCAAAGAAT GTCGCTCAIG CAAAGAATTT AATGTTCTAC TICGCCAGTT ACGAACTCCT CCAAGGATAT TAACGAATTC GTTCCAAGGG ANTIGAANIT TIGINCIACC CACTCCCGCA GGCATTICCC CGNITTAAAN AAGNITTINA ATACACANIT TITCCAAAGG GAGAATTTIG GGCAACAAAA AAAANIGINI TCCCCGANAA TICCCTTATTT INITAACNACC CCCCCTCCCC NGTTTCCACC GNIGAANACC NAANIATINAC CCTTTCCCCC AGAGATTTAC CAGGGCCNIN CAGGGGANIC CACTTTTTIN CTCCCGANIC AANAAAGGGA AANACCNINN GCTTTTGCCA GGNIGANAAA AAATCCNCCC CCCCCGAGGG		CATCITICTICG ATTICTICAAGG AGCACACGAA AAACOCTTACC ATCAGTICTIC CCCTCGAGAA	60
Geaagcaaag gtgaatgite agaattactt gaacactita geaagcaag tatetgacaa 24 AAAGATTICG ATTOURGCA AGITECAGCE TETGATCGAT GEAGAGGATG TEAGGGAGAA 30 ATACAAGGIC TECGTATECT TECCAACCGE CETTGGIGAT GATACTGIGT CGITETIACGG 36 ACTGTCCGCT AATCTTGATG ACGCCATCGC ATATCCTCGC CAGTCGICTA AGCAGTACAT 42 GGTAGAATCT TIGGAGGTAT CCAACGCTCA CGGAAAGAAT GTOGCTCATG CAAAGAATTT 48 AATGTTCTAC TICGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG 54 ANTIGAANIT TIGTNCTACC CACTCCCGGA GGCATTTGCC CGNITTAAAN AAGNITTINA 60 ATACACANIT TITCCAAAGG GAGAATTTG GGCNACAAAA AAAANIGINT TCCCCGGANCA TICCTTATTT NITAACNACC CCCCCTCCCC NGTTTCCNCC GNIGAANACC NAANTATNAC 72 CCTTTCCCCC AGAGATTTAC CNGGGCCNIN CAGGGGANIC CNCTTTTTIN CTCCCGGANIC 78 AANAAAGGGA AANACCNENN GCTTTTGCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG 86		CAACCACTC ATCCCATTCA TPTCGCTGGC GGACGTGCAG ATTTCCGAGG ACGTGACTGT	120
AAAGATTICG ATTOCTOGCA AGITTCAGCC TOTGATOGAT GCAGAGGATG TCAGGGAGAA ATACAAGGIC TCCGTTATCT TCCCAACCGC CCTTGGTGAT GATACTGTGT CGTTCTACGG ACTGTCCGCT AATCTTGATG ACGCCATCGC ATATGCTCGC CAGTCGTCTA AGCAGTACAT GCTAGAATCT TTGGAGGTAT CCAAGGCTCA CGGAAAGAAT GTCGCTCAIG CAAAGAATTT AATGTTCTAC TTCGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG AUTTGAANIT TTGTNCTACC CACTCCCGGA GGCATTTGCC CGNITTAAAN AAGNITTTNA ATNCACANIT TTTCCAAAGG GAGAATTTTG GGGAACAAAA AAAANTGINT TCCCCGNCNA TNCCTTATTT NITTAACNACC CCCCCTCCCCC NGTTTCCNCC GNIGAANACC NAANTATNAC CCTTTCCCCC AGNGATTTAC CNGGGCCNIN CAGGGGANIC CNCTTTTTIN CTCCGGANIC AANAAAGGGA AANACCNGNN GCTTTTGCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG	35	GAAGGCCTTC CCTAACGCCT CTGAGAAGAT CGTTCTTATG GGGCCACGCG ATGAAGGCGAA	180
ATTACAAGGIC TOOGITATET TOOCAACOGE OCTTOGIGAT GATACTGIGT OGTTOTACOG 36 ACTIGIOCGCT AATCTTGATG ACGCCATCGC ATTAIGCTCGC CAGTOGICTA AGCAGTACAT 42 GGTAGAATCT TIGGAGGIAT CCAAGGCTCA CGGAAAGAAT GTCGCTCAIG CAAAGAATTT 48 AATGTTCTAC TICGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG 54 ANTIGAANIT TIGINCTACC CACTCCCGGA GGGATTTGCC CONTITAAAN AACNITITINA 66 ATNCACANIT TITCCAAAGG GAGAATTTIG GGGAACAAAA AAAANIGINT TCCCCGAACAA TICCTTATTT NITAACNACC CCCCCTCCCC NGTTTCCACC GATGAANACC NAANTATNAC 72 CCTTTCCCCC AGAGATTTAC CNGGGCCNIN CAGGGGANIC CNCTTTTTIN CTCCGGANIC 78 AANAAAGGGA AANACCAGAN GCTTTTGCCA GGNIGANAAA AAATCCACCC CCCCCAGAGG 84		GCAAGCAAAG GTGAATGITC AGAATTACTT GAACACTTTA GCAAGCAAGG TATCTGAGAA	240
ACTIGIOCGET AATICHIGATIG ACGOCATOGE ATATOCTOGE CAGNOGICTA AGGAGIACAT 42 GETAGAATET TITGGAGGIAT CCAAGOCTCA COGAAAGAAT GICGETCATIG CAAAGAATITT 48 AATIGHICIAC TITUGCCAGIT ACGAACTICCT CCAAGGATAT TAAGGAATIC GITTCCAAGGG 54 ANTIGAANIT TITGINCIACC CACTCCCCGA GOCATTIGCC CGNITHAAN AAGNITHINA 60 ATNCACANIT TITTCCAAAGG GUGAATTITIG GOCAACAAAA AAAANIGINT TCCCCGANNA 66 TICCITATITI NITAACNACC CCCCCTCCCC NGITTICCNCC GNIGAANACC NAANTATNAC 72 CCITTICCCCC AGNGATITIAC CNGGGCCNIN CAGGGGANIC CNCITITITIN CTCCGGANIC 78 AANAAAGGGA AANACCNGNN GCITTTOCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG 84		AAAGATITOG ATTOCTOGCA AGTTCCAGCC TOTGATCGAT GCAGAGGATG TCAGGGAGAA	300
GGTAGAATCT TIGGAGGTAT CCAAGGCTCA CGGAAAGAAT GTCGCTCAIG CAAAGAATTT 48 AATGTTCIAC TICGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG 54 ANTIGAANIT TIGINCIACC CACTCCCCGA GGCATTTGCC CGNITTAAAN AAGNITITINA 60 ATNCACANIT TITCCAAAGG GNGAATTTIG GGCNACAAAA AAAANIGINI TCCCCGNCNA 66 TICCTTATTT NITAACNACC CCCCCTCCCC NGITTCCNCC GNIGAANACC NAANTATNAC 72 CCTTTCCCCCC AGNGATTTAC CNGGGCCNIN CAGGGGANIC CNCITTITIN CTCCGGANIC 78 AANAAAGGGA AANACCNGNN GCTTTTGCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG 84	40	ATACAAGGIC TOOGITATCI TOOCAACOGC COTTOGIGAT GATACTGIGT CGITICTACGG	360
AATOTTOTAC TICGCCAGIT ACGAACTCCT CCAAGGATAT TAAGGAATIC GTICCAAGGG ANTIGAANIT TIGINCTACC CACTCCCCGA GCGATTIGCC CONTITAAAN AAGNITITINA ATNCACANIT TITICCAAAGG GNGAATTITIG GCGNACAAAA AAAANIGINT TCCCCGNCNA TNCCTTATIT NITAACNACC CCCCCTCCCC NGITTICCNCC GNIGAANACC NAANTATNAC 72 CCTTTCCCCCC AGNGATTTAC CNGGGCCNIN CAGGGGANIC CNCITTITIN CTCCGGANIC AANAAAGGGA AANACCNGNN GCTTTTGCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG 84		ACTOTOCOCT AATCTTGATG ACOCCATOCC ATATOCTCOC CACTOCTCTA ACCACTACAT	420
ANTIGAANIT TIGINCIACE CACTECCOGA GCCATTICCE CONTITAAAN AACNITI'INA 60 ATNEACANIT TITICCAAAGG GAGAATITIG GCCAAAAA AAAANIGINI TOCCCCAACAA 66 TINCCITATIT MITAACNACE CECCETECCE NGITTOCIACE GAIGAANACE NAANIATMAC 72 CCITTCCCCC AGNGATITAC CNGGGCCNIN CAGGGGANIC CNCITITITIN CICCGGANIC 78 AANAAAGGGA AANACCNGNN GCITTTOCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG 84		OCTAGAATOT TIGGAGGIAT OCAAGGOTCA COGAAAGAAT GIOGOTCAIG CAAAGAATIT	480
ANTIGAANIT TIGINCIACO CACTOCOGA GOGATTIGOC CONTITAAAN AAGNITITNA 60 ATNOACANIT TITICCAAAGG GUGAATITIG GOGAACAAA AAAANIGINI TOCOGANAA TNOCITATIT NITAACNACO COCOCTOCOC NGITTOCNOC GNIGAANAOC NAANTATNAC 72 CCITTOCOCC AGNGATITIAC CNGGGCONIN CAGGGGANIC CNCITITITIN CICCGGANIC 78 AANAAAGGGA AANACCNGNN GCITTTOCCA GGNIGANAAA AAATOCNOCC COCCCAGAGG 84	45	AATGITCIAC TTCGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG	540
TINCCITATITI INTIAACINACO COCCOCTOCCO INSTITICCINCO GINIGAANIACO NAANTATINAC 72 CCITTICCCCC AGRIGATITIAC CINGGGCCININ CAGGGGANIC CINCITITITIN CICCOGGANIC 78 AANAAAGGGA AANACCINGIN GCITTITOCCA GGNIGANAAA AAATOCINCOC COCCCAGAGG 84	_	ANTIGAANIT TIGINCIACC CACICCOGGA GGGATTIGCC CGNITIAAAN AAGNITITINA	600
CONTROCCC AGREATITIAC CNOGGECONIN CAGGGGANIC CNCITITITIN CICCOGANIC 78 AANAAAGGGA AANACCNGNN GCITTTOCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG 84		ATNOACANIT TITICCAAAGG GAGAATTTIG GOGAACAAAA AAAANIGINI TOOCCCANCNA	660
CCTTTCCCCC AGNGATITAC CNGGGCCNIN CAGGGGANIC CNCTTTTTIN CTCCGGANIC 78 AANAAAGGGA AANACCNENN GCTTTTGCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG 84	50	INCCLIATEL WILLYACTACC COCCCICCCC NGLILICCNCC GALCAANIAC NAANIATNAC	720
		CCTTTCCCCC AGNGATITAC CNGGGCCNIN CAGGGGANTC CNCTTTTTIN CTCCGGANTC	780
TANGANCONN GNAAGGNENG COCNITTOGA GAATINCCC 88		AANAAAGGGA AANACCNENN GCITTTGCCA GGNIGANAAA AAATCCNCCC CCCCCAGAGG	840
		TAAGANOONN GNAADGNONG COCNITTOGA GAATINCOC	878

	(2) INFORMATION FOR SEQ ID NO:292:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 844 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1243RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:	
-	GATOSCTAAT CCCCAGGITT GTTTCAAGT CIGICATCAG TTGGTTCTCC ACATCTTICA	60
	GAATTCTAAT ACCCTCCGAT GCCAGTTCCT CCAATTCCAT TCCCACCTCG CCAGACTCTA	120
20	TCTTTAGAGA GTAATTTTCC ACACACAAAG AGTCAATCTT GTCTTGAACA TCGTCAATCA	180
	TATACTICAG TACATOGTIC ATGITTIGGIA GATTCACTGA GCTTTTGAGT GCGCCTTTTC	240
	CTACCOCCGA AAGGITICCCC GCTTCATTCG ATGAGAAGCC TAGAACTGAC ATCATGGCGT	300
25	GOCAGCATGT CTTCCGCAAC TGTGACAACC AATAATTCAA GACTGCCGGG CCTAGATAAC	360
23	AGGCCCCTTG CCCGTCTGAG TCATAGCCTG AAGCCTCCAA GAAGGATTTC CATAGGTTAA	420
	CATAATTATC ACCEPTATE CETICAGAATT GAAGITEGAT TAAGIAATGA TECTECTITIG	480
	GGATTITAAT CTGATATICG ACATCATTCT TIGTATGAGG GATACAAAGG TIGAAACGIG	540
30	OGATGATATO AAGAAGTTOT CITIOCOGTGA AAGTOACACO GITGACACGT TOGAGCTTTG	600
	CGAATTTGFT GOOGGATCTA GATGCATCOG ATTGTTGCCC AGTTCCCCTGG TATTCTGGCA	660
	GACTIGTIGTIC GATATACTIT GGAGATCCCT TGAAGGGATG CACTIGCCATT AGAAATACAC	720
35	CTIGAATOON CIAGIGAATG ATAGGINIAC COGAACOOCC ANTITIGATA COGNOCAGAG	780
	TITIGINCATO GOCCCCTION NOTICOTOCO CACATIGOCT COCNATITIA TOCTGAAATG	840
	CTTA	844
40	(2) INFORMATION FOR SEQ ID NO:293:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 865 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1243UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:	
55	CANTENER CACCACTATE CHACTAGET CHACTETET THEACATCA ACTORICAG	60

	GACGTCGATC TTTTCGTCGT AAAAAGGCCG GAAGCCGCAC AACACGGTGT ATAGGACGCA	120
	GEOGRATOCCE CACATETOGA CETTCATOGA GIAGOSTICG TOCTTCACCA CETCOGGOCC	180
5	GGTGTACCCG ACAGTCCCGC ACGGCGTCGT GGTGTTGGTA GCATAAATTT GCTTCCAGAG	240
	TCCGAAGTCT GOGAGCTTTA TCACACOGAT CCCGCCGCCC CCGATGCCAG GTCGGAACAG	300
,	SCCCTOSTICT TOTTTIGTCT TTISGGTCGTC CGACTIGTCTC ASCTIGCTCGC SCTTIGCTCGC	360
10	TATAAAATCA ATTOOOGAGA ACAGCAAGIT TICTOOCTIG ATATCCCGGT GGACAATGCC	420
	AAGCGAGTGC ATGTGTTTTA CCGCCAGTGC CAGCTGCCTG ATTACATGTC TAGAAAGGTC	480
	CTCCGAAAAA TAAGTGAGIC GCACGATTIC TCCAAAAAIC TCCCCCCCG GCAAGCAGCT	540
15	CCTGCACTAT GAAGTAGTAT GACTGGGTCT CCCTGGAAGT CGATAAACGT CACAATGTTT	600
	TOCCOGRAGE ACACOGOCTT GTOCRATOGTG ATCTCCTTCA CARCTOCTCT COCCRATGTOG	660
	COTOTITIOSC COCCIOCNOC CINCTIMINAC GOGCOCCCC NOGIOCCCCC ATCOTIAANA	720
20	GENNOCTTIT GCTGATCNCC TTGACGGCNC CGTTINNTAC NGNCNAAGIN CCCTTTCGCN	780
	CONCCTICAG COGNICONNOG ANNOCONOGN AAACCOCONCC CNATTINGCC NAACTINTCC	840
	CIVICAANICCAA GIUNICCGAANIC CCCCCC	865
25	(2) INFORMATION FOR SEQ ID NO:294:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLDCULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1244RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294;	
40	GATICCTECCT TATICACGASC CCCATICCGAA CTTICCCCCGG GATIGTCGTTIG AGAGGTAGCG	60
	AGCICACCIC CACAACTICC TCATCIGAAT CGICTICGIA TGIACTATCT AGCICTICAG	120
	CGICGOGGA TGCAGATTCC GCCCTGTCTT TCACCTGTTT CAGCACCGCC TGTGCGTTAA	180
45	SCTCAGAGAG SCASSCATIST STOSCACOCC OSTATATICTIS SCCCAGSTAA TACCCCGTIGG	240
	CCAGCGAAGC CATCGTAACG CTCAGTATCA ACGGTAAGTT GATACCTGCC ATCCTAGTTT	300
	CTGTTTGGTA TTCTGCATGC TGAGTGCGCA AQCCAAGITG GTTGAAAATT CCTTCAAGCT	360
50	CACAATOOCT GETOCTGOGC GCACTITOAAC ACAGCAAAAC TOAGAGAGAG GTATAAACGC	420
	CATATATAGG AGGAGACIAC TCTATTCACT GCCTWICTTT TCAGCCCACA GITOCTCTCC	480
	CTOCAGAATT GTGTTGTGAT TCCGCCAGCA TTTTGTTCAT CGTCTCGACA TATTCGTCCG	540
5 5	TTATGATTOG GAATOOGTOG AACATTOOGC COCCAGOOTG TTAGATTAGG CCACACOGCC	600

CTTGTTAGAC CATAGTGCCC GAGTGCGATT ACAGGTTATC CNTCGAACAC CATCCGTAGA	660
ACCAGREGOT ACNOROGEN GITTAAACCCC TACGOTINCCC TITOCACTINIC CGATAGROCA	720
TACOCOGAAT TTGGOGGCC AAAAAAGTOC CONOCAGGAA CNCAAACGAA GNNTCAACGC	78 0
CNIGINITEG GENEGIECEN TITICENCAAA NEAGIOOGTA NITNIAANCE NOCENETTAT	840
INICCCCCAT T	851
(2) INFORMATION FOR SEQ ID NO:295:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 859 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) Original Source: (A) Organism: Pag1244UP	
(1) (10111111111111111111111111111111111	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:	
GATCAATCTG ACAGTTGGAT TGATACCAGG TGCTATCTCC TTATCAGCCT TTACAGTGAC	60
GAAGGAGGA TIGGATIGGG GAATGGAGAA TAAAGATATT TITGATCCAT CACCAGAAGG	120
ATTIGATOOC TOTTICAGIG AGCATGOOCA ACTITITACIC TOGGAACGIA TAATGGGAAA	180
CTTTCTCGTT CCAAAGTCTG GCATCTGGAA TTATGCATTT ATGGGTGCTG GATTTAACAG	240
AGAGCIACGI TACGAGCIAT CICTOGACAT ACCACTOGGA TITTATGATG AACAGCACOG	300
TOCAACOCAT TITICIACAAT TCAACGAAGT GOCAGCTGAC GATACTITIGG AAGCAGAACA	360
GGAAGATITA TICTCCTAAG TACATATTAA GGATAGAGCC AAACTTGCAA CTAGCTTCAG	420
THOOGHATGA ATCCCATATA TGHATATATC AATACACGGG CCACTCATGG CHGGIGACCC	480
ATTTAAGCAA ATACCATATT TTTTAATGTT GCGGTGATTT TATAATCTCG ATATCATGAT	540
TTTMFTTATA GGAGATGACT TTTCCCTCTA CAACGCCACA TTATAGAAGA CCGTCAATGC	600
AGCACCCAGG CTGAAGCCAG AACGGAAATG TTGGAACCAG AACAGGCAGG TTTGAATAGC	660
TOGACATATG AACCTCCCCA GAACATGTTT TTTTTGAACA TONAATGANT TTCTGCCAAA	720
AACANGAAAA TOGACNOONN GCATCATTCA AAAAAAACON TOOTTGAACC TGACAAAAAA	780
TATOCACCON GATTITITGA TCACOGANNO TITITCITTAC NCCAATTAAA TAGGNCCCCC	840
NGAGATITIT ACACCCNCC	859
(2) INFORMATION FOR SEQ ID NO:296:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 833 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1245RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:	
	GATCAAAAAC AGAGTACCCT COGCACGAAC TITCCCATATG AGGCCCAGAG AGAACAACAT	60
15	CGCCGATCAC CTATATCAAC AACGGAGACC TIGGTCTGCC GAGAACGTCA CAGCTTATCT	120
	TATTATOGAT CGAATGGATG TTGGAAAGAA GATACAAAAT AACGCATAAT TOCTGAATAT	180
	ATTIGCACGCT TCTAACGCAA ACGACGAGGC TCACGCTCAG ATTICCATCAA GACCAAGATG	240
	TOSTICICIC TAACIGOOCC CTICACCITT CTCACAATGG TICIGGAAGT GTOGTOCAAG	300
20	AACTCAACOC OGACCTOOGT GACACCAOCA OGAGAACOGG TTOTACCTAG AACCTTGATA	360
	ACCITIAGCIA GAGTGACTOG OGTCTTOGAG TCCATTTTGA TCTATTOCTT CTTOGATATA	420
	AAATATCTAG TAAAAAGTOC TGAATAGGTG AGAGGAAGAT ATCATGAACA GOCGGTTTTT	480
25	TTTGATGCCC CGAAAAATTT TTCAGGTCTG CGATGCCCAT COCAGGTGAA ATGTGCTTGG	540
	GTTCTTGAAA AATCACATCA TACGATAACT ATGOGTGCAC CCAAAGGCCT TGGCAGCAGC	600
	GAAGTOCCCG AAGGTTAGCC AGCCCAGAAC GAAAACCTGAG AACAGGTTAA GCTCAGGTGA	660
30	ATTGTPTOCT TCTATTGCCT TACAGTTCAT CTTCCCGTAA TTCCAGTATC CGTTGATTCC	720
	CONCAGCIGA CCAGCOGI'IN ATTCCCGI'IT GAACTITICAG AGNICNIGAA ACCCTNGINI	780
	THICAACCON TEACACNIAT ATCNCCCCCT TATATGACTT COGTONATING COG	833
35	(2) INFORMATION FOR SEQ ID NO:297:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 864 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1245UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:	
	GATCCGGGTA ATACAACGCC TCGGACCCCT CGGCGGCTAA CGAGAAAATC GCGCTAAGCT	60
50	TOCACCOTAA TOATAATAAA AGGGCCATTG GTGGAAGCTT TOTGGTACTT ACGCGAGTAA	120
	ACAAAAGGGG CAAGGAGGTT TOAGAAGAAG OOAGAAGCAG CAATGAGGGA GATGAACTOG	180
	ATCATTCACA GAGTGAATGT ACTGGTCTCA AAACTGCCCA AAGAGAAAGGA TGCAGGCCTG	240
55	GAGAAAGAGT GCGCGCTGAT CAAGTTGGGC GGCATGGTAT CTAACCGGCGA ATCGGGCCCTG	300

	TIGITIOCAG AACTOSCOCA OCAGATOGAT COCACAGOOG TOCTACOGCA OCCATOGATT	360
	GICCAGITIG TIGIOCCCIT GOCCAACGAG CTATOCCGGC GTGCCGAGGI GCCCGAGACC	420
5	TTCTGGGGCA AGATATTGGT TCCGTTGGAT GGACAGACCC CGTTATTGAC AGTTACTAAC	480
	AAGAATOCAG OGTOCGAAGT TITTCOCGTAA TGTTOCCGGTC CATGOCCGGT TGGTGGAGGC	540
	OCTOCTOGAC COCCCCTIGT COCCTACGOC TCCCTGTCCG TCCCAGAATA TCCCCGTTGTT	600
10	SCICCASCIG TOCTATINNAC CINCOGGATT MICCOGGAGT TOMICACCOC CCITTACCCC	660
	CCCCCTINICN AGNATEGITG GNGACCNITT GNICGNITIC CAACITCCIT MINCCCCNCT	72Ò
	TITITICNAC NITGAANCNA TITITICCCCC TINAANICAA CONACCNGIT NINNCAACCC	780
15	CCCCCCCCTT TGGGAAAANN AGNAAAAAAN ACCTTTTCCA CCCNGGAINC CCTTTGGNCA	840
	NCTOGRACING NUMBUTIONS COTIC	864
	(2) INFORMATION FOR SEQ ID NO:298:	
2 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 830 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1246RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:	
	GATCAACAAT GATIGIGGGG ACGGGGGGGG GGGGGTTCAA ATTCTACGAC GTGCTGCTGT	60
	COGRATUTOC GOOCGIGTON GATATOCTOC GOCTOGRACIA GATOGRACIOC CTGRACGARGO	120
35	GETTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG	180
	OCCANGOCAC OGTOCATOOG CTGGCGCATG ATGAGATGTA CCCGTACATG CTAGTGAACA	240
	TAGGATCCOG GGTCTCGATT CTCAAGGTGG AGTCCCCCAA CGAGTGCATG CGTGTGGCCC	300
40	OCTOCTOATT GOOCOGGC ACCTIGIOGG GACTACTOTO OCTAATTACT GOOGGCAAGA	360
	CGTACGACGA GATCCTGGCC TGGGCAAACC AGGCCAATAA CGCGAACGTG GACATGTTGG	420
45	TAGGCGACAT ATAGGGCACC GACTATGCGA AGATGGGCCT GAAATCCAGT AATATTGCAT	480
45	CETECTITOGE GAAGGICTIC CAACGGGAGA GCCTCACGGC GCCCCTCGGC GCGCCTGACT	540
	TOGGOGTOTG OGACCTOGAC GTGTGAGATC OGACATTOGA AATGAGAAAT OGNNCAGGOC	600
5 0	CANTINITICC ATCOCTONIG TACCOCATOTO CANCANATOC COCANATOCT INCIGCAGOC	660
	AAATCCCCAA CICCAAAAAA NNICTTTGCG GTCNFTAINT CCCCGCCTTT TACCCCCTGA	720
	CCCTITACCC CCCCCTAACT CNGGTCNAAN GNITTTAACA NCCCNCCCCC TNAGGNITAA	780
	GGINNIGGCC CONGCCCCT INTIGCCCCA AAAATTICCC NNCGVITCIN	830
5 5		

(2) INFORMATION FOR SEQ ID NO:299:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 861 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1246UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:	
15	CATCOTIACAG CGTGAGACGG CACOBBOBGA GOCGOCAGGG COGGAGGGTG TGCAGOCAGG	60
	GOOGTITTCCT CAGCTGTACC GOOGGCASC GATATCTAGC TGGGGCCAAC GOCTGCAGAA	120
	CANCANTOCO CONCOCCOCO COCOCOCOCO COCACOCOCOCO COCACOCOCOCO	180
20	CCACAAGGAA AACATGGCGT ACATGGAGGG GCTGTGGGAG GAGCAGGGGA CGGCAGAGG	240
	COSCEARCIE TIMCAGAGCO TOGACCOCAA GETOGIGCAG GOETTGIACO ETCOGITIGCA	300
	TOCACOTOCA OCACOGACO GAACOCCOCO CTTAGTOCCO GAAGTOCAGO GAGCOCCAGO	360
25	CACTICOCTIC GCCGCCACCC GCCACCACCC CATCATCCCC CCCCTGCATC ACCCCACCT	420
	OCACGOOGC CTAGGOGGC CACAGGCTTC GATGCCAGAG GCCGGCCCA CCTAGGACCT	480
	OCCADCOCC CTOCACCATE COCACCACAT COCOCCCCAG CAATACCACT TCATCACCAC	540
30	ATGGACCATA TGAAGGACAG GACTTGCTIAC GAGATATCCA CTTCCTCCGC AATGAGACTG	600
	TOCOCCOCAG ACTOCACATO AACGACOCCA ACTITIATGAG CAGCTGCACG AGAATACTTC	660
	COGATIVITICO GAAAGAAANA AATAACTINGA ATOGATGAAG GOCACTGAAC COTGACACTO	720
35	THETINETAAC TENECGATTT TOCCGAATGC CETCCAACTT ACCOCCATE TOCCCCCCC	780
	CCGCAATTIN NICCCCNNAA CNGCCICNNC CCTTCGAAAA CCCCCCTTIN CCGGCNITCC	840
40	TCCCATTTCC ACVITCCCCA C	861
40	(2) INFORMATION FOR SEQ ID NO:300:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 810 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1247RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:	
55	GATCTGGCCG CCCACCTCCG GCCTCGTATT CCTCCCCTGC GTTACTGTGG CCCCGCCGCC	60

GIGICTTATT COSCATCOCG TACGOGICAC TAAGCCCCTC CAGGACGGGC ACAAAAAGCG	120
CAGGGGGTC ATAGAGCACC ACAGGGTCTG GGTCGGGAAG CAGGTGCATC CGCGGGGTGT	180
CONTROLICAC COCCURGINGO COCCURGOCCO CONTROCACO COSCOCAGOO CITIOCACCOC	240
CCCOCCCCC CCCCCCCCC TOCACTICTAC COCCACCCCC CCCCCCCACC CTCCCCCTTCC	300
GCACCOCCTT GATGACCCOC TTTTGCGCCCCG GCCCGCGCGC GCTCGCCCGA GCGAGGGCCA	360
OCCCOORCIG CACACRCATC ASCATCOCAT OCACCRCTT OCTGTOGTCT TOCACCACRC	420
TETEROCTICA AGCAGACTET COGCTATCTC CTCCCCCTCG GACGAAAGGC CTCGTCCCTG	480
CHOSACTOSC TOTOCCOSTA CTTCCGTOGA AGTACGCGCG CAGTOCCGCC GCGCGCTTCG	540
CCTCCGCCGC CGCCGGCGCC CGCGAAGGGCA CGTTAGGGCG CGGAGCCGCC GTCAGACCCCT	600
CCTCATCGAA TCCGAACCGC TCGCGCCCTC GCGCCAATCG CCCACGGAAC CANCCCCCG	660
OGGOGITHNOG NOGOCCOGOCC GOCCCCCTOC TITTINAAAAC GACNACCNCT TONAAANCCG	720
TIACCCCNCN CNNITCAAAC NCCNGGAAAA ATTTICGNCN ANNANNANN CCCCCCCCCC	780
MINCHNICAA AMAAMANCHOON GOCCCTINICO	810
(2) INFORMATION FOR SEQ ID NO:301:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 630 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1248RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:	
CATCAGATAC COTOGTAGTO TTAACCATAA ACTATOCOGA CTAGGGATOG GGTOGTGTTT	60
TOTTATGACC CACTOGGCAC CTTACGAGAA ATCAAAGTOT TTGGGTTCTG GGGGGAGTAT	120
OGTOGCAAGG CTGAAACTTA AAGGAATTGA COGAAGGGCA CCACCAGGAG TGGAGOCTGC	180
GOCTTAATTT GACTCAACAC GOOGAAAACTC ACCAGGTOCA GACACAATAA GGATTGACAG	240
ATTGAGAGCT CTTTCTTGAT TTTGTGGGTG GTGGTGCATG GCCGTTCTTA GTTGGTGGAG	300
TGATTIGICT OCTTAATTOC GATAACGAAC GAGACCITAA CCTACTAAAT AGTOCTOCTA	360
CONTITUCIE CITOCOCACT TCTTAGAGOG ACTATCOCTT TCAACCCCAT CCAACTTTCA	420
OSCANTANCA OSTICTISTICAT GCCCTTAGAC STTCTGOCCC GCACGCCCCC TACACTGACC	480
GAGCCAGOGA GTATAAOCTT GGCOGAGAGT CTGGGTAATC TTGTGAACTC GTCCCGTGCT	540
GOGGATAGAG CATTGCAATT ATTGCTCTTC CACGAAGAAT CCCTAATAGC GCAGTCATCA	600
CITECGITGA TACTICCCCT GCCCITGIAC	630

	(2) INFORMATION FOR SEQ ID NO:302:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 700 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1248UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:	
	CATCOCTAGA TOCCCAGGAT GAGACTOTTIC AGGITAGOCA GGTGTTGTAT GCGCCGCCAG	60
	ACCCARACCC AATGACTTTG CATAGAACAA ACCCGCCATC ACCCATGTCT TOCGCTGTAT	120
20	AGAGACIAAG GTATCTGACG ATCCCTTAGC GACTCTCTCC ACCGCTCGAC GACCCCATTG	180
	ASCICTIACG AACTOCACAA ACCIACIOGA ACTOIGITIC CAGACIICIT ICIGITIGIC	240
	TICAACTGCT TICGCATGAA GIACOCCCCA GGCTATITTT CITACCCGCC TGGTGITTGT	300
25	CTATATACCC GGTTGTATTT TTGATAAAAA ACTCAGCTCT TCCTCTACGG CAGAAATATA	360
	TATOCAGTOC TEAGOGOCAT GOCAAAATCE GOCTFFFFAC COCTGETTOT COCAGTOTTA	420
	GCACTGOCAG AAAAAAGATG TATOOOGTAT AGGCGCTGOC COCGGGAAA AAAAAAAAAA	480
30	ATAGAAAAAT AGAAAAATAA AAAGAOGTOG GOOCCCCCC GOOCAGACGA AGAAAAAATA	540
	COCCCACC CCTCCCAACC AGACGAACAG GOCAGACATA ATAAATCCCA CACCAGOGAA	600
	GARAGICTIG IGCACGCICC CECCICATAC GCIGCCATCI GITCCATCOG GMITGCAACC	660
35	AGTATIGGATG TICAAGCATG TCCGANGCTC COCTGCCTTG	700
	(2) INFORMATION FOR SEQ ID NO:303:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENCTH: 837 base pairs (B) TYPE: nucleic acid (C) STRANDFINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1249RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:	
-	CATCATOCAA CATTICTICT TRICCOBCTT TCTGCCTGTG CCGGACGGTG TGTCCCCGCC	60
	CCGCACCTCT GAGGAAGAGC TTGCGGACTG CAGCGAGCAT GCCCACAGTA CCTGGGGCGA	120
55	CTGCTGCGGC ATTCCCATAC CCAGCGGGT GGCCGCCTCC GAGGCCACTC GCAAGCATTC	180

TAA	ACCACIT	CCATTCGATT	GAATCAAATT	ATATATACCA	TTAAGTAGAG	CTACCATGCG	240
AAC	CTTAGCT	CCCACCCACT	AAAGATTOOC	OCTITICCAGA	TCAGCITICIC	CCCCTCCCATC	300
GAT	CCCTTT	TCTTCCCTAT	CACCTICTOG	TACCTTAGCA	OCACGICCIC	GTTCAGGTAC	360
AAG	ATGIGCT	GCCCTTGTA	ATATOGCAGT	ATGTTAAGAG	CCTTGGCTGT	GTCCAGTATC	420
TCT	GTAGTCG	TCACCCATGT	CATGCTACTG	ATTTCATCGA	TOGICATOIC	GCTGCCGTTT	480
TCG	ACTAGCA	GCTTGATCAG	OGITATOOGAC	CAATAGGCTC	TGTAGAGAGC	ACCCAAGAT	540
CAG	AGAGCCG	CTTCTCCCGGC	ACCCAACTIG	TTCTCCTTCT	TAGAGAGCTC	CATACGAAAC	600
TCA	ATCAGCA	COCTCCCCTA	CCCCATCCCC	TEGRACICAG	GCAGCGICCA	GAATACACGC	660
CAC	ATTGIAC	COGTCOGCCA	NICCITICON	TTOGANAATN	CCCACCAAGT	NGGTGCCCCA	720
CTC	ACTCCCC	TEIGITICITE	CANTAAAAA	AAGGICAANT	TCCTATNACT	CNICIGNICC	780
AAA	AAACITT	CANAAACNIN	GTTGCGNACC	ACTICCINNT	NCCCCCTCAA	TICAAAT	837

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGIH: 853 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDETNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1249UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

CACCTGCCCA TGCACNGCCG TIGGCACGTG ACTGCCCTAC GGTCTTTAGT CCCCCCAAAG 60 OCCATOSCOT TIGTOGOCAC ACOCAAGAAC TITGGCAATGA TGTTGACCAC GTCCATGGTG 120 TOCTIATIOT COTTGUACAT TGUGAAGTOC ACGCAGTTCT TGGAGGGGCC GTACCCCAG 180 TTAATGACAC CETTCTCGTC TCTTGTCTGC TCCACATAGT CCTCTTTGCT GACTCTGGTT 240 TTACCGTTCG CCACCCCAAT CTCGAATGTG TTCGACCCCG AAGTGACCGA TTCAAGCTCA 300 TRIFICAACG COTTOGRAG CACCEGIGG ATCITCGROC GROCAGOTTT GROSTCAAAG 360 CICCIGGIGG TITICCATITIT CGIGACGITC CIGTACACGG CCTCAATCIG CIGCATGICC 420 TECTOGOCCA GIAGOTOTAC CAGOTOGITIC COCAGOTOTO COTOCACOGO GIAGOTOGIGG 480 COCCUTTOCC CONTINUES CIRCUITICC TICACCIGGT COCCAGAGGT TICAGITITAG 540 CAGOCATTITI GAACCCATTG TCCCGCAAGT ACACCACTGT TCCATCCTTC TGGATCTCAT 600 TGACCATGAA GTCGGAATAG COCTOCTTGA TCTGCCCGCT AAACCCTGGT ACTCTGCTGA 660 CAGGTACTICT GTGATCCAAC GTCGATTCCT TGAGTCCATC GGTCTCCGVT TTGGCCCCTT 720 NCONCAAAAG TICCTGCCTG CICCNNANCC CCTCTNTAAT CCCCCGAAAN TCTGTACNNT 780

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TONONATTIC COMMININOC TACCINAACC CITCHINAAC CITCCACCON ANAANTCATA

	AATATTICCCC NCC	853
5	(2) INFORMATION FOR SEO ID NO:305:	023
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 834 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1250RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:	
20	ATCITAATIT AAAATITTAA TIAACTATIT ATAATITAGA AATATATAAT CTAGAGATAT	60
	ATRATCTTAA AATCATAGGT AAAAATACAT AAGATAGTAA GAATAAAATT AGTAAAATAA	120
	ATAGAAAACC ATAAGTTAAT TGATTCATAA AGAAAAATGG AATTATTTGT GGCATCTTAA	180
25	TTTTTATTAT TTAATTGATT ATTATCTATT TAACATAAAA CATTTTAAAA TGTTATAAAA	240
	TAAATAAGAA ATTACTTATA GAATATTTAT TAAATAGTAT TITAATTTAAT TITAATATTA	300
	AATATACCAT TTTTATTAAT AAATAGATTA TTAAGTTIAT TAATATTAAG TGATATATAA	360
30	TTTAATTAT ATAAATTATT TAATTTACTT CATTGATATA TATAATTATT AAATGTACCT	420
	TTCATAATAT TTATTTTAT TAGTCTAGTA ATATTTCTAT TTAATAGTCT ACCUTTAAT	480
	TOGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTFAAATCT	540
35	ANTAATTAT TATCTAAAGT ATATAAATTA ATTAAATCCT TITTTATTAT TAITTAATTA	600
	TTATTAATTA GIAAATTATA TTTATTATTT TATTAACATA ATTTTTTGAT AATAATATAT	660
	CCATAITAAA TOGTAATTTA TTAATAATAT CCTTTAATGA TITNATGATA ACCNTATTAT	720
40	TATGANATTA GITAATAGIG ACCITAATAT COCNATOONA ATATAINIAT TIATTINIAA	780
	NAACANANAA CITCITATINI CATATTTANI TINANIATIN ACCNITIOCN NINT	834
	(2) INFORMATION FOR SEQ ID NO: 306:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 847 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1250UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:	

	GHORRAL TORONTH CONTINUE HOLDING CONTINUE	00
	CATCATTIAG TITATTAGGT TIACTATTAA CITTAGCTIT TACTATACAT GGTATTATIG	120
5	GTAATATTTA TOCTTTATTA TTATCTTTAT TAGTAGTTTT ATTACTAATA ACTITATGAT	180
	TTAGAGATAT TGTAOCTGAA CTTACTTATT TAGGTGATCA TACTTTAGCT GTAAGAAAAG	240
	GENTEACHT AGGITECCEN TENTEGRIG TATCEGNAGE ATTANTITET OCCUPANT	300
10	TTTGAGCTTA CTTCCATTCA CCTATAAGTC CTGATATTCT ATTAGGTAAT GTTTGACCAC	360
	CAGTAGGTAT TGAAGCAGIT CAACCAACAG AATTACCATT ATTAAATACT ATTATTTTAT	420
10	TAGCATCAGG TCTAACTATT ACATATAGTC ATCATGGTTT AATTGAAGGT AATAGAAAAC	480
15	AUCCUTIAIC AGGITTACTT ATTACTTTCT GATTAATTGT TACATTTGTA TTATGTCAAT	540
	ATATTGAATA TAGIAATACA TCATTTACAA TTACAGATOG TATTTATOOG TCCAGTATTT	600
20	TROCTOGRAC TOGTTACATT CTTACNTAIG GRTAGRITTAC TAATTAGGRA GGINCTATTA	660
20	NCAANAACAA GAAATTNOCT TTAACNOOCN COCCTOOGTT NGANATNNAA CONCACCTAT	720
	TATTACNVIT TTINAAAATA NIGAANACCC CANNATTGIT NIAANGAAAG GNVIAACGIN	780
25	NACINCACCON TAGNINITING GTCCCCCCCC NTOCTACCCC ATTITICNICCC CCCCCACAAN	840
	AACCCCC	847
	(2) INFORMATION FOR SEQ ID NO:307:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 825 base pairs (B) TYPE: nucleic acid (C) SIRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1251RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:	
	GATCAGGAGG GITTIGOGGI OCTGCCCCAC GCCGGGITAG AGGIAATGCT CCTGCCGAGAG	60
45	GATGACAAGA CTGTCCCTGT GTACCCCCAAA GTCCCAGAAT AGTGTATACT ACATAGTCAT	120
70	AGITATAATA AACAAGOOGC GGCGGGCTCT AACCAAATGC GGAGITGCCC ATGCCACCGG	180
	GGCCGCCGGG GCCGCCGGGGGGAAAC GCGCCGTTCCA GCGCCCACCG GGCAACAAAC	240
50	CONSCIONAT GCGCONGFTCC GCGNGGTCCG CGNGGTCGAA CTGCCCCCC TAGGCCACCC	300
	GOOGGETIGGS COGTTGTAGC CGCGGATCGA ATATCATGCC GCCCTGCGGG TTGGGCGCGG	360
	GAAAGGGCIC AAAGGGCITT GGCCGCTICT GGCCGCCTGG ATACAGGTCG CTGTCGCCGT	420
5 <i>5</i>	ABOUTGOAGG GUTGOCAGGU AGOGGUTGOG CGGCGGGGC CGGGGGGGAG AGAACCTCGT	480
	ACTOGTOCTO GAAGOCAGGO ATGTCTGCTG GCAGCCTGCG TGCAGGAACC TGCGGCGCGA	540

	Traces describes citarasacti civinaricale describited affectiones	600
	CCTTCTCNTC CGCCCACCAG GGVAATTTCC CINGNAAACT TWCCGAACTC CNCCCCCTTA	660
5	AAACTGCCCN CNCCCTTTTIN CCTINNCNSCT NTCCTCCTGC NNCCCCQNTTT CCCCCTCAAN	720
	ACCONCCTAC CONTINICINT NEWTHOMAC OCTACANCCT THOMACTAC TOCCCCONCC	780
	ATMICCIONI IMIATONIAA AATIITOMIIM CTITITIACOO COCCC	825
10	(2) INFORMATION FOR SEQ ID NO:308:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 856 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1251UP	
25	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:308:	
25	GACTGITOCC TGTTGAGGAA GATAATCAAT ACCGGAATCC TCTGAGCTTT GCTTCGGCCT	60
	CCATTCOCCT ATTACGAAAT TCCCCTGCTG CTCCTAACGA TGTTGTACCG TTTATACAAC	120
30	COCTIGITGA TOCCTITITIA CCAGAACCOC GITTITICCAC CGACAGAGAT GACAACCITT	180
30	GCTACTICIC CGATCCAGIA TIGITCAGIG CIGIAGICAT CITGCGATCG TIGGTAAACA	240
	CATATACCCC ATCCCACTTG GACAAGATCG ATACCACGIT GCTTTCGCTC TCATTTCACC	300
35	CATTAATTIC GCGCCTITTA TIGTAAAGGT GCAGCACCAC AGAAATACTT GATAAAATCT	360
	TAGGCAATGG CCATATTGGG AAGTTTATAT TACTAGCACG ATGGTTGCTC ATCCCGGCCT	420
	TGIGCIGTIC GITCIAGGG GCCCTGITAC TACCITIAGT CCTGIGTTAC TCACAGCTIG	480
40	TTACCOGCCC GOGCTTCTAT GCAACTATTA TATTTGCTTC TAATATATAA GTACTGACAT	540
	TITICATACCE GOCTACCTAC COCTOCTTIG TOTICOGIGA CICIOTICAG AACAGOTICT	600
	TOGANTATO TIGINCTATO AACCATOGAG ACACTGITAC GCCACACCCC GACCAAAAAGG	660
45	AGAACCEAAG GACAATTTIG ANCCTOCCTT TCCCCCGAAT TANGGVITNT GAANATATNA	720
	ACCOSCACUG GGITCCCTINN TCCCCCOGOGT ANITINCCCNIT TAAATTCGIN TAAANTTANN	780
	AANOGINIAT GOOGNGAANG AACCCCANCT GACCCNAAAN GIINCNIGGG GITTAACCIN	840
50	CTINITINGSCC GTINGGG	856
	(2) INFORMATION FOR SEQ ID NO:309:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 834 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genamic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1252RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:	
10	GATCTCCTAT TAGTGGGTAG CTAGCTAGTC GGCCCGGCTG GCCGGGCCGG	60
	GEGIGOCAGE COGAGIGACT AACACTOOGE GITCITICIGI CICITECCAT GOOGAACATA	120
	ACCATGOCCA CTTATATAAG TICOOOCOOC GTGCAGTCGT ATGAGCCCGT ACGAGCAAGA	180
15	CGTCCAGCAG TITIGCAGCGC GGTAGTCGGG GCGTTGCAGT TGTGTATATA TTGCCACCCT	240
	TOCCAACTIC CACACCCTIA TOCTOCACC COTCACTACT AACCACCACC COGTCACTCA	300
	AAGTAGAAGT COGATTIGTAA AGGACAACAG ACCAGTOGGG GTACGGACAG CAGCGGGCCA	360
20	ACGTAGTAAT AAAATATGAC GAGAGATATA CAGAACCACC TACTCTTOGA GACGGCCACG	420
	GAGGIAGCGA ACAAGGICGG GGGCAICTAC TCGGIGCTCA AGTCGAAGGC ACCGGIGACC	480
	TECECTICAGT ACAAGGACCA CTACCACTGT ATTGGGCCCC TGAATGCAGA CTCGGTGCAG	540
25	ATAGAAGTOG AGGCCTOGA CTGOGAGGAT GACAGCGTGT TGGACCCGGG AGATTGCTGC	600
	COGGTAAAAC GTCCCCTGCA GCACATGCGG AACCCCGGGT TGAACTCCGT ATATGCCGGT	660
	GELLINGLOSAY GELINGCOCCE GLIALCLIEL LCYARCIELL CCCELACCCC CCLCCLCCAC	720
30	AATTGAAGCC ACCTGTTGAA CACTGCGGAT CCCCCCCCCC	780
	CCATCOGTIA GGINCOCCING NCTGTCOCCOG AAATTAANOC CGANCONCINC TCAN	834
	(2) INFORMATION FOR SEQ ID 130:310:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 858 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL252UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:	
	GATCHTTAIC GCAACNITHT OCHTCIGTIT CCACHTACOG CCCTGGCGGA CCACACCCAA	60
5 <i>0</i>	ASCOCCASCT COGAGTGIFT TOCOGAATAT GTAGTCOOCT TTGTTCACAT ACGAGOCTOG	120
	THEACCIGIC ACCITICIOGA AGAACTICGI CAACATETIG CCCTGAGACG GAGGACGATC	180
	CTOCOCCTIC GATECOSTICTT COSTOCTOCTC CCCTACACCC TTACCOGACIT TTCCOGGTOCA	240
55	ACTAGTGAAC ACTOCCATAG CCTCOCAGTT AAAGTGATGT GOCAATATTA TATTGTAGTT	300

	HEHETHI CHANIET HASCISCE GALASCOAL GASGIGNASI INGIACACI	360
	TCACACATCC CAGCACTGCC ATCACGACAG ATGITGAAGA TCAAATTTCG CAGCTACATG	420
5	CTOCATTGIG GTOCTIGGGT TAGCAGIAGC GOCTAAGTTG CAACTACATT GTCCCCATTC	480
	ACTOAGAAGT ACCTOGGITA AGCTOACTAT GCOCTTATTIG COGAGOGAAG COGAGOATTIG	54 0
	TTACAGCAAT GATGAGAAGA GOCTATTOGT ATGTTAACAT AACGCCAGTA GTGTTATATT	60 0
10	TACCACTAAC CATAGAAAAA GTACAGAATA TOOGTAGOOT ACGAACTGAA TGAATATNI'T	660
	OCTIOCOCNO OCCORNOCNTA TACCAATGAA TAATAAATIG GAITIOCTAA TAICINOCCO	720
	ATATOGNOCO GGOCCCCCGA NINCCCTINCAA CITATTGGIN CACNCINCON TGCCNCCINCN	780
15	TITTNITTIN TONNOCAACC COCCOCCCGI CATONICGIN TGININAANA TGANIACCCT	840
	CCCTTGNICC CCCNCCCT	858
	(2) INFORMATION FOR SEQ ID NO:311:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 841 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1253UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:	
	GATCCTAACC AAGCTGATTG ACTOCAACTT TOCACTTGGC ACATTGGACA AGCTGTTGCA	60
35	GAGCTCCACG OCCGTGCCCC CITCGTGCCTC CATATTCCCA TCACATGCTG GGTGTACAGA	120
	CACCGAGGCA TTGGGACATG ACCGAAAAAGG CAAGAAGTTG GAGCCCCCCT TCCCGGGGCCC	180
	TCCCCCGAGC GTGCCACTCG GCCCCCCCCA TCGCCCGATAT AATTCTGAAT TGGCCCTCAA	240
40	CTACTIOCOC CACAOCAACG COCACOCCAG CGICATOCTC COOCAGGIGC AGCAGOSCIG	300
	GAACACAGCT CCTCCACAAC AACCCAGACA ACAGCATAGA CAACATGGGC AGGCCGAGGA	360
	AACOGGTTCA CCACCAATGG CTCTTCGCTA TCCCCCTCCA ATGTTAATGA ACAGCAATTA	420
45	TACATTCCCT GCCCCCCC ACCACCCCCT CGGCCCCCAT CCACAATCCC GTGCCTCGAC	480
	GCAGCAATCT GATGTCCCAG CTACCCTCCC CGGAATATCG GCGTAGCACC ATCGTCCCAA	540
	CTTCCCACAG CCCCCACCCC TGACTIAGTCT TTTGTCTAAA CATCAGCCTC ATCACTCGCA	600
50	OCCTAATGAG CTGCCTACCT CCCATGCATA TGTACAACAG ATTTGCCTAC TCCAATAGCC	660
	CAGITICIGAA GICIGCITIGC TIACGITIGCG COCTICTOCOC TIGGOCAAIN TAITOCITIGIN	720
	NUVAAAACON AACOCNNGIT COCCTGTGCC NGAATTICTA CTTTTACCGT CCGTTATTCC	780
55	WOOCHANDO REPEACHER TARGASTICO TITOCOGRAMA ACTRESCOCA ATACACIM	840

	C	841
	(2) INFORMATION FOR SEQ ID NO:312:	
5	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 842 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1253UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:	
	GATOGACGAG TIOGATGITG AGACGITCAA GAAGCIGITT GOGAACIGCA TICOCAAGGA	60
20	TOTOGRATORIC COCCACCITO TOCCOCRACITA COCCACTICATA CTOCCOTORIC ACCACCOCCC	120
	TOGOGTICOGO COCOCOGOGO COCGTICACOC GOCCGAGOGO GAAACOGAAAC COTITITOGCA	180
	CCAACACAC AAAGAGATTA CCATCATTCT COCTCCAAAG CCAATTCCCA TTCACTTTCT	240
25	AAAGAATGTG TOOGAGAACT GCTGTGTGCT GTACCGTTTC TATCACCGCC CGACTTTCAT	300
23	CASSANGUIG GACCACCTET ATGAGACAGA COCGOGTIGAG TACACGCAGG AGCAGCTACG	360
	CIPICTIOCCE TIGIOCTACE CIGICATOCC ASTOCGOCCE CIGITICICIA OCTOCATOCI	420
	CCCTGGTCGG GGAAGCGAAG ATGCGGGGCTC TGCAGGCAGA ATAACAGCGG CTACATTGGC	480
30	GGATACTGAC ACACGGCACG CTTATCTGCA CGACGAGGGC TACCGGTACT ATGTGGCTGC	540
	GAAAAAGCIA GIGATCTCAC GAACGCCCGT GACACCGAGG CGAATCAAAC CTTGTTCCCG	600
	TETGIGETICE COCCAAGETICC GOOGOGETCNC COCCGGCATOC GETETTICEGC CCNGCTATINA	660
35	ATTOCNOCON OCTINIAGANT OCACOCACOO COCCOCGANA ANTAAAAAAA TITOCCCCCC	720
	CAACCEGAAN TOOCHCCCCG MITTACCCCC CTTANAAANG AGGITTITTIA AACAAANCOG	780
	GENECOCONO NOCOCOGENN CININACATOS COCOCOCTABA TOGGABNATT INNOCEABACO	840
40	œ	842
	(2) INFORMATION FOR SEQ ID NO:313:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 836 base pairs (B) TYPE: nucleic acid (C) SIRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1254RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:	

	discourse Attorection Assertation Assessment Attorested Total Assertation	60
	TGACGACATT GTCATCGACG CCGAGAACAA TGCCATCAAC CTCCTTGTGC CAAAAGAAGA	120
5	AATTGAGTOG COOCGCCTC GCTGGACCCA GCCGGCTCCA CGCTACAAGA GCGGCACGCT	180
	COCCACCTAT TCTAAGTTAG TCTCCAACOC CTCCAAGGGT TGTGTCTTGG ACAGCGACGA	240
	CTAGCACCTC GACGCAAGTC ACTATTTATT AACAAGATTA TGTATATAAG CACCCGCCA	300
10	TGTCCATTCA ATOGACCOCA TATGTAACAA AAATCGAGGA TOCTTCCCTA TCGTCTACAA	360
	ATCICAGGAT GITGAGTACC TYTCAGGIGT CTGACTGAAA TAAATGITGA ACTYTGATAG	420
	TACTITITATG TITIGAAAAAT TITTAAAATTT TATTGTATGG CTGTCACCAC GAGTACTCAT	480
15	CTTCACCCCA CATTACCCCT ACCTGAAGAG CTTATCTATC GATAACATCG CCACTCACCA	540
	GCCGTATTT ATCCCCCCA ATAGCCAGAC GAAGGITGCG GACTTCTATT TGCCCGACCAA	600
20	GACTUTCCAT TOGACTOGAA AGTOCATOCT CTATOGAATC COTTOGACGA ACNCATOCNG	660
20	GNGTTINNGC CATTGAAGGC CNCAACCCCGA GNIACTCGGN AATTIATGGG GCNAAAAACT	720
	TITIOGICACN CICNNOGAAG CACAAINCIT COOCAAGNAA NAAAAANGGA AITIGNOCNAT	780
25	TTGGAGCCCN AAACCINIAC NINGCNIGGN GNOOGIANC TOCONTITOCN ANGICN	836
25	(2) INFORMATION FOR SEQ ID NO:314:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 850 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) Original Source: (A) Organism: pag1254UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:	
40	CATCTCTGGT ACCCCAGCAG CCCTGGCGGG GACGTGGCAT TGGTGACTTC TCCCCCAGGT	60
	AACCGGGIGT GCTCTCAGCC CCTTCCCCAC ATTGAAGTTA AGCTTGTTAG CGGTACTCCG	120
	CITCATTIC TGIGCCOGGI CGACCGGIAG CGICATAGIC CCGCCGIGIG CCCGACCGCG	180
45	GGCCGCCATC ACACGTATCT ACACGTTCAAC GGCCGCGTCG CGATCCCCAAG CGCAGTCTGG	240
	AATCTCGAAC GGTGCTACAA AGAACGCATG CGTGGCAGAT CGAAGCTATC GAGAAGGTGG	300
	TESSECANT CACTENANCE ACACEANSE ASSISTENCIAS ATCTOSTACE TETESCATAC	360
50	ACTACCACAA GCACTICOGOG ACGCTICTICA CAAATCAGOG CACTICTOCAG TOCOGGGAAG	420
	COTOCAAACO GAACTICOGAA ACAATICOGAC GGACCTACTIG CCAGGTICCAA GCCCTTTCCA	480
	COGTIGICACA OCTAAGATOG TOACTOGOCCA ATAATTIGIC ATOCTOGTAT TOGTGIGIGG	540
55	ACCATTATOT ATTOGGITCA GOOGITCATA TITTAGGTGOG CTGCAAACGI GGTGACATCA	600

	CONTIOCACT GIAININGS TOCAGIAATT COCATACACT GAAAATCIVIA ATAATCAATA	Udd
	ACCCATIGOEN CNACTOGNICA ACTITONOCINO TITONOCITOCN OGTIGAAATOO OCTTOACTIAN	720
5	TTTTTTTCAT TOCCCATINN ACCGAACTIT ACNAATNATG CAATGANAAC CNCCCCTCCC	780
	AAACCTANAT CCTTTTNTIN NGGGTCCCONN ACNGTTNCCN TTCCNGNCNA NCCCNCTTIN	840
	ATTCCAANAC	850
10	(2) INFORMATION FOR SEQ ID NO:315:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 827 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
20	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1255RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:	
25	GATCGTGTGG TCAGGGTGCA TTGCAGTGGG CCTGAAGACG GTGGGGACTG ATGGGCGCCC	60
	GAAGAACCTG TCGCAGCTAC AGGCCATTGC GGCTGTGGGT CAGGGCCGGC TTAITTGCGCG	120
	GIGGGACTCC CTCTTCAGAC CGITICAACGA GAAGATTCCG CAGATTTTGT TGACACGGAA	180
30	CGACATAGIT GACTOGICOC AGTATAAGAA COCOCAGAAT ACGTTICCACG AACTOCTOCC	240
	CATCOCCCIU ACCCCCATTG TCAACCACAA CCACACCCTC TCAATCACCG CAGTCAAGTT	300
	TRICOGRACIAC GACACRETIGA GTROCGATICAE ARCHROCTIG ATTCOCCOCAG ACTIVICITIST	360
35	CCTGATGACG GACGTGGACT GOCTATACAC CGACAACCCG CGGACGAACC CGGATGCAAA	420
	GCCCATCITG GIGGIGCCGG ATCTGTCACA GGGACTGCCC GGCGTGAACA CCTCTAGTGG	480
	GTCCCGGTTCA GGTGTGGGCA CCGGCCGCCAT GGCCGACGAAG ATCCTTGCTG CAGACCTGGC	540
40	AACGAACOCC GGGTGCATAC GATTATTATG AAGAGTGAGC GGCCGTCGAC ATGGTGCCGCA	600
	TOGTOCAGIT CATGCAATGG COCAGCAGTG CACTGCAGTT TOTGCTGAGG CGAGACTTGC	660
	AGACOGACGA OCTGAATITG TTOCAGACCA COOCGTCCCA CTACACACCC NCTTCNTOCA	720
45	ACTITICACC TOCTIGAACNA CNGATTIONTIG ATCCCNOGTIC TIGTIGACNOGG NOGTATCTIAA	780
	CAGOGOCINA GOCCOCCCA AACAACTONT COCACGTINT COGTCAG	827
	(2) INFORMATION FOR SEQ ID NO:316:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 836 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5 5	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIG	INAL SOURCE	Ε:
	(A)	ORGANISM:	1256RP

· ·		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:	
	GATCTAATIGG CATTCTCCCT ACCAAATIGGG CCCAATTGTA TATTGCCGAT CTTCCTACAG	60
10	CONTROL TACCOUNTICA COCANCATOS COACACITOS COTOTICIA TICOCCACAT	120
	TGIGTCGAAA ACACCASCTG CAAACTTGAG SCCATATGTC ACTGTCATCA CAGGTCCACT	180
	TATCCGTGTT GTTGGCCAAA GGTCTACCAG TCATATTAAG GCTGCTATCC TATATGCCCT	240
15	AAATGTTCTC TTTTCGAAGG TTCCACAATT CCTGCGGCCA TTCATACCTC AACTACAGAG	300
	AACATTIGIT AAATCICTIT COGACICAAC CAATGAGACC TTAAGATTIGC GGGCGGGAA	360
	GOCACTAGGI ACTITICATAC AATATCAACC AAGAAITGAC CCICTOGIGG TGGAGCTAGT	420
20	AACAGOCGCT CAGCAGOCCA CTGAAAGGGG AGTAAGGACG GCTATCTTGA AGGCATTGTT	480
	GGAAGTIGIC TCCAAAGCTG GCAGCAAGAT AAGCGAAGCT TCCAAAGCTA ACATCATTAG	540
	ACTIGIOGAG CAAGAGATOG CATOCACAGA CAGCAAGTIT OCAGTOGCTT ACOCCAAGCT	600
25	TCTAGGTGCA CTTTCTGAAA TCATGTCTOC GGAGGAGGGG CAGACCATAC TTCACGAAAA	560
	GIGCITICATO CAATTITICAA GANGCACNOT AAATTICOOGI CNOACCOCAO TOTATOOTNO	720
	TACCCCTGIA CATTCTCCCG CCATACACCA ATATTGACIA TINGTGGIGC ACGGATCACA	780
30	ATCCTTCCNN CACACGITIN CCCNINGNAT TCCCCCCNAA NGAAAGINAN CCCCCC	83€
	(2) INFORMATION FOR SEQ ID NO:317:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 841 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAGI256UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:	
	GATCAACTGG TCGGGCCGGC TGCACCACGC CAAGAAGAGC AATCCTTCGG GGTTCTGTTA	60
	COTCAACCAC ATTOTTOTOG CGATTCTGAA TCTOCTGCGC TACCACCCAC GCGTTCTGTA	120
50	CATTEACATT GATCTGCACC ACGGAGACGG TGTCCAAGAA CCATTCTACA CTACTGACCG	180
	CGIGITCACG GICTOGITCC ACAAGTACAA TGGTCAGTTT TITCCGGGAA CGGGCGATTT	240
	OGATCACATO CICATOCTOCO COOSCAASCA CITTITOCCTIC AATGTGCCGC TCAATCACGG	300

360

CATCGATGAT GATICGIACA TCAACTTATT TAAGAGCATC ATAGACCCGC TAGITACATC

	ATACAAGOCA ACAGTAATTA TICAGCAATG TOGAGCAGAC TUTTIGOGGC ATGACAGACT	420
	GOGGIGITIC AATCIAAATA TCAGAGCCCA CGGCGAGTGC GTCAATTIGT GAAGTCGTTC	480
5	GOGATACCIA TOCTATOTOT COGTOGTOGA GGITACACCC CCAGGAATOT GICOCOCCIA	540
	TOGACCTACC ACACACCCAT CCTTAATGAT GTCCTCTTAC CTTCACATAT CCCACAACAT	600
	ATTOCCTIOC GCGAATGGIT COGTCCAGAC TATCTCTGCA COCGGTCCTT GGATGANTIN	660
10	TOCAAAATAA ACNOCCAAAT TACTOGANAA NATAOGING GVITTAAAAN NTAAATINIG	720
	CIVESCOCAT TITICINCNICA NINCGAATATC CTCCAGATTI CCGTITAACN AAAAAAAAAA	780
	GATCOGAANA ACCAAAANAT NCCITGNTAA CANINAAGAA NTTTGCCGNN ACTINITANT	840
15	c	841
	(2) INFORMATION FOR SEQ ID NO:318:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 841 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1257RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:	
	GATCACTOGT GTCACCAAGG OCTACAAGTA CAAGATGAGA TATGTGTACG COCATTTTCC	60
	CATCAACGIC AACGITGICG AGAAGGACGG CGAGAAGTIC AITGAGATCA GAAACTACIT	120
35	GGGTGACAG AGAGTTAGAG CTGTGCCTGT CAGAGAGGGC GTCAGGGTGG AGTTCTCCAC	180
	CAACCAGAAG GACCAGATTG TTTTGTCCGG TACCTCCATC GAAAACGITT CTCAGAACGC	240
	TOCTGACATC CAGCAAATCT GCCGTGCCAG AAACAAGGAT ATCAGAAAGT TCTTGGACGG	300
40	TATCTACGIT TCTCACAAGG GTGTCATTGC CGAGGAAGCC TAAGTGCCTT ACTGACCGTA	360
	TCTTGATAAA TAATATGAGI ATTATGTAAT CAAAGAACTC ACTGCTTTTT ATTGGTGGTG	420
	TTITCGTCAA ACOCTCTTAT TAGCGCCGGG GTTAGAGTGT GGGAATACTG GCGTTATATG	480
15	CTTTAGAAGT TATGITAAGT AAATTTAATG TOCTATCAGG GOCACAGOCT TAGCAACTAG	540
	GIGCAGGIAC TOCTITAGCT TOCCACIGIT CIGGAACAGA AGATATATIT TATCIGICIC	600
	GTTGGCACCA TCGTAGACAG GTTCACCGCT TCCTTGCAGG AACGATGGAA CGCCAGCTTT	660
50	CCGCGGTIGGA AGTTATACCA ATTATGCATT CCAATGACAG TIGGTGTGTT AACNANCCTG	720
	ATTIGICCAN TITICOGTICT CAGAAGCTING ANTIGNITICON TGACCINANCA AACCOGGAN	780
	ACCCCTAGGG CTGNVAGGCT TGAATGCNIT AAAANANIIT CNITGANAAA NCAITGNIAA	840
55	?	841

	(2) INFORMATION FOR SEQ ID NO:319:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 856 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1257UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:	
15	GATOGOGOGO CTCACACACT CAGGTACCTC AAAGGAATAC GAGTTTGTCG CAGGCTTCCC	60
	GTGTCCAGAT GCACAGAAAA TCGATATGTA CATCAAGGAG CCCCAAAACA AGTACCTCTT	120
	TICCOGAACA GAGIACACTI TOCAAATCAT CTOCAGCCCT GCAGACCCCC TCACTICACGA	180
20	TOCATACGAC GOCCAAGOOG CTGCGCCAAA TGTGATAGTC GTCCAGTCCC CATCCGGCAA	240
	CATCTACCGT CTCAAAAAGG CCCAATCCCA TGTCGAATTT CCCGTATGCG AACCTACCCT	300
	AAAAGTOCAC GAGCCAGGOG TCTGGCTGGC CCTAATTACC TCTGAGGCAG GTGCTGGTTG	360
25	GIOCACTITO OCGANGIOGA TOTGIGITTA ACACCTAGAT OCTACACAGT CATOCACCCC	420
	ACGARATTAR TACATACTAC GOSTACATAC ARGCCCTATA GITTCTTARC ACACTIOCCC	480
	TATATTGAAT ATGTCTACGA AGTATATGGG CGAGGCACTT TCAAAATCGG TGAAAAAAAA	540
30	TOCACCACTY CGARATCCAT GITTIATGAG CTTARACARC AGTOGITIGIT GAAGAACART	600
	ACCCIGOCAA GCAAATGICA GGIACIGCAA CCAGCICTCA ACAGAITICIT AAAGAITIGOC	660
	AGTOTTOTAA COGAATOCAC GTTOOCTGAA TOCTGOCACC GACATOAGAC COTTOCATTG	720
35	GTACAAAATC ACTICTATACG CNGAGCGCCT GTNTGCCCCNA AAAANAAANA CCACGGAAGG	780
	ACIVEATIBIC ACTIGNACING ACIVEANIBIE TIMENETENDE COCNINITITE GNITICAACICE	840
	CCAAGGACAA NAACGC	85€
40	(2) INFORMATION FOR SEQ ID NO:320:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 724 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1258RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:	
55	CATCCAACCT TCTACTAGGG TATTTTTCCC TACCTCAGCC TGCAATTCCA TGCCATCGCT	60

AACCAAGATA ATATTCTCCT CCAGTAGATC CATATTCTCT CCCGACTTCG CACTAATCCG	120
GATGACTOOC ACGTTTOCAC CCAGATCTTC ACCATGTATT TCATGCTGTA CCAAATCATT	180
CATTATTTIG TIGATCACAG TITICCTTTIC TITITOCCGAC COGAGITTIGT CCACCTTOGT	240
TATGOCGACA ATCACCICAT TCCCIGATIT TITGACATOC TTAATCCCIT CAATGGICIG	300
GOGTTTAATT GAGTCTTCGG CAGATACTAC CAAGACAACG ATATCGGTAA TATTCGCGCC	360
CCGLICCCIC ATCTICAAAA ATOCTITOGIG CCCCCCCCCTA TCCAAAAACG TGATCTTCCC	420
CTTCGAAACA GGTGTGACAA CCTGGAACGC ACCAATGTGT TGTGTAATGC CACCAAACTC	480
CTGCGAAACG ATGCTCGACT TCCGCAGATA GTCCAATATG GTGGTTTTGC CGTGATCAAC	540
GIGACCCATA ATOGTCACAA CAGGIGGCCG GICCTICAGG GCCTTCGGGT CTGCAGGCTG	600
CTTCAATTCA TOGTAAACGT TCTCCCGCAGT GACAATTCCC TCCCGGAGGG CAGITGGTAG	660
CTATCTCCTC CCAATATAGC TCGATGTAGT CTCCTGGAAA TATGTAGTCC GCCTGGCTTT	720
TCAA	724
(2) INFORMATION FOR SEQ ID NO:321:	
(i) SPQUENCE CHARACTERISTICS: (A) LENGTH: 853 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1258UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:	
GATCCTGTTT ACAACTAAGT TCGCATCCCT ACCAGGGGAA AATATGAAAT ACCAAGTGTT	60
GTATTCCGAA CGCTAGAATT CTTGTACAAA AACCGCGCCA TTCAGGAAGA AGGTATATTT	120
AGGITAAGCG GATCCAGITC TCTCATAAAA TCTTTGCAGG AGCAATTIGA CAAAGAATAT	180
CACGIOGATT TGTOCAATTA CAACGATAAA GITTCTGTCA CACCAGGAAA CGAAAATCAG	240
GOOGGICICT ACGICGATGI GAATACCGIT TCAGGITTAT TAAAACTATA CCTAAGAAAG	300
CITCCICATA TGAICTITGG GGATGCIGCA TATATGGAIT TTAAGAGAAT CGIGGAAAGA	360
ANCOGAGATG ATAGCAAACT AATAGCACTC GAGTTCAGGG CAITGGTTAA TTCCCGGACGA	420
	480
ATTOCCAAAG AATATGTCGC CITAATGTAT GCATTGTTCG AGTTATTGGT GAAGATCACC	400
ATTOCCAAAG AATATGICOC CITAATGIAT OCATTGITCG AGITATTGGT GAAGATCACC GAGAACAGCA AATATAACAA GATGAATCTG COGAATTTGT GTATCGTATT TTCCCCCAACG	540
GAGAACAGCA AATATAACAA GATGAATCTG CGCAATTTGT GTATCGTATT TTCGCCAACG	540

	THE SECTION TOTAL PARTICULAR ADDITIONAL MICHELLARY CARRAGES	700
	CCATTEGATT TACACCINECE TOTGTAANGA CNTCTAGCTT GGTCATCCCA NETCTCANIT	840
5	NCTCCCCCTT NCA	853
	(2) INFORMATION FOR SEQ ID NO:322:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 836 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1259RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:	
	GATCACACGA ATATTECCOG AGTATTTCTC CATCOTTCOC COCAACGCGG CCTGCCCCATC	60
	OCCOCTIGACC CATTOCCCCT COTTIGATEAT CACACTCTIG TACCTCCCCC CTACCCCCTC	120
25	CGATCCGCTC TGGAAATCCA CCTGCTCCAT CTGCGCAATC TCCTTCAACA ACTCCTGAAT	180
	CACGATCCGG TCATTGTGCC CCATGTGGCT CGGCGTGATC TCGATGTGGT ATGGGCTGCT	240
	GACGACGFIG ACCICGAGCT TCTIGITAGA TGGCGTAACA AATTGCCGCA CATCAATCTT	300
30	TAATITGIAT ACACCIGCIC CAAAGATACT TGCAAGGAGC CCCATGCACC GIGICITCIT	360
	CCCACTICCA TICOCCCCCT AAAGTAAAAT ATGCGGCAGG TCCTTCGCGAG AACCTGCTAA	420
	ACCCICGAGC IGCIIGGTAA GCCAIGCCGI ATGIGAAAGG CIGGICAACG ACTICGGICI	480
35	ATECTIGICA ACCCAAAGIC ACATATICCT GIGIAICCIG ACATOCOCIT TIGIGIGITG	540
	TAGGGAAGGI GAGCAATICA GICGCAATIA AAITCATITA GAITCGCGIT TIAGCACAAA	600
	ACCATATOCC CTCAGTAAGG CCAGAATACA TACAGGTACT TOGCCTACTA CTTTTGACAG	660
40	AASTAAASCT CTCACGAGAT COCTOGAGGA GATGGCATGT ATATAACCCN CAATTACTCT	720
	GATGONAAAA ATGITGCACC CNIGOCTITT TANITONGIC GACAACTANN AGAGCCINIA	780
	TONAGTOCAA ATTTINOCAA ANCIGOGAAA ACCTININOC GIGGINIAIN AACACA	836
45	(2) INFORMATION FOR SEQ ID NO:323:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: mucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1259UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:	
5	GATCACCCCC CAAATCAGCA ATAACTGGAA AACTGTGCCC AGTACCTTTC AACGCGCATG	60
	AACCTAACOG CGCGCAGOOG TCATGOGTAC TCGACTGCCT TTGTATCCCT CACACTGCCC	120
	CICLICCRICI OCCOCACCIC CLICITCATC CIACCOCCOC COCCOCCIC ATCIAACCC	180
10	ACGICTOTTI GTACGTGGGI CTCACGTGCA CATCGGTCATC CATCCGCTIG CGAATCAGIA	240
	GATCAGCACG GAGACCATGC TAGGCAGGGC OGTTGGGGGA GGTGGAAAAGG TTGCAGCATT	300
	GAGGIGGAGC ACCAAGAIGA CAICACAGGA TAGTAGIGGG AAGAAAGAGC TATGIGCAGC	360
15	GIACAGOGTA GIOGATGAGO COGTTTOGOG CAGOATGGAA GAATGOOGAC GIAGAAGGIC	420
	GCACCITCTA TICCITCCCC TTTCIAAACT CAAAACCTCCC TCCCATGTGG CCATACTGTA	480
	CGAAGAAATG GGGCTGCGGC ACTITGGAGA GAACTACGTG CAGGAGCTGG TGGGGAAGGC	540
20	ACCAGACTIG CCCCCCCATA TCCAGTOCCA CTTTATCCCC CCCCTCCAGA GIAACAAGTG	600
	CAAGGACCTG GCGAAGGTAG TGAACTGCAT GCGGTGGAGA CCATGGACTC GCTAAGAAGG	660
	CGCGCAAGCT GAGCACGCCG TGCCCAAGTTC CAGCGGAGCC CCCGCATCTG TGTTACATTG	720
25	AGIGAACNOT CITOCOAACNO AAAGNNGTTN CNOGATGAGO NACNGTGCAC TGTGATTICTT	780
	CINCCAAAAC AAACCTTCCC TGCCCGACGA TAAATGGTCC TGCACCCTCC CCGCGAAGGG	840
	AACCGATCCC C	851
30	(2) INFORMATION FOR SEQ ID NO: 324:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1260RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:	
45	GATCCTCAGA GGGCCCCCAA GAAGCTTCGG CCGAGACAGT AACGATGTTT GGCGAGGTTG	60
	TOCTOTATCA CAGTIGADOT CTAGGITIOCA CTITICOGAAA GAGOOCTACO GTAGOTOCAT	120
	GAAAAAAAG TAAGGCTCAT CAGTTTATGC AGAGGCAAGA ATAAGTTTGG TAGAGCCTTA	180
50	CTICACAAGC GIOGCICTAG CGAGCCATAT TATICTAIGG CCGGCAAGAG AAGACCGAAG	240
	AAGOCCACAG CICCATATOG AAAGIALOGIG GCGCGICAAG GGITTGIGCA TACCIALOGG	300
	GITTCCAGTA CTGAGAGTTC ACCACACGAT GAAAGCGGTT TGTTCCCCGC AGACAGTGGG	360

GIGCAGGIAT CIGACGAIGA TATTGCGAGA CGACTIGTIG ATATGACACT TICCUCAAGC 420

55

	GENERALITY COORDENSE GREATHAN CONTINUES GREATHAN GREATHAN	400
	TOOGAGCTOC AGTITITIOGI TCTGTCCAAA TOCAAAACTA TTGAAACACA CTTCATGCAA	540
5	GIGIGCAGGC GGIGGIATAT CATGIGTCIG CCATTGATCT ACCGAGCACC AAGGCTCTCC	600
	ACCAAGACTT CTACAAGTTT GTOGAGACAC TOGTOGCAGC CCGTAAACAG AATTACCOGC	660
	AATATTOCTC GATCTOGACC GTOCATGAAT ACCINVANOGC AAACCTTTTC CAAGGTOCTC	720
10	COGNITIONICO CACOCTIGAE ATTICOGGOCC CAAACACTOG TATICOCOMIG AATICTITACOG	780
	CNNCCCNNTT OCAACCGATT TGTCTNTTCC CAACGTTANC GAACNCNTTG AG	832
	(2) INFORMATION FOR SEQ ID NO:325:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 846 base pairs (B) TYPE: nucleic acid (C) STRUMENTE: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1060UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:	
	GATCGACCGG CCGCCCACGC CGGTGCCGTG GGTGAAGTCG CCGCCCTGGA TCATGAAGTT	60
30	GOCCATGACG COGTGCAACG TOCAGTTGAT GTACCCCOCG GAGGGTCCT GGCTCTTTGC	120
	CACCISTRACE AAGTTOCCCA COCTECCEG ACCTACCTOC CCCACCACCAC	180
	ACCOCCCAGT GOUTCGTCGC CGTGCTGCAG ATCGAAGAAG ACACGGTGTG TGACGGTGGG	240
35	GTCTGCGAGC GCGAACGCGC AGAGCAGCGC CTGTGCGAGA ACGAAGAGGA CCTGCATTGG GCGTGGCTGC GGGAGGCGCG GGAAGACGCC CCCTTTTATA CCCGAAAAAG	300 360
	CITOCITICOSC TACGITAGCIA GAGATACAGA GOCGIGGACT TGAGGCICTG CAGCATCAGG	420
	COGTICCATICA TICTOGROCOT CAGCACGTICE GAGTACCOCG COGTICGCOCC GTICCAGCOCC	480
40	COGSTCARCG CTGSCGCAET GSCGCTAGAC GCGETCGTGC CACTGCCCGC CTGCACCGAG	540
	TICTCCITCA CCECACGAA GOCCOCCCC TGGCCAGCCT GGAACCCGC CAGACCCTGA	600
	TOSCOCCEAS COCCOCCEAS ACCITOSANCE COSTOGAÇÃO CASCOCETIC TOCACCACAC	660
45	TOTACGOOGE GOCCOCCIGTA COTTCCCCINA ANANGINTAT CITICACGCAT CACCOTTCCG	720
	CCCCCCCTCC TTCCCAACCA AATCCCTCCC NCTTAACCAC CNTTTCANSC CNTCACTTCC	780
	ACNOTIGNOCA CACNOTTONO GETTACGITOC CAATIGOOGTIC TOCCONGGGO GOTTAGGING	840
50	OCTOGT .	846
	(2) INFORMATION FOR SEQ ID NO:326:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 835 base pairs	

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1261RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:	
	GATCATAAAC GAAGAATTCC TAATTAACAA TITGTCCTCC ATGTACTTCC TCAGTGAGAA	60
15	ATAGOGATAT AATCATTAGA AAGCTTCCCC GAGCACTTTA GCAGCACCGC ATGCCAGCAT	120
	AACCCCCTGG ACTCAGGGCA GTATGCCGGC TGGCACCTCG GCACCTCATC GCAGGCGAGA	180
	CAGTOCACCA CTGOCAGCAC CGTAGTATTT ATACTTTTCC AGGTTGAAAA ATTTTCGACC	240
20	GCCCCACGCC GCACAGGGCT GGACGCGCAT TAGGGCTCAC AGCGGTCGAC TGCCACTGCT	300
	OCCCCAACAG CGCCGCGCAT GTAACGTGAA ATGATATATT ATACCTTCTG ACTACAATGT	360
	GAAATATACA AAGGTGGCTC ATAGGCCCAT TGCATTTATT CAGACGCAGT AGCTCTGGTG	420
25	TAGATAGOCT GCTTGGAGTG CTTGGAGATT GOCTTGATGA TGCCCTCGGT CTCCAAGTGT	480
	CTCAAAGCAA CICTGGCCAT GGAACCGCCG ATCTTCAATC TGTCGACCAA CACGGACACA	540
	GAGACGIATO TGTAGGTTGG GACCTCCTTT AGGATTCTGT CAAGCTTGTC CTGGTCCAAG	600
30	ATGACOGCOT OCTOSSOCTT GTCCTTGTOG GACTTCTTGG ACCACTTCTC TTGGACTTCT	660
	TACCACCGGC CATGOCOCGC GCGCCTTCIG GCCCTTAAAN AINFIGITIT TGGIGCATAT	720
	ACNOTOTICC CINTATACTOT CCOCACCACT COCINTCTICTG CONAGOSTICS TGASCITICCS	780
35	TACTOCNOCC OCTACOCNOC COCCONNENT TGTOCNITTC NYCHNOCTA ANICT	835
.	(2) INFORMATION FOR SEQ ID NO: 327:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 852 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1261UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:	
50	GATCTGCAAC AACACCATTC CATCGCGAAG TCTTTCCAAT TTCTGTTCTG	60
	AGGAAGITIG AGAACGATAT IGGGAGCGAT GAIGAGGAAG ATCCCTTOCA GAICAACGAT	120
	TIGGACGAGE AGAAGACCIT GOGCATGCIT TCIAACCAAG CCTGITICIT CGGCTACCTG	180
55	ATGOCCGAAG GTCAGGTAAA GTTAGATGIT TTAAAACATG TATCCATTAT GOOGTTGAAC	240

(B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear

	TCTGACGGGA GACTTTTCCT AGAGAATCTT CTATTTCAGT TTCTGTTGGC CTCAGCCAAA	300
	AAAGCAGAAA CTAAAAAGAA GGTGGGGAAT ATCAAGGAAT GGTCTTACAG AGATGACTTG	360
5	TIGCAGOGOG COCTOTCOCA TOGGATCCAG GCCGAAAATA AAAAGATAAT CTGCAAATCG	420
	CTCAGGATGT TTATGAGGAA TTTTAGATAC ACGAACTATA TTCGTGGTCA GCCTGCCTCG	480
	AAGGAGTATC AACGTGACAT GAGAAGGTTG GACTGGGCCG TTAAGCGTTT TTTGGAACTT	540
10	ATAGATGAAG AACTOGATAG TOCAGATTGT GAAGAGCTTC TIGTCACTAG TCTGAATGCA	600
	TATTACGIGI AACATTGAAC ATACGIACTC TATATTAAAG TOGTGAAAGT GATGAGAGIA	660
	TGACGTCCNT CCTTTTATTG CATACCACTT NTCAATTACA GITATTCCGT GAATCACNAC	720
15	AAACANGTIC CATTACTTAC TIGITGACNI CGCCNCGACC ACCACCCGG CCACACCTTT	780
	GITTACCITA TAAAAATCIC CACNICCONC GIATANAGCC TNAANAATIC MITCOCICAT	840
	GCGGTTTIGA CN	852
20	(2) INFORMATION FOR SEQ ID NO:328:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 831 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1262RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:	
35	GATCITICCA CACOCIOGIA AIGITICOCA CTAACTOGIA TITTICCTIG TCIAGATAGT	60
	CTOCCGTAAA GACTCCCCAC GTGATCGGCC GGGCACGGAC GCCCATCTGC TCCAAGGCCG	120
	TCACAAGITT CAGGITCTGT TOCAGAAAGC ACTOGOGAAC TACTGTCATG GTCACAGGAT	180
40	CAGITACOCG AATTOCTTCT ATATATGAAG OCTOGATACC CTGAGCCTCC AATTTGTTAT	240
	TCACCTGOGG ACCOGTGCCA TGCAGCACAA TOGGATAGAG CCCCACATGG TACAGGAACG	300
	CCAGGCATGA AGCCAGTTCC GGCAAGTTGT CGCTGATGAT GGCACCTCCA ACTTTGATAA	360
45	COCCGANTIG CTCCTCCCAG ACGGAAGIAA AGIACTICAG GIACTGTTCT ACTTCACCCT	420
	TAGAGCCAAT ACTGTTGAGA AGCTGGATCA CGGTGGACCG TGTCTGCAGA GACCCAACGC	480
	CCTCGTTGTT CCCGGTTCTT GCATAGTTCA GCTTCTTTAT AGCGGCAGTG CTGAACAATT	540
50	COCCCTTGTA TGCGGCACGG ACAGCCCATG GCGTCCGGTT TTAGATCCTG CTACCAGCGA	600
	AGCTCTACTA AACAGTAGAG AGTGCTCGCA AGCATCTTGG TACTCCGTTT ATCCCAGTCG	660
	CGCGAGTTCT ACCTCTCGAA ACCAGTCCGT GTGCCTTATA GCCTAANTTC TCTTCGGTTC	720
55	CATAACCACA AACCGTCTCN TTGNCTVITCC TGANTTTCAA GACCCCUANA TTTTCACAAT	780

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	TINIGCATIT NICONGNANA AGOGIOCNAT TTATINITOC AINCNITTAA A	831
	(2) INFORMATION FOR SEQ ID NO: 329:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 865 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1262UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:	
	GATCACAAGC TIGITGAAGC CAACTGCTCA AAATGTCTCC TACGAGAAGA AACCATTCCT	60
20	TOCACTAGGA GACGTIGTIGGC AAATTITAAA AGGAGCCAGT AAGACGCAGA CTAGCCCCAG	120
	CAGAAGCCCC AGTAGTTGTT AGGAAGCATT CCAGAGGGTA TACGACACTT TGAAGACGGA	180
	CAGCGITCAG AGAAGACAGA GACAATCAAC ACCAAACAAA CATGGAGAAT OCTCACGTAC	240
25	ATGATAATTT ACAACACATC CAGGOGGTGT TATGGAACTA GGACACATGG TTTCTCTCGG	300
	ACGATGAAGA GGACTACTGT COGCTCTGCA TGGAGCCTTT GGACATCACC GATAAGAACT	360
	THAAGCCGIG TCCGTGCGGG TATCAAATCT GTCAGTTCTG CTACAACAAC ATCAGACACA	420
30	ACCORGAGET AAATGOOGGG TGTCCTGCGT GTCGGCGAAA TATGATGATG AGTCGGTGGA	480
	GIACATIGIT TIGAGOCCOG AGCAGCTICAA ACTIGAGOCCA GOCGAAGCAGG CGCCGAAGGA	5 4 0
	GCGCGAGCGC AAGCAGCGCG AGAAGGAGCG AAAGGAAAAC GAATATGCCA CCGCAACATC	600
35	TOGOCOGICAT GOGOGITATO CAGAAGATTG GIATACGITA TIGOCOTGAA CCACCOGTAC	660
	CCTACCACCA CCTTCCTCCC CTCTTCCCCCT CCCACACTTA CTTTCCCCCT TNCCCCANAT	720
40	TTACINATION TCCGTGAACC GCAAAAACCCC CCATGACCCC NACGGINTGG AININITITCC	780
40	TTCCCTNGAAA AAGAGCOOCC CINTINCOCC GTGCATGTNT TTTNTCANCC CCNCGTGACG	840
	GOGIFACGACC NATIVICACIN TITTIC	865
45	(2) INFORMATION FOR SEQ ID NO:330:	
50	(i) SPQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: UNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1263RP	
<i>55</i>		

	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:330:	
	GATCOCOCCA TROGCTRCTG AATGGTRCCT CACAGAAGGA TROGTCTACC AATGGCATTA	60
5	GITCAGOGAG GICCTCOCTA CTAACAGAAT CGICTIGIOG AACTCICTIT AGGAAGGIGA	120
	ACAGTICATO TATOCTITCA AAATIGATAC TOTGAAAGGG TICATTIGGG GOGTTAAACA	180
	TACTAGATGC AGTCATTAGG GCGGCACTTT CTTGGTTAAT ATCGTCAGCT ATCCTTTTTA	240
10	GIGCITCITC CICATITICA TIGOCCTIGA ATAAACCICT AGCTATCAAA AACTCAATTA	300
	GIATCTTCCT GACCTTAGTA GITGGTCCGT CTGTGGGCCT AGTCATACTC ATTAAGTGAT	360
	GACGGAGCTT TTGCACACCT TTGCCAGAAA ACACACAAAA TATTTGACGT TGGTTAACGG	420
15	TAAATTCACT AGGAGGAGGT CTOCAAAATT GTGTGATATC TOOCCTGAGA AAAGAAGTAC	480
	COCAGTICAAT GACAAATGAG AGAGCTITIGG ACAAGCCATT ACCAACTCAT ATATTOGATA	540
	AATAGICAAA TIAGIACAAT ATGATAGGIG AACTCTITCC AATGIGICAT TCCTACCACG	600
20	CARAGCARTO ATATITIARIA ACCICATOTO TORICIGAGA ACATICACOA ACCOTATOTI	660
	TITAGITIGI TAATICCCCA ATCATATAAG TATGAATIGI CCATITIGIA CACAACNATC	720
	CNCTTCTGAT CNVOGANATC CTGATTCAAC CTTATCCCCN CCCNGAATGA ACNTGCCCAA	780
25	NGANATININ GITTITICCON CITGAAANCT CNAAAINCAT ACCCCGCTTA CC	832
	(2) INFORMATION FOR SEQ ID NO:331:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1263UP	
40	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:331:	
	GATCTTAAAA GCTGGCCTCC GCAGATAGAC CTTCTGCGCA GAGGCTGGAA ACCTCAACTA	60
	GCAAGTCGCC ACCOGAATCA GATAAGCACT AGAGTCGTTC CAGTAACAGA GGAAGCGATC	120
45	AAGGAAGATA GTAGAAGAGG ACACTGCTGC CAGGCTTGAT CGGACAGAGG GTTTAGCTTT	180
	CIGITGAATT TTAGAGITIC 0000CTTIGT TTACTTCGIT TCATTCTTTC GIGIAAAGAA	240
	CONSTITUCA COCTOCCATO ATTICCCAST COCCASSIAS CSTATICCAS COCCACCSAS	300
50	TOOGTGAAAC AGAGCAGGAC OGAGAACGOC GATAGACAGG CGITTGTTTG TAAGCOGTGA	360
	GASCTGAAGC AGGTCAAGAG GCCGGCTTGG GCAGGTTGTG CGGCGGCGGC AGAGCACAGC	420
	AGGGCATCCG AACAAGGCGG AGCGTGCGGA CAGGAGCGCA GGCGGCGAA CAGGGGGGTG	480
55	TGATGACGAG CCAGACGAAC AACAACAACG CGGCGAGCTC GAACGGCGGG CAGCTACGGC	540

600

CATCGGGGCT TCCGGCCGAGC TGGTTTACGA CGCCATTCCT GCGCCCTCGA CCACAGACAG

	ACAGCAGIAC TCCCAGAAGT TTCGCGAGCG TGTTTCGCGG TGAGGCCAGC GCGCCAGAAC	660
5	TATTITICCA CITACCAACC GOCCGNAATG CCCCCCACTT INTICNCCAA ANACCATTIT	720
	TOCHOCAGON COCHCOCING TAAAACCATT TOTTACHOGG NOGAATGAAA TGGGTTGWIT	780
	TTCCCCCCCC NGAGAACACA TTTTTCCNCA CTCTCACCCG ANTININTIANT CTCCCNAACA	840
10	TIATITITIC C	851
	(2) INFORMATION FOR SEQ ID NO:332:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 801 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1364RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:	
	GATCTOGTTT TIGTAATGCT CTAGCTCATA TITGTTGAAG GAGAAGGGTG AAAACAGCTC	60
	CGAGGCTGCA ACTACTGCAA AGAATAAGA GCAAAATATG GCACATAAGA TGTCTTCCCA	120
30	ATTCATTIGG TACAGCTCTA ATACTGIGAA CCCTTAATCT COGGTAGGCG CAACAGTTAT	180
	GCGGCCAACC ACGITAACGI GATAATCAIG TAGGIACCCC GGIGAAAAAA AGAGIATGIG	240
	GAACCOCCCA OCTGAACCAA GOOGATGAGA CATGOCGAACC ATATTCGAGC ATACTTGACC	300
35	ATGATGACGC AAAACTATCT AGCATAGTTA GTCTTGCAGC TGAGACAGGC TTCAATCGTA	360
	AACCTCCCAC CITCACTATT GTCACGIGAG AGGCAACATA ATTGATCTIG TGACTACCAC	420
	CCATACATTT TOCTACCACC CATACATACT AAITAATGGG GAAAATAGCG GCTGGTACAG	480
40	ATTETTOCAT CTCCCTGCCC CAGAGGGCCG CGGGGCTCTC GTTCCCCAGC GCGGGCAGGC	540
	GSCCGCAGGC CGACTGTCCT ACTACGCTCT CCCTGTTGGC CCGTGGTTAC CGCGCCTCAA	600
	ATTACCAANC CTCCAATTIT IGANATICCC CGACAGTINT GINOCINTIT ITTACCCCAA	660
45	TICCOGRATT TOCCTATIAA ANOGIAACAC CONNVITTAC TITIGIOGAN TAACCINNOG	720
	COINCTINING GENVINCCIT TINITACINGS COCCUNITONA GOOCHTTIGG TICCCTAAAA	780
	CCCCTIVAAAA AAAAAAACAT T	801
50	(2) INFORMATION FOR SEQ ID NO:333:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genemic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL264UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:	
10	GATCTCATGT ATCACAACCA GACTATGATG CGACTTOCGG TGACTATGTC TCCTTTOCCC	60
	ACCCETTICAG ACAACGAGTIG AAAGACAAGG ACCTTATTTT GATCCACTICT CETCACAAAC	120
	CTACCOCTAA TOCTCTCACT CATCTCACTA CTCCCATGOC TYTCAACTCA ACCOCTATCT	180
15	TTAACCTICA GAAACTIGAC TIGITAACTC TOOGTAATCA TGAACTGTAT ACCCAACATG	240
	TOGTTCOCTT GGAATACTAT GGAACAGCAA TOGAGCCTGA GCTAAGTGAT AAATATGTCA	300
	CAAGCAATGT GCAATTTATC ACAGAACATG GOGACGTTGT ATOCGTTCOG CAATAAATAT	360
20	AGGIACTITIG AAACGCCAAA CCAGAATCTA CGTGTATTGG CGTTGGCATT CATGTTGGAT	420
	TTTCCCCGTGG GCTGCTAAAA ATGTTAGGTT AACCCCTCTG GCCGAAGAGG TTAAAAAAGGA	480
	CTGGTTCACC CAAACTGTGG AAAAGTACCC GCTGACAAGC TTGATATTAT AGTTGTCTTC	540
25	CGTCATTTAC CAGTCACCOG TOGCCAAAACG AGAGCTTCTG CAGTTACACC AACGACTAAG	600
	GGAATCTTAC CCCGACACTA TTATCCCGTA CTTCCGAGTG INTIACTCAGT CNGAAANTOC	660
	CINGITITING ANAAAACSAN TOCITTACCA ACGOCGAAAT TOCIGAAACA TOGAATOCNA	720
30	TCAANANNIG TITCNCAAGA AACCAAATIT TOCATICNAT AIGACTTAOC CAATICCTIT	780
	TCCCCTCCING NITNANACTC CAAATTCCNT CCAAGGAAGA ANANINACNC CC	832
	(2) INFORMATION FOR SEQ ID NO:334:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 800 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1265RP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:	
	CATCITICCIC ACAAATAACT TOCATTGICT CCACTATTTT CICAACATTA GCATTTATGC	60
	ATGICACTAG GCATTGCGTT TCAGGTAATG CATTCCCAAC AAGTGGCTTA CGATCTGGAA	120
50	CAGATTGIGT TOTTTGIGAT TOTGGIGGAG COGTACCTOC AAAAGTIGAA TOTTCGITTT	180
	CCCCCGACCA GGAATTCCAT GGACGAGACT TCTTGTCAGA CATAAACTCA AGTCGCCCCG	240
	CICHATCIGA CATATCITCC TGACICICIT CIOCATAGGI GOGGITACCT GGGIGIAGIT	300
55	CGICCICAGI CCCIACGICI CTICTICCAT CCATATOCCI TGICGICAGA TATGITICIC	360

	TUTTUUGGIT AGAAGUGICU TUATTIGTAG GATUTTGAAC AAAAAGTAGT TIGTTATICT	420
5	CCASCIOCOC AGICICITOC AGGITITACT TOCCATOCIT ATTAATACIG GITCITTIAGA	480
,	TOGITICCCTG ACTITICCCTA TAGGCCATTIG GTTCCGGCGA CTTGTGAAGG TATGCATTGA	540
	CAGTOCTOCT OCTTAAAOST CINCTOCCCC CCTTATTTTA NCACCOCTTG CCCOCAATGC	600
10	TACACNAVIC ACTTAATONO NECOCCITOC NCITOCATOC TGT0000000 OCACOCACAA	660
10	COCNAACTIN GOOGCOCACNA TTICOCONION CCAAACNIVIT TOOCCNAAAA AANAATINIT	720
	CCCCCAACCN NCCANNACCC ATACCCCCAN ATCANCTAIN TIGICCCCCN AACCCCCNNA	780
	ANCOCCHOCC CCCCNENCEAA	800
15	(2) INFORMATION FOR SEQ ID NO:335:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 820 base pairs (B) TYPE: nucleic acid (C) STRANDENESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(V.) ORIGINAL SOURCE: (A) ORGANISM: PAG1265UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:	
30	CATCOGGICG COGCIGGIGA AGGCAGGGAC GIGGITGIAC GGGCAAGGGG GCCIGGGGGC	60
	GUICTACCIG GOCAACGESC TCAACGICAT CAACGIGTIC CCGCACICGE CCATCAACIT	120
	COSCILOGILIC CASCILOGOCA ACCOCCILICA COCCACACACACACACACACACACACACACACACACA	180
35	CEASCICICE COCCIGICEA CGIACGITEC GOGGGGGTT GOCGGCATCA TGGCGCAGIT	240
	CTCCGTCTAC CCAATOCACA CCTTCAAGTT TCCCCATACAG TGTCCCCCCC TGCATACGCC	300
	CTGCCGCGGT CTGCCGCTGC TAATCAACAC GCCGAAGGAC ATGTACCGCG AGGGCGGTCT	360
40	COCACTOTIC TACOCCCCC TICSOCTICG CATTITICOCC GIGITOCCCG TACOCCCCC	420
	TOTACCITOG CACCITOTOG COCCICAAAC COTOGIACAT TACCOGRODO GCAAATOCOC	480
	TOGGCATCTC CCCAGAACCA AGTOGTCATG ACCATCTCCG TGTGCTGCCG AATGCCCCCT	540
45	TOAGOOGTAC GTOOGGOCA CGTGTOTACC CTATCAACCT TCTACNGANG CONTCCCAGC	600
	CCCAGGNAGT INTONONCCC CCCTCCTACA ANGNITICAAN INTITICCGAA AACACCNON	660
	AGGCCCCCC GCTTTTACAA GGTTGGTTCC NACATTGCCA GGTNNCCCNC ATCCCACNCT	720
50	MITITITING NAAANITAAA NNCCANCOOC OCNAATAAAG GCCCCTTNIC CCCCCNACOC	780
	CINGGAATAAN GGITCGGACT NWAAAAACCAA MACNCCCCCC	820
	(2) INFORMATION FOR SEQ ID NO:336:	
55	(i) SEQUENCE CHARACTERISTICS:	

5	(A) LENGTH: 819 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: 1266RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:	
15	GATCTTATCT GGAACACCCA TICAGAACGA TITATCTGAA TATTTCGCCT TACTAAAITT	60
	TAGTAACCCT GOOCTICTOG GTACOCOGC ACAATTTAGG AAAAATTTOG AAATACCCAT	120
	TCTACGGGGT CGGCATGCTG ATGCTACTGA CAAGGACATC GCTGCTGGTG AGGTGAAGTT	180
20	ACATGAGUTA TOOCAGATUG TGTOGAAAUT CATUATOOGG AGAACCAAUG AUATOCUATO	240
	GAAGIACTIA CCITGIAAGI ACGAACATAT TCTATTCGIC AATCTCTCTC CGATGCAAAA	300
	GGCAATTTAC GAACACTTCG TGACGTCACG AGAGGTTCCC AAGTTAATGA AAGGTACAGG	360
25	GICGCAGCCA CTGAAGGCGA TAGGTTTGCT GAAAAAGTTA TGTTACCACC CTGACCTGCT	420
	AGATOTOCOG GATGAGATOG COGGTTOTAC AAATTTAATT CCAGATGACT ACCAGAAGTG	480
	CTAGTGACAC ACACTCCCCC CCCCAACAAN TTCCCCTTTT GNATTCCAAC GANACATTCC	540
30	ATCHAATTIC GCNATTCCTA GAACSTTTIC NGFTTTAGAA TCCAGCCNTG ATTCNAATGA	600
	AAAAAATGIC CCNGATTICT ACNINCCCCCC ACCITIGGATT TINICCAAAA AATNINNCCN	660
	COONCCCCON GOTTINITOC CANCIGAANG NNOOCNONAA ATTAANNANC TTINAACCTT	720
35	TIGAAAATIC CAAAACCCCC GGCAGAATIT NICNITINIT TCCCCCNGCN CNGGGNNGGG	780
	NICCCCCTTT NGGCCCCCCG NGAANTTIGA CCCCAAAGN	819
	(2) INFORMATION FOR SEQ ID NO:337:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 807 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1266UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:	
	GATCTIGTCAG CATTCACAGA AACCATCOCT ACGAAAAGIT TCCTACAAGI AATCCCACCC	60
55	ACCOGNAGEN CHOCCOGTIG GGHOCHGHAG COGHCTTGOC ACCOCACAGT THOCAGGACT	120
	TGTCTTCTGT TGGTCAGAGT ACTAGGCAGG ATGCGTTTGC TTATTCCAAT CACAGTGTTG	180

	TOSCTAATGA TOSCCAGOOC TOTTTACOGO GAAACOOTGO COCAGACTOO ACGITUACTG	240
	COGASTITAA CCAGCIOCTA TCTGAATCCA GCAACTOCCT TGAGCTTGAT TCTATATTCT	3 0 0
5	CAGGCAACTC AGTTCTCTGG AATGGGGAGA CCTTAACCTC TGAAGCAAGA GCTACCCTTGG	360
	ACCOCATOTO COCATOTO TOCCAAGATC COCCOCGACGA CAGCCACCCA AATTOTOCAC	420
	AGANICOCCI GAAGIAITGA GTCTAGOOGA CACTGAGTAT GOOGACCTGG ATAGTTTGAT	480
10	CACTAATTIG TACTICTACC ATGCGAGGET TOGTCCCGCG GGTCTGAAGG TITTGTTATA	540
	ATGATOGATT TTAGAAAATA TAAGAACOOC CTTGAATATG AATACNENON NITAACOOCC	600
	GGGGGTTGCT GATACCCCCC CTNTCCCCCCN CTNGGNTGAA TINTTACCCC NGGGNGGGA	660
15	GANAAANAAT TOOTGOODNIC TIGGOTTOON AANOOCCATT COOTTINIVAA TNAAAANIGO	720
	TICCINCION INTIAAAAA AAAAACCGIG TICCCCCNAT AACCAAATCC CCNCGCANGN	780
	AATTICCTOG GTICAACANC COCTCAC	8 0 7
20	(2) INFORMATION FOR SEQ ID NO:338:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 792 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
3 0	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1267RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:	
35	GATOCATTOC ACCOGATIGE AGCAGCIAGI GCATITIGGOC ATACGCOCGA TIGCCCTITIC	60
	TTATAATGAA TOOOGGCTTG TAGAGCATCA TOOGGCACTT CACGTGGTAT TGAATAGCTC	120
	CTCATAACCG CACCGGAAGA TTTCAGGAAT ATATCTGGTT GIGIAGIGTA GAGGTIATCA	180
40	CIGIOGATIC TGATATOSCT GITISCASCIT GAACATICCA CIAACCICOG TICGAATCOG	240
	AGCACGAACA ATTITITICANC TINAANOOCINA NATTITININOO OCTANAATAN TIGGACTININOO	300
	AAAATCATCA MATTIMAATT TITTCCAAAA CTTTGTCCCGT GACCGGANIN GAAATGAGGG	360
45	NAAGTOGAAT GICCAACACG GGNACCCNAA ATTAGAATTC CAGGGAAAAT TOOTACANTA	420
	NANAGETICAC ACCONOCINA ACCOCCCCCO GOGANNACTE GACCOCTITINA ACCTENGAAT	480
	OCCUPATIVICC ANCOUNTING COCCUCCOUN TRAINCHAI TACCONCOCC	540
50	TNCTTTTCCC NAAANNGATN CCCCCCCCNCG GAAAGGITICN TTNNNANCN TAGGAGGCCC	600
	CITINGGICCG GAAITINGNIN CCTITICTINIC TOCCOCCCCA AATOCNGGAC CCTGNAANINC	660
	CCTUNINGCC CCCNITTIAC NNITTICCNN GNAANINGTT CCCTIGGCCC ATCCCCGGAC	720
55	NUMBARTIGGG GNITTAANGG CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	780

	CCCCCCCTIN CN	792
	(2) INFORMATION FOR SEQ ID NO:339:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 824 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1267UP	
15	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:339:	
	GATECOSCATE GITTIGFICA GICATACIAE CTOGACOCCA TGITOGCOGA OCTOGCOCCG	60
20	CCGGCGAGIC TCGGGTCACT GGTCGGCTTG TGCAACGCGG ACTGTGCCCC CTCCTACTGG	120
20	TIGGAGGTAC CCAAGCACGG TATCCTGTTC CTATGTGCGA TTGCGAACCT CGTAATCACG	180
	CACCTCGTGA ATGTAGACCC AGCAGCAAGG GACATGCACG CCTTCTGGGA GAAGGTGAAT	240
25	GCGCTCTTCT TGGAGAACGG CTCAGGGGGG ATGCTGCAGA AGGAGGCTTT GGTGCCCCAA	300
	CCGAAGAGT GCCACAAGGA TGGCGGGGGG GCGAACGTTC CTGCGTCCCC GATTTCCCGT	360
	TOGONGACAC ANTACACATO GOACCAGGGC AGCAATTACA TGAACCCGCA CGCATTCGGC	420
30	ACGCCCCCC ATCCCCCCCC CACACCCCCC TOCTCTGTTC COCCTAACAC CCACACCCTC	480
	TOTOTOCOCAC TOCOTTCACA CAACOCCTOC GOOCCACAAG COTTOCCCAG ATTOCCATACO	540
	ACACTTOCTC ACCCAGOSTC GAGGACGCCA TCAGACAGGG AGCTTOCTOC TTTGACCAGA	600
35	AGGGCTTGAG CAGGATTCCC AGGACGACAC GACGGCNCTG TAATGCAACT GTTGTCCTTC	660
	CNATTIBOOC CCTATCOCCC AATOGAACGC CACTCCCCCNG AAAAAAAAAA AATITTCCCN	720
	TOCATATTIC ATCAATICAA TTACAAAAAT TACIVITICIN NIVATTCTTOC OCTOCCACAA	780
40	CAATTGOGAN TNCTAGACOC GOGNOCTGOC MITNOGITTI AAAT	824
	(2) INFORMATION FOR SEQ ID NO:340:	
4 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 787 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) Original Source: (A) Organism: Pagl268RP	
<i></i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:	
5 <i>5</i>	CATCCICACA ACACTITUTC TGTGCAGGCT TATCAATGCT CITTCTATCC GCAGCTTCTT	60

	CCAGGCAGAT GAATACTGGC AGTGGCTGGA GCCTGCGCAT GTTAAGGCGT TTGGATATGG	120
	TOUGCTGACT TOUGAGTOOC AGCATOOOCT GCGCAOCTAT GCATTCCCGA TGCTCTTTGA	180
5	ANTIGICGIAC TAIGICGCGT GGATACIGGG TGIGGCCACC CGCATGCCGC TGCAGGGGIT	240
	OCCACATOCS ACCOCCCTGT GTGCCCCCGT GGTGCCCACC GGCCCGCCGC GCGTGCCCCCC	300
	GATGAAGGCC GTCTGGGAGC TGCCGGAGGC AGCGCAGGAA CTGGTGGAGT ACTACGGGGT	360
10	TATTICTACCO CCCCCCAAGT CCTCATCCCC CCCTACCAC CCTTCCCCCCA CTTCTACACC	420
	GIGCIGCIGG TIGCGCAAGC TGTATCIGCG AGTCGCGGAT AACGGCGACA CCAGAAGGCC	480
1.5	GACGCGCCC GTCAGCCGTT GCGCTGATGC TGACCATGAC AACTTCTTCA ACTGTTTCTT	540
15	CCCCACCCA ACCITICATCA CICCTICCAG ATCACCCTCA CCCCTOCCCC TCTACCATTG	600
	ATTGAACGGG CCTCACTTGG TTCTCTNGCT TCNCCCAACT TGCGGTGGCT CTTTTGCCTG	660
20	CCTCACGCCA MIACTITTIA TCTGGCNCCC TGCTNFTCTT GGTGNCANCC TGTTCCCCCN	720
.0	ANNOTOCINO COTTITAACO CONOCCAAGT TECCOCCGAGO COCTEGGGIN TITICAATICCA	780
	MANA	787
rs	(2) INFORMATION FOR SEQ ID NO:341:	
80	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 840 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
95	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1268UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:	
	GATOCAGGTA TACCOGCCTC CGTCGCGCAG CGAGCTGCGC AGCCGCTTCA TCGCTGCAAC	60
o	TGAGAATGCC CTCGACCTGA TGTGCGGTAT GCTGACGATG GACCCGCACA AACGGTGGGA	120
	CACGACTOGT TOCCTOCTCA GTCAGTATTT TGTAGAGCTT CCCGAGGCGA CACCTCCTAC	180
	GGAACTICCA AAACTAAATA AGTAATGACT ATGATAACCT AGATOGTATA CTCCGACGTT	240
5	TIGIGITIGI OCTTIGACOC GAIGACATIG OCTTITIATOG TATCOCAGAC GITOCCIGAA	300
	AAAGATTCAA OGTCTOOGTA ACAGATTTOC GCAGACTACT TGTTGAAAGA ACAAAGACCA	360
	GAGCOCTOGG ATTOCTCACCC CAATGACGAA COCACTCCOC CITATITOGCG CTGGCTGCAG	420
o	GTTCCTTAGC ACCAACAATA GGCCGCCACT GCACAAGATC TTTCCCTCCC AAGAAGCTGG	480
	TGAACAGGAT OCTGITICGAC CITGATAGCC GACTGACCTT CCCOGAAATT ACTGCCTGITA	540
4	TACCACCAGT TGTACACCCC AATTACACAG TAGTACCCCG ATTTGTAGTA CCCCCCCCGT	600
	TGAGUGGGC ACGACGITTA TGATTCATGA AAAGGTGCTG AGAAGACTGG CCCCCCAGAA	660

	CGAGAGCTCC CATCGCCNTC TACTTGCNCC GGANAACAAC TGCTTTACTT GCTGCCCANT	720
	GGANACNAAA ATOCACONOC NCTNCCCTTG ANCCCGTGCA CCGVITCGCC NAAGGANGGA	78C
5	AATGAATTIG CAATTI'AGNI CINGATTITAC INCTICTOGNIC COCCOCCCCA CTGANNGANC	840
	(2) INFORMATION FOR SEQ ID NO:342:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 787 base pairs (B) TYPE: nucleic acid (C) STRANDFINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1269RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:	
	GATCCCACTIC TYGOCAAGCT ATACGGTGAC ACTATCATAG CYCGCGGTGG CCTCTACGAG	60
25	ATGGAAGACA ACCTGGGGGA GTTCTTGGAC AGAGAACCCA ATAACGAGGC GTACCTCAGA	120
	GATCAGGGCC TAGCCTAAAT OCTCCTTCTT TICGCCGCCCT TCCTGCCCTC CTATGTATAT	180
	TOCASCIAGA GAATOSCAAG CAASCCATAC TIAGAAATAG GATAITGITC CGGGAACACT	240
30	GATTTACTGT COGTTACTCC TCCCCGAAACT CACCTGTTCG GTATCGAATA ATTACCGTTC	300
	GACTACCOCC AGIGIGATOC TITCTITATA CCGGCATACT AAAACAGGGT CCTCAGIGGA	360
	ATCCTCTCTC ACTGAATATC ACCCCCTCCA TCACTTCCCA TCCCCTACAC CCTCCTATGT	420
35	GCAGACCATA TCAACACCCT CIGIACACGC GIGGAGTICA ATATACGCGT ACGACGCACA	480
	TACAATAGTA CGIGICOCCA ACCGITATAC GAAGACCTGC GTICTGATTG CAGCATTTCC	540
	CAAGCCCCCG AAATACAAAA CCGCATTTIT AGCCCAGTGC GATAGATGTC CTGAACCANG	600
40	GAATTACANC GAAGGNOGAT TOCTACTACN ANCATCANCC AGGGCTOGNG TATTTCTCAT	660
	CCATCCCCCT CNAACNAAAA ATCCCCANTT TYTAAATYTC CATCCAAACC AINCANATOC	720
	CONTTINGAT ATTONOCOCAC TOCCOCCCO NOCCCANIVI ANCHOTOGG ATCONENATT	780
45	ccccct	787
	(2) INFORMATION FOR SEQ ID NO:343:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 820 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1269UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:	
5	GATCGAACTC CATGAAGGAG CGTAATGGCC TCGTGGAGCT GCACCGCACT GGGTGCGTIAC	60
	ATAGOGGAT GTAGGAATGC GGGGATAACG ATTCGCAAAA CCTCACTGGG CTGCGCCTCT	120
	AGCITCAGCT CAAGCTGGCG CAGCAGCGTT GCTATAGGCT GTTGTGGCCGA CAAGGTGCGAC	180
10	ACTICACITG CACTAGGACC ACCIACCATA CCACTACTTA TATOCAACIG GTGCCGCTIAA	240
	TGAGGATGAG GGTCAATTIC TGGCTCCGAG CGCTGGCTAG CACCACAATT ATCACCAAGT	300
	CCATACCTCC ATGCAATTCT GAGATCTTGG CTACGTGCGA CGGGTTTTGC ACCCCCTCCG	360
15	CCTAAGTTT CCACCGTGAC CTTCGATTCC TCCTGGGAAA TGCGAGATTT CITTACCTCT	420
	TRACCIGIGC CCIGGAATAT CCCCGGCAGC TCCTTCGCAT ACTGAGTGIT GABCGTGATG	480
	ACCACCACAT GOGIFATOCC COCCCCTIGN GGCCCCCNAN TITICCCCCCCC GGTEATITICT	540
20	GICCCIGGGC CIGCAANAAC TICCANITAC GANGCAATCT GGICCCCCTG TICTTCCCCC	600
	AAAACATCTG GOOCATTGGA NOOCATATGC OCTAGAACON ATOCAATCTG CANCOCONGA	660
	MITTITOGAA ANNAATTACC GONAAGGANC AACCCGGAAG NAAAGCCCGC CCCCCCTGTG	720
25	CACCONACTT CCCCCCCCC NAAAACONGA ANTINVITTIT INVITTIGOCC CHANCONCON	780
	TTTTCVGCCC NGCCGGGANG GCCTTAAAAN TTCVTCCCCC	820
	(2) INFORMATION FOR SEQ ID NO:344:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 806 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1270RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:	
	GATCATATOG TGAACTTGGC ACATACAGTT GAATCATCCC AATAGCAAAG AGAACGTAAG	60
45	ATTIACCIAG COCOGCATCA CCTOGAATAT CTAGCATTIG CAGCOCAGGT GAAAAGAATT	120
	TCTCATGAAT TGATTGGAAA TGTGGTTCCG TGTGTTCCAT TGCTAAGCCC GCTAGTACAC	180
	CATAATCATC ATTACACTCA CAGGITAGAT GOGCCTTCAC TGITGCCTTA TACCAGTCTA	240
5 0	ATAGAACCTG CCTGTAACGA GCATATTGAT CCTGAAGAAT AACCACCGAT GOGTCAACCA	300
	TOCAMITICAG CAACAATGIC GOCTICATICA COGTITICAGI CATGICACTT COGGICAANT	360
	TCTCAAAGGA ATTTAATTIC GGTATCAACC CCTTCAACAA GGAAGCTGTG AAGATATCAT	420
55	CANCATOCCA TITICTIANOCT ANACCITICCC GCATCCATAG GAAATCAAAA GTGGCTQGCA	480

	AAGCATAGIT TGCGCTATTG GCTTTGACTA ACTGCGAAGT TAGAATACTA CFTGTGGGCG	540
	CCAGITIGAA TACCAGAGTT AGACATTCAA COGATTCINA GAATATAATC CTNOCGAATT	600
5	TATOCATION OCTANAAAAT INTITOONOC TIGATOCANA ACNANAAAAT TOOGTIGAOO	660
	NCTGAAGACC TATTOCINCC TTINAAAGAC CTOCNCATTC TTCNATTTCC CNAANGNVTC	720
	CCGITCTACC NAGAAANITC TIGCATGOON NCATGGTTIN AACONAAACN TCCTTTGANG	780
10	NIANINACIT COCCONNCCC AATTEA	806
	(2) INFORMATION FOR SEQ ID NO:345:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1270UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:	
20	GATCCGATTC TCAAATTTTC TGAATGGTAT GGTAAGAAGT TTGGGGCTGG AAAGGCTAAC	60
	AGIOGIGITA TATCITICOG TGATATITITA GCITGOGICG AGITCATTAA TAGIACCIAT	120
30	AAGGCATTGG CTTGCCCTTA TGCTTCATTA ATCCATGGGG CGGCAATGGT ATTCATTGAC	180
	GCCCTTGGAA CCAACAACAC AGCGTACCTT GCCGAGAGTG AGGAACGATT AGAACACCAG	240
	AAGCAAGAAT GTCTCAAATA TCTGTCTGAA CTAGCAGGAA AGGATTTAAA CAAATACATG	300
35	TOTOGROCAT TOGATOTTAA GATTGACGAT GAAACTOTOC AATCCGGGCT TTTTAGCCTA	360
	COCAGAGITT CTTCCTCATC TGTCCAACCG GTTTTCAATC TTGGCGCACT ACTACAGCCT	420
	ACAATCTCAT GAAAGTTGTC AGAGCAATGC AAGTACAAAA GCCATCTTAC TGGAAGGATC	480
40	ACCIGGIGIT GGTAAAACCA CATTAATTIC CGCATTGGCT GACTGTACCG TTACGAATTA	540
	CCCNTTTAA TTATCCGAAC CAACTGATTT GAATGAATTA TTTGGATCCG AAGCNCCCCG	600
	AAAAAAAAN GOVAATTINI TITGNGITGA TGCCCCCNIT TITNAAACTA TGCCAAAGTG	660
45	GATGGITTIN TITAAATAAA ANNANATIGC NCCCCANCON TITTITAACON CNNACCCIGT	720
	TIGINNOCNI GCNCAACCCA NICCCAAATT TAANAAAATT TNICCCCCCC ATCCGCTTIT	780
	TIGNINOCCA AACCCANACA GGGGNGGIGA AAAGGGNIGC CAANCTICCC TC	832
50	(2) INFORMATION FOR SEQ ID NO:346:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	IN TOLOGOT: THERE	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI271RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:	
10	CATCATTATA TIATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT	60
	ATTATATTAA TICTCCATTG GAGCAATTTG AGATTAGAGA TITTATTAGGT TTAACATCAC	120
	CAATAATAGA TITTAGTITT ATTAATATTA CTAATTITOG TITATATCIT ATAATTCITT	180
15	TATTAGTAAT TITACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTICTA	240
	ATTEMINITE ANGICANGAN ATANTITATIG ATACTATTAT ANATATAGIT ANGACACAGA	300
20	TTOGTOGTAA AGITATGAGG TTATTATTTT CCATTAGTTT ATACATTTTT TATTCTTATT	360
20	TTTACTATAA ATTTAATTAG TATAATCCTT ATTCATTTGC TATAACTTCA CATGIAGTAT	420
	TIGIAGIAIC AATAAGIATA ATIAITTGAT TAGGICIAAC TATTATTGGI TITIATACIC	480
25	AUGITTAAAT CITTIGTTTAT TITACCACTA GGTACACCAT TAATITTAGTA CCATTATTAG	540
.0	TATCCATTGA ATTATATCCT ATTTGCTINIA ACTTATTCCA TAGGITTITIA AAATACACTA	600
	ATATATACCG GICCATTTAT AATOGITATT TAGANGGITT AATATINAAT TNAAAACCAN	660
10	AATATTIACA TITTATOGIN NOONOOCAAN AAGGCATTOG TITGGIINIT TAAAAAGGON	720
	ACCIATATON CCITATITATIN CCCCCTITTA AMANCNATT TIMOCITAT	780
	TAAANTAAAT C	791
5	(2) INFORMATION FOR SEQ ID NO:347:	
o	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 834 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
5	(A) ORGANISM: PAG1271UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:	
	CATCAATCIT TOGATCATTG TOCAATATTC COCACTOCTG TATCATATAG ATATTGATTA	60
o	TAATTICIAA ATCAACGIGA TIGITCTAAC TITAATTAAC AATTATGAAT TITIGGCTAG	120
	TTATTATTT TTAATTAACT AATACCTAAA TCATTATAAG CTTGACTTAA AACAAATAAT	180
-	TATTACATTA TICTITATIT ATTATTIAAT ATTITAGITAA ATTITAAGIT CATTATTCTT	240
5	AATITITACT CACCAGIACA CCACTTATIA ATACTATIAA TIAATAATAT TAACGITICA	300

	TICOCATOTO TAATOTCCTT AGTTAGCOCT TAATCTGAAC CAACATCATG TICTCATTAT	360
	TATTAACTAT TTTTAATTAT TTTAAATAAT TATTTAATAC GAAAGTTATA GCATTCCAAC	420
5	CTATGAAATC ATAAAGATTT ATAATAGCTC AAATATTACA CTTTAAACCA CTCAGTCAAA	480
	CTTTCTTAAT ATATATACCT TATATATOGT TTGATAATTT ACTTATAATA TATAGTATAT	540
	AATTTAATGA TAACTCTTAT CATTTAGGTG OGTAGGGTTC ACCCCCCTAT TGCTAGTCAG	600
	CATATGAGGT ACCICCCCC AATGATAAAA GTTATAATAT ATAATATTAT ATTAAGTATT	660
	TAAACAANAT AATATAATTA TITAATAATA TITTITATITA GONAATAAA AAAAANITIC	720
15	ANVIPTOAAA NANGGIOCNG AGAATTANAA AAAGONAATA ATATGTICAA TTTGACCCAT	780
	TAANAATGIA GINCNCTGAC ATCNCCTATT TCCTATANAA ANTTTANAAN AANA	834
	(2) INFORMATION FOR SEQ ID NO:348:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 813 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1272RP	
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEO ID NO:348:	
	(AL) SEQUENCE DESCRIPTION. SEQ ID NO. 340;	
	GATCAAATCT AGGTTCTCGG ACGGCAACGG TGAGGAGTTC GTGAACGGCG TGAAGCTCTG	60
	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGAGTTCTT	60 120
35	GATCAAATCT AGGTTCTCCC ACCOCAACGC TGACGAGTTC GTGAACGCCC TCAAGCTCTG	
35	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGAGTTCTT	120
	GATCAAATCT AGGITCTCCG ACGCCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCITTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCAGGAAGT TTGAGTTCTT CAAGCCTCCA AAGGAGATCC TAGAAGAACG CAAAGCCAAG CTGCAGCGTA AGCAGAAGTT	120 180
35 40	GATCAAATCT AGGTTCTCCG ACGCCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCAGGAAGT TTGAGTTCTT CAAGCCTCCA AAGGAGATCC TAGAAGAACG CAAAGCCAAG CTGGAGCGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG GGGTGGGAAA ATCCAGAAGG	120 180 240
	GATCAAATCT AGETICICGE ACGGCAACGG TGACGAGTIC GIGAACGGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGAGTTCTT CAAGCCTCCA AAGGAGATCC TAGAAGAACG CAAAGCCCAAG CTGGAGGGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG GGGTGGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC	120 180 240 300
40	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCAGGAAGT TTGAGTTCTT CAAGCCTCCA AAGGAGATCC TAGAACAACG CAAAGCCAAG CTGGAGGGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG CGGTGGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT	120 180 240 300 360
	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCCC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCAGGAAGT TTGACTTCTT CAAGCCTCCA AAGGAGATCC TAGAACAACG CAAAGCCAAG CTGGACGGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG GGGTGGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA COGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG	120 180 240 300 360 420
40	GATCAAATCT AGETTCTCCG ACGCCAACGG TGACGAGTTC GTGAACGCCC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGACTTCTT CAAGCCTCCA AAGGAGATCC TAGAACAACG CAAAGCCAAG CTCGACGGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG GGGTGGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTGTT GGGCTGCCAT	120 180 240 300 360 420 480
40 45	GATCAAATCT AGGTTCTCCG ACGCCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGAGTTCTT CAAGCCTCCA AAGGACATCC TAGAAGAACG CAAAGCCCAAG CTGGAGGGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG GGGTGGGAAA ATGCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTGG TGTAATCTTA TCAAACTATA TATAGGGGGA CGGACAGCTT CAACGGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGGCCA TATGCTGCTT GTCTCCCAGC TTTTCTTGTT GGGCTCCCAT CTGTCGCCAG GAGGGGAATC CGGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC	120 180 240 300 360 420 480 540
40	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCAGGAAGT TTGAGTTCTT CAAGCCTCCA AAGGAGATCC TAGAAGAACG CAAAGCCAAG CTGGAGCGTA AGCAGAAGTT CATGGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG GGGTGGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTGG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTGTT GGGCTCCCAT CTGTCGCCAG GAGCGGAATC CCGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC AGAAGAGGCT GATAATTGTA GTCNCAGCAC ACCATAGACG CCGAACAATG CCCCAAGCCCC	120 180 240 300 360 420 480 540
40 45	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCAGGAAGT TTGAGTTCTT CAAGCCTCCA AAGGACATCC TAGAACAACG CAAAGCCAAG CTGGACGGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG GGGTGGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CGGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTTGTGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTIGTT GGGCTCCCAT CTGTCGCCAG GAGGGGAATC CCGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAACGC AGAAGAGGCT GATAATTGTA GTCNCAGCAC ACCATAGAGC CCGAACAATG CCGCAAGGCCC AGAACAGCGCT TAGTTTGAAA TCCCAAAACA CTTCGAATCA TCGGTTCCCC GGAGGCCCAA	120 180 240 300 360 420 480 540 600
40 45	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCC TCAAGCTCTG TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGACTTCTT CAAGCCTCCA AAGGACATCC TAGAAGAACG CAAAGCCAAG CTCGAGCGTA AGCAGAAGTT CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG CGGTGGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGCCA TATGCTGCTT GTCTCCCAGC TTTTTCTTGTT GGGCTCCCAT CTGTCGCCAG GAGGGGAATC CGGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC AGAAGAGGCT GATAATTGTA GTCNCAGCAC ACCATAGACG CCGAACAATG CCCCAAACGC AGTGCTGCGT TAGTTTGAAA TCCCAAAACA CTTCGAATCA TCGGTTCCCC GCAGGCCCAA TTIATCCGGAAN TTGCCTTTTTA AANTCCNAAT ACAANGANTG CGCCCCONTGT CCCCTGTACA	120 180 240 300 360 420 480 540 600 660 720

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 844 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1272UP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:349:	
15	CATOCACOCO COCOCOCATOS COCOCOCOCO COCOCOCOCO COCOCOCOCO	60
	OCTOSTOTAC ATCOTCACOG TOSCCATOTT CACCAACGAC TICTICATOT COSCUTTOTS	120
	CCICCOCACO TICGOCOCC CCICCOAACOC CCACCIGCIG CICCOCCIGCT CGCIGCCCCC	180
20	COTOCTOCTO COCOTOCTOCT TOCTOCTICAT COCOCTOCTOC COCTOCTOC COCTOCTOC	240
	COOCTACOCC COGCTCCCAG ACCTCCGACAG COCCAGTTTC TYCCTGCTGC TCCCCCCCCCT	300
	OCCOCCTION COCCAACONOC TOURISCITCON COTOCATORIC GROUNITONA COTICCACOCT	360
25	CGACTCCTTC CAGAGCCCAC TOSTCTCCAC CATTICCAAC GACCTCTTCC CCCAACCGCC	420
	TOCCCCCCCT CTACCCCCCCC CCCCCCCTCC CCCTCCTCAT CCTCCCCCCTC CTCCTCCTCC	480
	GCCIGCIGGC CACCOCACAT CCTGGCCATC TACCTCATCG TOCACCTGCT GTCCGCCGCC	540
30	GROGICOCCG TCAIGCIGCT GCCTTCTGCC CGCGCCCCCG CGCGCCCTGT TCTGCCTTGG	600
	AGCTGATCGG CGGCCGCTCC GENGGGCTGT CTGCGTTCTC NICTTTCCGG CCATCTATAA	660
	COCIMINOCN CNANCESCENC SCINICICIATI TATIGNAANG NOOCTACTIN AATAANSESSG	720
35	NACTINASCA GOCINGICATI TOCOCCCANIN GOCAACTGIT TITOCOOCANA NAANITONOC	780
	CTGGGNCCC GITGGNCCCN CCCGGANANT CANGNTAACC NCAGGGGAAN TCCAAANCIT	840
	CINC	844
40	(2) INFORMATION FOR SEQ ID NO:350:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 792 base pairs (B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1273RP	
50		
	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:350:	
	GATOCCAATA CAAGCAATAT TGTCGCTACC AGAATGCCCC ATTTGCGACC CATATAATCA	60
55	CAAGCGAATC CCATCCCCAC CTGCCCTATG ATAGTCCCTA TGAGTGATGC ATTTCAAACC	120

	CHIGHASHA CAICIGCALL AIAITCIAIC ICACCHALL GAPPICHGAA TALAEGSTIT	100
	AACATOGACA TGACATTATT TTGGTAACCA TCTGAAATAA GCGCAAATCC TGCCGCCAGG	240
5	ATACTGAATA GATGTACCCA TTTCCCCTTC TTCCCCACAG CAAAACGTGC TTTCCCCACAG	300
	TOGGOGTCAT ACTITAGIAA COCTGTOGTG GACATOGTAT TICTOCAAGC COCGGCTATC	360
	CGANTANTAT CTACCOCCTC ANGOGITAGG TIGCTGCATT CTATATTATA TATTTCCTCT	420
10	CICTACCACG TOCAAATITA CCIGIATGAT TATOCTOCAA TCTCCOCGIT CIACITCCTT	480
	TOTTOGAÇÃO COCTACOGAC TOTOTTATGA TITATOGOTIOC ACCATATIGAC GICAAGCAGO	540
	ACTAGCTTTT ACCTGIGATA CCTTCCTTEA CTAACTGNAT TCCGAACTAN TTTGNNCCCA	600
15	TACTATATOC TICCOCTAGA GIGAAATAAC CITCCATITA GGPINNTOCC ATTCCCNGAA	660
	ACAGTITITIA AANAAANACA ACCTITATOO TINAACOOCA AACOCOOCAA AAANAAAATT	720
20	TCCCCATTIN CIAGFITTIT TCNOCCNOGA GOGAAGAAAC CCCCCCTAAC CCCCTAAANA	780
20	ATTOCICING CC	792
	(2) INFORMATION FOR SEQ ID NO:351:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 833 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1273UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:	
	GATUGGUGTA TAAAACTGAA AGTTUATGTA TOUTGTUTTG AATGCAGAGA CGUGGUGCAC	60
	TTTACACATC GGCAAGCCTT GTGTTGCGAA TGAAACATTA AGCTTATGTC AAATACCATG	120
40	AACTGTATGC CAAATTTAGT AAAACTCGTA CGTGCTGCCA GCATAGATAG ACCTGTTACC	180
	GATATOTOCO TIGAGOCTAA AGOOGAGCAT TGOGTATTAA CTIGOCTIGGA CTATITOGGAA	240
	TCAGAGCITT CAGATTOGIC TICATCATGG TCAGTCATCA AAGTOGICGA TGTAGGATGT	300
4 5	TCTATTTICC CACCGCAATA AAGIGCAGIA TICATGCAGI ATTCAATAAG CTTACCTCTC	360
	ACCTOGATAT CTACCACATC ACCTGGAGOG GAACCTAACC ACACACGAAG TTTAGTGGCC	420
	ACCICTICCA CCACICAAAA TATTICITCG TCCCCCAAIG ATCCTCATCC CCCATTATAT	480
50	GOCGTAACGI TAGGTACATA CCIGIGACAC CCAACAAAGT ACAGTIGCTA ACGTCCCAAT	540
	ATCTTAAAGG ANCCGTTTAA ACCNCATATT AAGGTGAAGT TTATGAACCT TTGANAGTAA	600
	CIGNVICNIT ATACCECAAT ACCANANNAA TAACCACCIT GITANGGNAT CIATCGAAGG	660
55	MITACITICON MITOGANCAT TITATAGITIC MINCTATTAC COCCEANAAA TITIGAACAAC	720

	CIVICAGAAAA GITIVIINIOCIN CINGGGAAANG AAAANIINIINC ITIVIGANIICC CCCCGITI'AC	780
5	CTTGAAGNIT CTCCATTONC GAGATTCAAA TTTTTINTAAN AAGGANITIN TAA	833
	(2) INFORMATION FOR SEQ ID NO:352:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 803 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	·
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1274RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:	
	GATCAGAACC AAAAAGCAGT TOGAGTATAT CAGTAAGCAC TOGGAAGTIT GOGAAATAGC	60
	AGTIGCTGAGA GTTACGGGAC AGATTGGCAA AGACACATTT GCGATGGAAT TTAATTCGCC	120
25	GCAGCCAGAG CACGCACAAT TACACATTCA CCCTAAAGGT GCAGCCCGGC TOCTGGGAAA	180
	ACTIGUACIGOS GAGGISTOGOS TIGATIGUACICA OGAAGATAAC CAAGAAAAACC GGGISCOGIGGA	240
	AGGACCOCTG ATTCCGTCAC COCCGCTGTC ACCACGAATC GOGCCGGGAG AGAACCGGGG	300
30	COCCETINGEA ACCIGAATCCC CGAACCCTTT TINITACCCC AACTTECNIC CCNOCCTIAN	360
	TITCAAACCG NITINCAAACC CONNOCCIGG GITINFINGC CONNINCOCA NIANITGGGC	420
	THOGGGGGGG GGGGCCCINGN CCAAAAAAAA ANGOGGININ CCINGGGNGGC CCCCNGITTIT	480
35	ANCAAAANAT TINCCCCCCC GGITCNCCCC CNNAAAAGGT TITTCCCCCCC CCCGGGGITT	540
	ACCAAAAANC CNGCCCCCCC TTTGCANGGT TTCCCCNVTCC CCATGGGGGG TTTTCNCGGG	600
	GCTCCCCCCN GCGGAACCCC AAAAAAGGGC CCCCCCTTTT NTGGGCCCCC NAAANNCCCC	660
40	CHINATTIC CAGANGOGIT NOCHCCOCCC TITITITICC CCATTANNOG GGAANTCOCN	720
	NINITOCCCC CTTTNNCCCC CCCCCCAAAA ANNAATTTTT TNNATTAAAA GAGGGCCCCN	780
	NGAAAAANAA NACCCONNCCC CAC	803
45	(2) INFORMATION FOR SEQ ID NO:353:	
5 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 814 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1274UP	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:	
	GATCAATTIGC GGATACACGA GOCACAGGGC GATAGGCCAA GCTTCCAAGA ATGGGAAGAG	60
5	TACCTAGTCA GGGTCGTCCT GGTAAGACTG AACCGCTGCA AGCAGCTCTA TACACAAAAT	120
	GTAGAGATTC TATTCGATAT ATATCCOCAG ATAGACCOCC CATAAACACT AATGATACOC	180
	TAATTCATAC ACCTACAGCG TGTACATCAA ACACACACAC AAGTTTGATG CACACGCTTT	240
10	ATTIGITICCT TOCACACACT TGATTTAGAC GGTCAACACC CTCAAGGTGT TAGAGTGGCC	300
	AACACCAGAC GOGAAACOCT GAATAGTGAC AATAGTGTCA COCTCOCTCA GGATACCAAG	360
	CTCCTTCCAC TICTCCACAC CCAAGITCAA TCTCCCCTCG ACGTCATCCG TCCACTCATC	420
15	ASCIGOCICC TOTTCOTAGA CGAATGOCAA GACACCICIG TOCAAGIGSC AGIXICIGGC	480
	COCTCCTTGG TTTCTGGTCA CCATAACGAT TGGAACGTTT GGCTTGTACT TGGAGACCAT	540
	CIGIOGIGIT CACCOGAGGI TGATACACGA ANAIGCCTIG GCTTCTGCTC GAANINCCGC	600
20	GAAAGCAGCA CACAAGNOCC CGAGGIIGAA TIGGCTIGNI CATITICCIGA GICACOGIAT	660
	TIGAACGITT GGAAGGCCTG CNCCACNAIC AAAATCTCGC CAGNCNTAAA CGTNAATGGT	720
	TGANACCCTG GOGNICCCCN AAAAATAANA TCNCCCGCCN GAAAAGTTCC ACTTOGAACN	780
25	CCCCNGINGT CIGGITITION TOGTANOCCA ACCG	814
	(2) INFORMATION FOR SEQ ID NO:354:	
<i>30</i>	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1275RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:	
	TGACTOGOCT TOGTGAGGAA CTGACGCTPT TACTACATGT AGATTGAAAC COGTTTTCCT	60
	GENTOGOCTO GROTOGITGO TIGGINTOTT TGCCANTOCT COTGAGRGGA COCTGCCTGT	120
45	AGAGGATCTT COCGATGOOC CAAACACGCC CCACCAGCCC AAAGACGTTG GAGAGAGGGC	180
	TGAAGAAGGI TCATTGACCT CCTTTATGGC TTCAAATGCT GACGGAAGIG ACAAATGGTT	240
	CCCAAGACGC ATGTCCCGACA ATTGTCTGAC GGTGGACTGC AAGACGTGGA TGCGGCTGTGC	300
50	CCTGGTCTTT GATATTCTAT GCATAGTGGC AATGTCCTTT GACAGTGTCA TGTTCTGGTT	360
	TGTCAGGITT AGGITATCAA GITGGGCAAT AGCCAGCTGC TCTGCAAGIT GGTGGITTTTC	420
	TOCACCAGCT GIGOCICTOT GIGITICAGG TCTGTCATCA GITTICITTIAA GCCTCTCCTT	480
55	ATCOGCCCAT COTOCACCIG GACTONIAIN THITINOCAC NOCCATINNN CCATAATTIG	540

NINAAGNAG TNOOCCNCCG GAATTINGNI COCGITICCA NAGNICOGNC COGGGATAAT	600
TTAAACNITT AAAAATTANC CCCCGGCCCTA NITCCTTTIN CCNAATNNIN GINCCCCCCN	660
QUAANVITIT NCAANVCTIN TONVOONIAN CCTTTTTNNC CCCACGGTTI TINVICCCCC	720
CCCNTCCCCN ATTINGGANT TCCCCCCNTIN CCCC	754
(2) INFORMATION FOR SEQ ID NO:355:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 842 base pairs (B) TYPE: mucleic acid (C) STRANDHINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genamic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1275UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:	
-	
GATCGCCCAC ATTATGTCTC AGGGTACTTT GTAGGTTAAG AAGACCTGCC GCTGCATGCT	60
GCCTCAGAGC ATCGTCGAGC ACTACAACIT GCACGTCTCT ATTGTCGATG CCCACAAGAA	120
CCAGGACTIC CAGAAGAAGT TCCCATTGAA CCGCCTCCA CCGTTTTCCT GTCCGGCTGG	180
AAATCTAACT GAGACCATGG CCATCACCTA TIACTGTAAG TTGCCACCGA CTACACACCG	240
AASCATGGAG COCTAGIGIG ATGAGAAAAC CTTTCGAAAA AACAGTTATC CCTGTCTGAA	300
TOSSCATAAT ATCTOSTTGC ACATGTGTCG ACACACCATA CTCTGATTTA CACCTACATG	360
CGAGGTTCCG AGGAACACGT ACTAACCGAA CAACAGTGGT CAACCTAATC CAGGACGAGA	420
AGGCCAAGGC TGCTCTGCTT GGCTCCACGC TAGAGGAGCA GGCACAGGTG TTGCGCTGGG	480
AGTOTITICAC CAACACCAAC TICATIGACG ACGITGOCTIC TGCCTCCTAT ACCTAGAGAG	540
GGIGIGGICC CNITINCACCA ANNONACATG GAAAACGNON TICCCONGNOG CGAAACNITIN	600
CCCNAGNOTT TIMMAAAAAA GAAATAACCN CITCCCTCCC TTACCCCCCG AAANTTTIMT	660
TINCCOSCAN NCCNIGNON TNOOCCOCT GAACHNANIT CCCCACANIT NCCCCACANIN	720
MIGGGNOONG GCCCCCCCCC CCCNNNNANG GITACCCCTT GGGTANCCCC MWINAAAAA	780
CNNCCNCCC CCCTTNCGTC GGACCNAAAG GCCCCCCCCCCCAAANGAAAA AAAAAAAAAA	840
AA	842
(2) INFORMATION FOR SEQ ID NO:356:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	

	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1276RP	
5		
	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:356:	
	CATCOTATT GITGITGACC AGTACCACTT TTTTCATCTT COCTTCGACG ACCACCIOGG	60
10	CCACGITACC GAGGATC	7 7
	(2) INFORMATION FOR SEQ ID NO:357:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 77 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1276UP	
0.5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:	
25	GATOCTOCGT AACGTGCCGG AGCTGCTCGT CGAAGGGAAG ATGAAAAAAG TGCTACTGGT	60
	CAACAACAAA TACGATC	7 7
	(2) INFORMATION FOR SEQ ID NO:358:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 822 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1277RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:	
	CATCOGTCAC GGACAGACTG AATGGTCAAA ATCAGGTCAA TACACAGGCT TGACAGACCT	60
45	TCCGCTGACC GAATATGGTG TCGGCCAGAT GCGGCCACT GGTGCTGCGA TATTTAGCGC	120
	AAAATACATT GATCCTGOOC ACATAACATA CGTATTTACT TCTOCACGCC AACGCGOOGG	180
	GAACACTGTG CACCTGGTTT TGCAAAGCCT CAGTGAAGAT CAACGTGCAC GCATCCAGGT	240
50	GETGETGEAC GAGGACCTAC GGGAGTGGGA GTACGGTGAC TACGGAGGTC TGCTGACAAG	300
	CCAGATTATC GAATTCCGTC GTAGCCGTGG CTTGGACTGC AAGCGCCCAT GGAATATATG	360
	GOGCGACGGC TGCGAGAACG GCGAGAGAGCAC CCAGCAGGTG GGCCTGAGGC TATCACGAGT	420
55	CATTOCCCCC ATCCACCCAT TACACCCCCA CCACCAAGCT CAGGGACCCC CCACCCATAT	480

TOTOGRATIT GOGCATOSCO ATOCTOTOG TTATTITTOT GOGCTOTOGA TGAAGATOGG	540
OGTOCAAGOG COGAGGCCAG ACTGCCCCAT GCCCTCGAGT AACCGCAATG ACCATCCGTG	600
COCTTOCTOC GCCTGGAGCA ATCCGTACCT GCAGGACACC CCACTTCTTG CTAGACGCAG	660
GROCCATOGG TGTGTTGTCC TACCCCCNCN ATTTGAGACC ANTCTACTCN CCTGGCCNTT	720
CVITIOCCCCC COGAGATICCC CCCACOGTINA GTCCCACCGA AAATTITITAT ATICTACAAGN	780
CNETCCCCCC ATGAATATAC CNTATCTTCT TAATCETCON CN	822
(2) INFORMATION FOR SEQ ID NO:359:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 818 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1277UP	
(xd.) SPQUENCE DESCRIPTION: SPQ ID NO:359:	
OCCUPACITY TOCOSCICACE OCCACTOCAG CTOCCOCCAC ACOCCCACG ACCOCCACT	60
GOCCAGGOGA TAGTACGOGT ATGOGACCAG GCCCGCCCC AGCACGTTGC TTGCCCCGAA	120
GAACCAGAGG AACCGCGAGC GGCTAACCAG CTGCACCAGC TGTCCGTAAT CGTGCCGCAG	180
COCCECCO CACOCCACCO CCATGCCTIGT GCCCACAGIC CCCAGCATCA CGCCCCCCC	240
GCAGATCAGC ACCGTCCCGA CGCACGTAAG CATACAAAAC GGCTCTGCGA GCAGCCAACA	300
OGAAAAOCAG CTGTTGAACA GCAGTCOGCA CGCCTGCAGC GGGGCCAGCA TCACCAGTGG	360
TAGOGTICICA ATCTICCATOG TICCTTICCICAA CACGTITCICT AGAATGAATA GOGTICAGACC	420
CATCHOCCAT AGGCCCCTAC GGTACACCAC CHGCACAGTT CCCCGTGCCA CTTGCAGGGC	480
AGOCTIGOGO TGAAAGTACO AGGCOCAAAA GACTGCATAC GCTTGAAACT ACCGCCACCA	540
CGACCCATAA TAACCAGTTG ATCGACCATT COCTTOGATA CCCTGCACCC TTCGCTGCAG	600
AGUACICTAC TG19G00GCC TTTTGGCTCT AGGTCTCTAC GCTATGCCAA ACATACTGGC	660
TOCOGUICOCT CAUGUICOCAT COUCHAUGUC ACGUCACCGA TGACAGGGUA COTGUCGGUT	720
CTCTTCCGGT TCCAGGGNAT GATACCGAAA NCCGAAATTA NCCGGATGAA TTTCCCGACC	780
CLICCENNIAC CYCNOCYYCN CCYCYCOCOL LLILINIGI	818
(2) INFORMATION FOR SEQ ID NO:360:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 828 base pairs (B) TYPE: nucleic acid (C) STRANDERNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: INA (genamic)

5	(vi) Original Source: (A) Organism: Pag1278RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:	
10	GATCTTCAAC CTGCTTCCCC CTATGAACAT TCTGTTGTGA TTGAGAGGGG ATACCGCCTC	60
	CACCITICIT CGAGCCIGCC CCCITITICGT AATCCATACG TICTICCCCA TICTITICGT	120
	ATTOGTATAA GOGATGCAAA TGAAAACAGC CTCTTGAATA CAAATGGACT TGCCTACGTA	180
15	TAAAATTATA TITTTATCAG AAACITGGCG AGCATCAAGC TCGGCTTCAT TGATTCATAT	240
	ACTABACAGA ATACACTACA TOCTACOGTO OGAAAACGAA TAATOTATTT COAATATATA	300
	TATATATATA TATATATATA TTATAGTIGI ACTITATAAA TCTGAACTAG GTCATACAAC	360
20	TCTCAAATCA AACGATATTT ATTCTACATA TAGCACGGGC GACGCACCAA TTGAAGACTC	420
	TAGGOCOCCT GAACTTGOCG CTGCCCTGTA TCTTTAGCCT GTTCCTTTAC AGGGTCATAA	480
	ACATAGTACA TACOGCOCTO TAGTTOGICA TACTOGATOT TOCTOTOTT CAGCTOCOCC	540
25	CARTITICGI GAGGGATATO COACCCACAT TICTGAGCTA TGAAAGCTGC AACGTGGTCG	600
	CACACCCCA GIAACITAGS TCAATTOSCG TOCTIAACSG GICTOCTATG ATAGTACTIG	660
	TOGIACGIGA OCIOCACONI CITTACATON COCAAACTOC OCNOCTICAN CINITCNATO	7 20
30	ANCINCARTOG CATINCANNIT CIGGCNANIT TITTIGANIC CATGACCCCC CCNAAANINI	780
	TICCOGUINNE ACCCACACOC CCTIGAAAIN NCIGATIVIEN AGANOCIC	828
	(2) INFORMATION FOR SEQ ID NO:361:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 855 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
40	(11) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1278UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:	
	GATCHTGGAT GRACIGOGGG CICATACTIC GOCTICIGIT TCHTGTCCTT TTTGCCCTTC	60
50	TOSCOCTIGO CATACGIOGA TOCTOCTIGO COCATOTIAS AGATATOTOS IGIOCOCTA	120
	TOGAGIAACG CTTCTOCTTG CGAACTCTAA GTAGTGTTAT CAACTTGTGT GTATCATTTT	180
	TOCCACCTOG AATOCATCAA TITICACCTAG CCCAACCCAA GCTGCGACCT ATCAAAAAAC	240
55	AGGAGCAGGA AGCTGCCTGA AGAAGCGCTC CAGGGGTCTA CCGACGGGAA AAACTACGAG	300
	CACTOSTIGCT ATGACATECT TOCOGGGATC CATCOCGAGT TOAGTGCTTT OGAGCTGTAC	360

	AATTOCGICC GASCOGTICGG AGCGCAAGCG TOCGTCACAAC ATCAACCACC GTATCCAGGA	420
	OCTOCTCAAC GTGATTCCAG AGGAGTTCTT CCAGGACTAC TACCAGAAGA AGAAGGACCA	480
5	OCACTOCCAC ACCOCCACOC COCCCCCACAAAAAC AACGCAAACTG GCACCCCCA	540
	COGCAACCCC AACAAACCCA GATTCTCACG CACCCCGTCG AATATGTGAC CTATCTGCAA	600
	ACCACTOCAT CTGCGCACCC CGAACACGTC CACCTCATCC TCAACCTCAC CACCTCTCTC	660
10	COCAGACCOC CACCATCCTIC AACGACCTICA ACTAGAAACA CCATTGCCGA CTCCCCCTCG	720
	CAAATOOCCT TOCCCNCTCC ACCCTOCTCC GCAATTNTGC GCCCNCAGGG CAGCACACCC	780
	NOGCAGCACA CCGCCCCAGA CCACACACTC ATTTGGGTCC CATTCGGACG CNTAGATTTT	840
15	CNOCTEGNOT GITTT	855
	(2) INFORMATION FOR SEQ ID NO:362:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 831 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1279RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:	
	CATCCTTCTG GATOCTGGTA GCTCCGATGA GGAAGTCGTA CTTTTGGTAA TGTCACTGCT	60
	OCTTAAGCAT CTACTITICAA AGOGTIGATAT ACAGAGAGOG TITIOCTAAAA GIGGTIGGATA	120
35	TAGGITACIG TICTCCATAT TAAAAGATAT CCAATCCGGG CITACAGGAA AAGTCACGAA	180
	TOTATTGIGG ACCTATGCAT TTGGAAATCA TATTGIGGCA ACACACAGGG AAAGCAGGIG	240
	CCITCITATT AGACCGCAAG GCGATGGGCT ACAAAGGATA GITTICGAAC TICATTATIT	300
40	GOCAATTOCA TIGTTACAGA TAGCOGTGAT AAAAGCCCCA AAGGAGGATC AACAAGAGTT	360
	GAGTAAAAAC ATTATTACGT ATATCAACCA GTTGGCGTTA CTTCATAGTA CTCACTCTCG	420
	AATATOOCIT TITGATCCAA GCGIATOCCA ACTICATGAG AGATTGITAA CITTGITATT	480
45	AACTTTEACA GATCCCAAAT ATCAGGGTTT CTATATACAG GCTATTCTGG ACATTGAACT	540
	TOTATTGAGT AACAACATAT CTTTCACTTA AAGAATGATG ATOCACCACC TTTTCGAACT	600
5 0	ACTIGCAAAA TATTITGGIA ATGAAAGGGA CATCCGATTA GIOCTAGCAG ATTACAGITA	660
50	GIAACAAAGG TOCAATTATA TIGAGACCAC TATATINI'AA AATIGIOCOC NIGITATIGA	720
	AAACTINIGC CONSOGIACA CITATISCIN TICNACACOG TOOTGNAAAA ANIGIGNITI	780
55	GITACCATTA ACTOGITTOC TIGATICACO AACTITITONI TITTATCATA G	831
-	(2) INFORMATION FOR SEQ ID NO:363:	

5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 841 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1279UP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:363:	
15	GATCAAGAGT ACAGTTGATG AAAAGGAGTT CCATGATGAA ATATGTAAGA TGGACTTGCT	60
	TRAGARATTG ATRATATARA AGGCTACGAG CTTCARTATT ATRATACGCA TTGCATARIT	120
	TAPTACATTA AATTGATATA OGTATATTTT TCTTOGAAGA ATTAATTCTA ATCATTTCCA	180
20	TGTGAAGATA TGGCCCTCTG TGTTACCTGC GGATATTTCG ACTCTTAGTA TATCTACATA	240
	TTTTTGGCGAG CCATTATTTA AACTOGCCAG CTTGACTCTG GACCCAAGAG CCGTAATGGC	300
	AGCAGCTCTT CCTGAGCGCA ATTTCTTCAA GCAATTGAGG CACCATGTGC CGTTCTTTAA	360
25	TICAAGCACA TATAAACAGA COGTOCOGTO AATAAACOCT AGCACAATTA TATCCTTTTC	420
	TITICCAATAC ATGTGCCGAT ACCTGGACAT TICCTGAGAT GCAAAGTTAA CAAAGCTTAT	480
	AGCAGTGATA TCTTGCGTTA GAGACATGCT TGCAAATTTC GAACCGTTGA GGTCATAAAC	540
30	ATGAACGITA TITGAGAATA TCAACCACCC ATTAAATGAA CTGTACCTGT TTGAAACCGC	600
	AATGCACTGG NYINNCINGA AATATTONCC AACCONCCCT TAAAAGNGIC CCCCTTTATT	660
	NVENCCINGC TATTCCCAAA AACNIACCCG NITCNITGIG NCNCCAAGGN NITTINNCNI	720
35	TMTTGGCAGC CTTTTAGAGN TTTAAANATN TTOCAANCOC CAAATCCAMT TTTTAAAGGN	780
	CTCCCCINAA AANNICNIGA AIGANCAGON GAAITICGITT GOONITTAAC TICCCAGINA	840
	G	841
40	(2) INFORMATION FOR SEQ ID NO:364:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 826 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1280RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:	
55	GATCATCAGA CCTGTCGGAG CCTTCCGTAG TGGAACCTCT TGGTAGGGGG GAGCCGCTGT	60

IGIGAGECTI GAGEGETET GGAGALGGGG GETTEGAGTG AAACCGAGCT CGTATCGGGG	120
ATCCCCAGAT GIACTCCCCC CACCTTAATC CAMITITICIT CTCGAACCAC TITICTCCCCA	180
CGCAGCAAAG TCTTTCAAAT ATTGACGCAG AGCGGCCCTT TGAGATTTGG CTCTGCAAAG	240
ACCORTETITE CAAGGECOCE COCAGCITTT CITECOGIOCT TOCAGCOCIT OCCOCAGGIG	300
CAAGCACGOC COCCITICOCA AGAACGOGAC TCTGCTTCAG TAGGCTTGTC TTGGTCATCA	360
TOGGOTTOCAL CACCAGOGGA TOTTTIGTTOG GCAGOGGCAC AAACATGITIG GACCGCOGGA	420
GOGTICCOGTIC ACCOCTICOGC CCAATICACOG CTCCCCGTCCG AAACCTICAAC CTCTTCTCCC	480
GOCTOTTOGA CATOGAAACO TTOGTOTOGT TGATGOGACT TOTOCGAGTO CACCTOCTGT	540
ACCETICATET GETECCOCTIC CTGCGTGCCC TOCCOCTICCN GNOCKCONGT TCCTGCCTCC	600
CIGACINFIC CCCCCCCTTT AGGGGAACAC GGGAACAAAA NAANINCCCT TICINNCCCG	660
CCCCLLCIC LCCCCCCIN NAMOCCCCI CCCIMANAN VARNCANAN WACCANCAIN	720
NVNNAAAAT NTAGGGENGE CAAAAATONG GITACNGTOC CCCACCNGAA CCCCAAAAAA	780
AACCNCCCAT GINICCAGGG NCTINATGAN CANCTICNEN NICCGA	826
(2) INFORMATION FOR SEQ ID NO:365:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 840 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genemic)	
(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1280UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:	
GATCATAATG CCACTATCOC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT	60
CACCOTTOCA TICTOCOCCA COSTGACGIG COTGIGIACA AAGOCTCAGO GOTGCAAGOG	120
COCCATOTICA TOCCOTATICA CGAACTATICA AACTOGAACT ATTITICACTOT GAATOCTOGT	180
GAAACACTAA CACTTCCTGT GTATGAACCG GAGTTAAACA TCCAAGGCAA CATTGTCGAG	240
GGGCGCAGA TIACCAATIT AACTCAGGGI GIACCAGGGG ATGICCCGAT TICIATICIA	300
GACOGGAACA ACTATACOCA CTOGCAGOCG TTOGACAAGT CTGAGAGOGC ACTCTTGTTG	360
ATTEATTIGE GITCCGAAGA GCAGIACCAG ATCACAACGG GITAAAATTI TGIGGGGCC	420
TOGICCOGOG AAGAACTICT CCATCICTAT TCTCCCCAAC TCAAAGCACA TCACACACAT	480
ATTGACAAAA CTGACGOCCA TGATGGACGG CCGGAATAGG GACTTGTCTC CTGCTGAAAG	540
TOCCACGOOG TOTOTTOCTO GCAGCATOTG CTCGGCGGGGC TGGCGAATGT CACCGATTCC	600
isothern referred describes crossesse resemples of continue	600
ACCOMACTOG COCCCATTGA TGAAAACCTG GANNTGTTTT TAAAAAAATTT CNGTTOGACT	660

	MCANCICCI NONTICALII IMEECANAG EGCAAINAN GANCICCINA GECCIGNAA	720
	CACCATINAN CNICCACCIA CTCAAAAGIN TICIATOCOC CAAINICNIT TOCAACACAA	780
5	CGATCTOCTA ATTICNOCONO CAACCATCAC TINNTOCATO ATTITOCCAC AACAATGNGA	84 0
	(2) INFORMATION FOR SEQ ID NO:366:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 833 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1281RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:	
	CATCCCACCT TCACTCCACT CTTCCCATT AAGGTTTTCA ACAAATTCCA AACTCATGTG	60
25	TITAATGOCT TGIACCATAC CGATGAAAAT GTAITTAITG GAGCTTGTAA GOGCTCGGGT	120
	AAAACTOCAA TOOCAGAATT AOCTITATTG AGTCACTOGA GAGATOGTAA GOGACGTOCC	180
	GICTATATAT GICCATCTCA GGAGAAAATT GATTTTCTGG TGAAGGATTG GCGAAACAGA	240
30	TITTIAAATG TOOCAGGIGG AAAGGITAIT AATAAACTCA CATTOGAATT AACTAACAAT	300
	CITCGAACGC TAGCCCAGTC GCATTIAATC TTAGCGACTC CAGAGCAGTT TGACCTGCTT	360
	TOTOGTOOCT GGAAAAGAAG AAAAAAGATT CAGACATTAG AGCTGITGAT TOTAGATGAT	420
35	CTICATATGA TCAGTAGTGA CTTGCCTGGC GCAAGGTATG AAAATATAAT ATCCAGAATG	480
	CIGITCATTC GOGGICAACT TGAAACOGCC TTGCGTATAG TCGGTTTATC TACCTCCCTC	540
	GCTAATGGTC GCGACTTTGG AGAGTTGGCT CCGAGCTAAA AAGCTACATT TTTATTTCTC	600
40	CTTTCACGAA GGGTTATGCC CTTACAGATC CNCTTACATC CGTTCCTAGA NGCATGAAAN	660
	TCTTTAATTG AACTATGGCC AATCGCTTCC TGACGNACAA CTCTGTGATA CTCCCANINT	720
	TANCTITIGT ICCATTAGAA AIGTITCAAT TCTGTCNCTG CACGCCGCGC GGANGAAAIC	780
45	CIGGICNOCN ATPACTICISA ACCATTOTAG CINAAAAGAC TOTTATOOTA ACN	833
	(2) INFORMATION FOR SEQ ID NO:367:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 853 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1281UP	

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:367:	
GATCTGAACG TATGAGAGCG GGTTTTTACT AATTATAGAA CCATATGAGA TAGAAAATCC	60
GOCAGTICCA AAICCAATAA TOOGATICAC GIGOCTICAT OCCICCATIG CAATCAAACC	120
AGIGITIGAG AAGITITIOGT CAGITATTAT TACATOGGG ACCATTICIC COCTIGACAT	180
GTACCCTCGA ATGCTGAATT TTGAGACAGT TCTTCAAAAA TCTTACTCCA TGACGCTGGC	240
GCAGAAGTCC TTCCTCCCAA TGATTATAAC CAAGGGGTCA GACCAGGTAG CCATCTCTTC	3 0 0
TCGGITTGAG ATCAGGAATG ATCCCTCAAT TGTCAGGAAT TATGGTTCCA TATTGGTTGA	360
ATTIGCCAAG ATTACTCCTG ATGGTATGGT AGTGTTCTTC CCCTCATATT TATATATGGA	420
ATCCATTATT TCAACTTGGC AGACAATGGG GATCTAGACG AGGTTTGGAA ATACAAGCTC	480
ATCCCTCGTG GAAACACCAG ACCCCACAGG AAACCTCCTC TACCTTTAAA AACTNACCNA	540
AGGCCNGCCC NNAATGGGAC GGGCCANTTA ATTTCNGTGG CCCNGGGAAA ATTCTNAGGA	600
ATGGATTING ACNOCCIOGG NOGGAGIGIT TGAAAATGGA TOCCTCCCTT NACCGANAAC	660
GITINITIAG OGAGOGITINI NICCOVINANA AAANATOCAA ACCOOGAATA CITTITICCIT	720
NNAGCATGAA NCCCCCCCT TITICGGAAAA TICACCCCGG AGGAANATAT GGITAATGIN	780
CCCCCCANCN GNINCONNAA AAAAANCACT CCCAATIGTCC CAGCNCCTIN NENACCACTT	840
CINWWAITG GAT	853
(2) INFORMATION FOR SEQ ID NO:368:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 598 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1282RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:	
GATCCOGAAT TATAGAATCG ATGAGCAITT CATTTAGCAA CCTTCTTCCA ATTCGTAATG	60
GTICATATAT AAACTOOCTA GOTTOOTOTT GATAAATOOT TICAAGAACA GCACOGTOGC	120
AGICTOGGIT TATCTITATA TTATTTCTTG TTATOCAACT COCATOGICT ATGAGGICCC	180
TACATACATT TAGGICGCCC ATCAGTACCA COCTOTTCCC CAGATTCTCT ATGITCCTCA	240
CACGITIGAA TAGAGITTIC AGGAAACGCA GCCTAAAAAC TICACCCTCC TCAGIGITCA	300
TAGAATTAGC AGGGCAGTAT ACGGAAATGA CCACCACCIT ACAGGCCAAT TOGACTAGAA	360
OCCATCTOCC CTCACTGTCT AGTTCCTGTG CATTAGCATC ACTCCCATAG GOCAAGCCAT	420

	CATAACCACC AATACCAATG GTCCCCTTCCT CCCAATATGC TACCAAGCCG CCATCCTTTT	480
	TEAMPTITT AGICTOCCIG TAATACCICC TCCCCCCTIC AATACTICIA AIGAITAICG	540
5	CAACCATCCC CTCCTTCACC CATTCTCTTC CACNCCCACN CONATACCCT TCTCCTCN	598
	(2) INFORMATION FOR SEQ ID NO:369:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 622 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1282UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:	
	CATCHOCOCA AACACCCCCA CTCTGTGTAC CTCCTCGATG CTGTCAATCG AGTCCTTGTC	60
	CATGCTTCTA TCCTTCAGCA GGAACGCGCC TAGGTACGGG ATGTTCCGGC GCAGCAGCCC	120
25	OCAGATAGOT TOGATGACCE CERCETOGIA CACCETCACO GACTIGIAGI ACCOCRIGAA	180
	GAGCGGCCGG TIGCICATCG GTAGCACCAT CAGCTCCTCG TACTTGCGCG GCACCTCGCC	240
	CLICACLICARC CARLLICATOC CARCACACACA CACCACACATA CATOCACATAC CACCACACACACACACACACACACACACACAC	300
30	CCCCCAACAA CIACCCICCE ACCACCCATT CCCCICCICT TCCCCIGCCT CCCCCICCCC	360
	CICCICGICG COCACCOCTT CCICCICGCG CCCCICCICC GCCCCCCGC GCACCTITIT	420
	GTCGTCGCTC TCGTCCGCCT CCCCGGTCCT GCTTCAGTAT GCAACTGCCC GCCGCGTGTA	480
35	TOCCOGRACIE CIECOSCAAG GOCACICITT TIEGGGGGGG GGGGGGINNG NNWOOCCONC	540
	CCCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCCCCCC	600
	CCATCCCCCC CIMMITTIC CT	622
40	(2) INFORMATION FOR SEQ ID NO: 370:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENSIH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1283RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:	
	GATCAGGAAA TCGACGGAC TGGCTGATTG TCTTTATAGT CAAGCATATT AAACACAGT	60
55	GACTIAAACT AGAITTACAC GIGACATOCA ATTOTOTOGT TICTTTTTTA TTIGAAAAAC	120

	CTOCATOGAG CTATTAGATG CTCATOGACA CTAGTIGTACA AACCAGTICAA GOCTTAAAAG	180
_	CTCTGCAGCA TGGACCAGTC GAATAAGGAG CATGGTOCTA AAAAGGAGAA GGCGACAGCT	240
5	AAAAAGAAGC TGCACTCCCA GGGCCACAAT GCGAAGGCAT TCGCGGTGGC CGCTCCGGGA	300
	AAGATGGCCA AGCAGATGCA GCGCAGCAGC GATAAGCGGG AGCGCGCCCT GCAGGTTCCG	360
	ATGGTGGACC GGACGCGGGA CGACGACCCG CGGCCACTCA TTGTTGCGGT TGTAGGTCCC	420
10	CCCCCCACCC CTAAGACAAC NCTGATCAAT CCCTGCTCCC CCCGTTGACC AAGACGACCC	480
	TOOGOGAGAT TAACOGTOCG ATCACOGTICG TCTCCGGCAA GCGCCCCGT CTGACGTTCA	540
	TIGAGAGGCC COCOGACGAT CIGAACICCG ATGIGGACAT TGCGAAGGIT GCAGATTTGG	600
15	TOCTOCTOCT CATOGACOGT ACTITOGITC GAGATGAGAC ATGAGTTCCC TGACCTGGCN	660
	CACNOCACGG ATMOCCTTTT NOTGGATTAC AAMONONCAT TITTCATTING NAGGOONCTC	720
20	CNOCTONAAA ACTITINVACC TOGITCTGAC NATTITINOON GOOGNICANT COCCTTOGIN	780
20	TITITIATON NONCONI	798
	(2) INFORMATION FOR SEQ ID NO:371:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 829 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1283UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:	
	CATCOSCIGG COCCATOSCOG AGASCTATGT SCATOSCOTIC ATAGTOSCOT TGATACGTIGT	60
	CTCAACCAAG ATTIGTIGGAAG ACACCGTIGCA CTCCCACGAG TATTTCAGCA AGGTCTGCGG	120
10	CATATOGAAG AAGCTOTTIGA TOCGCOTOGA GOTAGCCOCTIC ATACTOGTICC TOCGCOGGGA	180
	COSTITUATE GICACOCCIE CACCICTAAA COCIOCCICA AACOCACGIE CICCOCCIICO	240
	CGAGCAGTOT GOCCTGOCAG CCCCTGCTGC TCAGTGATAA TCGCCACTTC TAGGCCCACA	300
15	ATTCOGTTAT TTAATAAGCA ATAAATACTC CAACACTAAT AGTATACACC GTTTGCGAGA	360
	GTAAGCAGGC AGCAGGAGGI GGCAGCITITI CIGGTACCAC CICAAGCCCC TIGCCATIGC	420
	TOCCTATICTIC GITTAGOCAT CAGCAACCTT AGICAGTTTC CAACCCGTGA TATATGTTTC	480
50	GAACACGITA CCTITTCOGT GAAAAGAAAA AGCCTAAAGG CGAAATGITT TCCATGITAA	540
	CACAGCAGAT TAGAGGTACC TIGIACTGGA TATTCTGTAG GATCACGGCC TACGAGCATT	600
	CATCCAGAAG CTTTGAACTT ANGGTGTTTC NGGATGOCAG TINGGGACTT ATNCCGTGGN	660
55	TMTAAAANAA TACTTOGTOO TAGTCTTTGG AACAAACNIG CATTTGTTGT TCTTNGTTTG	720

	GANNATCOGN AAGACANOCT TTGCCCTGCT AANAAGACNG TTGGGAAGNG NNGCCINNTGN	780
5	CCCNCICCEA GYONGAACN GGCCCONI'IN CIWITICINICN GGGGWINNC	829
3	(2) INFORMATION FOR SEQ ID NO:372:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 817 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1284RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:	
20	GATCCATCIG GICAGGICIA TITGIGGCAC CGATGACAAA AACATTITIC TITGCATTCA	60
	TACCATOCAT TICAGITAAC AATIGGITAA CGACTOTATO AGAGOOOCCA CCAGCATOAC	120
25	CCATTGAGCC ACCTCTAGCC TTTGCAATGG AATCTAGTTC ATCCAAAAAG ACAACGGTTG	180
23	GCGCTGCGGC TCTAGCTTTA TCAAAAAATAT CACGAATGTT GGACTCAGAC TCACCATAGC	240
	ACATOCTTAG CAACTICTOGA COCTTCACAG AAATGAAATT AOCAGATACT TCAGTTOCGA	300
30	CTGCCTTTGC CAACAACGTC TTACCAGTAC CTGGAGGACC GTAAAACAAC ACACCTTTGG	360
	ATGGCCATAG ACCAAACTTA ATGTATTGGT CAGGATGCAA GACGGGATAC TCAACGGTTT	420
	CCTTCAACTC CCCCTTTATG TCATCCAACC CACCAACATC GTCCCAAGTA ACGTTAACCG	480
35	ATTCAACCAC GGTTTCACGT AGCGCGGATG GATTGGAGTT CCCAAGTGCG AATCTAAAGT	540
	TATCCATTGT AACTCCTAAG GAATCCAAGC ACTTCAGOGT CGATTTCATC CCTCGTCCCCA	600
	ATCAATTAGA CTCATCTTCT CTCTAATCTG TTGCATTGCA	660
40	ATATCAGCAC CCACATACCA TOGTTTCAGC AGCTAGCACT TOCAATCAGG TCATCAGCCA	720
	TCTCANFTCT TCVTGTGGAT GPTTAAATTC CCACCCTCCA GTGCTCTGGA NACCANFTTA	780
	TINNNETCAA TITACCAACT TITAGNOOGN TINNATOG	817
45	(2) INFORMATION FOR SEQ ID NO:373:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 831 base pairs (B) TYPE: nucleic acid (C) STRANDERNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1284UP	
55	(,	

	(XI) SECONDE DESCRIPTION: SEC 15 NO:373:	
	CATCAASCIG ATATGIATIC TOOGGCTACT GGTCGTATCC GTGGTAATCT TCTTCGGCGG	60
5	COCTOCCAAC CACGACOGTA CTOOCTTCCG CTACTOGAAG AACCOGGGGC CCTTTGCGAT	120
	GAGCCICOCC CCACCAAGCA COGGCCGITT CTTGCACGTG TGCCGCCGC TCATCAAGTC	180
	GOCCTICGCC TICATCCTAT CACCAGAACT TATAGGCATT GCATGCGTCG AGGCGCAGGA	240
10	CACCOGGGG AACACTGAGA AGGCATOGAG ACGTTTCATA TACOGTATTA TCTTTTTTCTA	300
	TGTGAGCTGC GCCCTCATGA TCGCCGTCAT CTTATCAAGA ACTGATCCCA AACTCATAGA	360
	COOCCTOCAG ACACOCCCC CAGGOOCTCC CTCTTCTCCC TTCGTCCAGG CGATTCCCAA	420
15	COCAGOGATT CCCGTOCTOG ACCACGTCAT CAACGTCGCG ATCTTGTCTT CTGCGTGGTC	480
	COCACCCAAC TOCTTCATGT ATGCATOCAC GCGCATGGTG CTAGCGCTTG CGCGCCAGGG	540
	AAATGCGCCA AAGTTCCTCA CCAAGATCAA CAGATATGTG TGCCCTACAA CGCGGTCATC	600
20	GICTOCACOC TOGICOCCTG TOTTOCCTAC CTGAACGTCA AGACGACTCC GCAATGTGTT	660
	CCAGTGGCTG TOGAACATAT GCACCATCTC CGCTTCATCC GCTTGTTCGC CATGGCTCCC	720
	TTATATCCCT TCCCNOSCCT TCTTTTCACA CTCCNANCCN TNCCCINCCA GITCCCIGCA	780
25	CONTRONC ACTATICONT INTRATGINE CETTITINGAC AATGEFCCCE C	831
	(2) INFORMATION FOR SEQ ID NO:374:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 817 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
35	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1285RP	
40	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:374:	
	GATCOGGGTC CGCCACAAGC TGCTGGTCCA CATCGTGCTG CTGCGCGGCCC CCCCCGACGC	60
	OCCUSSAAAG AAAACUSAAA TCAAGGCCAG CATTCOGGTT ATGCTCTACA TATCGCCGCT	120
45	CGTACCTGTG CAGGGCCGCA CCGTCCTGGT TGATAACGCT GGCCGCTTCC ACATCCGTCC	180
	COCCOTOCTO ACAGACCTAT TCCGGACGGG GAGCOCGGAC TCACTTCCGA GCTGGGACGC	240
	GCCGCCGTCC TACCAGTCGC GCGTGCACGA TCGGCTGTAC GATGGCCACG TACGCTCGCT	300
50	TOCTICOGOC AGGOGGGCCC COCCCGATIC GOCGGCCCCCC CCCCCAGAITIC	360
	OCCACTOGGI CTCCTTCCCC CCCTTCACCC CTTGTCGTTG GATGATCTAA GCAGOGTCCC	420
	CACGUACCAA CAGCAGCACG AUGGACACUC CCUGCCATUG CAUCACCUCT CCCCCCCCCCIA	48
55	TOCCOCCACC GCOCCACCNG CCCCCCCCCCA ACAGUSCACN TGACAATCAC TINTGCGGTC	54

	Considered consistent confedence maynered concernate concernation	600
	CCCAATAGOG TCAAACCGCG GNETTGGNAA TTTNCTTGNT CNGNNNCNG NNCNGETTIT	560
5	GEOCCOCCCC GETTINCCCCCC GENVANTTINGC CCAANCGGAA NCCGGGGGAGG GTTININGTIGN	720
	NNCNGTAAAA ACTINTACOC OCCONCTITG GGINCCNGGC OGGNGGGITT TITTTITOCC	780
	COCCURRICOC COCCUNICOS ACCIVITINOS NACIVATIT	817
10	(2) INFORMATION FOR SEQ ID NO:375:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 831 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1285UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:	
25	GATCTTCTTC ATGACOCTAC TGTAGACAGT TTCACAACCG ATAGCCTGAA GACACAGTAC	60
	AACCAGAGCA AAAGATATCA ACTIGTITCGG ATTCCGGATT CGGAGCATTC CAGCTITAAG	120
	GACCTAAGTA TITTCOCAAC CACGATOCAG ATGAACOCCA TTCGATCTAC AGTGAACCTG	180
30	OCCICITIOS AGAIGCATOS CATGIGGTIC GACACTIGGT CICGIATTAG AAACGAAAAA	240
	TACCTOCGTA AATTATGATT ACATGTTATA TATAGTAAAA GATAACACOC CACTCAGTGT	300
	TARATOGICC ATCATGCCIC TAGGACTOGT TGTCGTTGCT CGACAGAACT GCAGTCCCCA	360
35	THISCOIGGE AGGITTLIGT GASSCRITTT TOTALTIGIC TALTITALAG TOCTGALTAT	420
	TATOCTOCAA TIGIOGAATG AAACACACAT GTACCACTAG AGGITCAGCC OGATGGCTGC	480
	AAAACGOCAT ATTIGICATE CAAATCATGC COCTOGICCA ACAGITTAAT AATGICTCTG	540
40	GAACTICGAC TACGICCOGA ACTOGICIAT CATCIGGAAT ACCNOCICCT GITAIGCNIT	600
	ACCATANICC CCTCCCTTCG TCCCCNAATT CTTAANCAAT TTTTCNTTAA AINCCCCCNT	660
	OCTINACIAA GIINAATIOC NATIOOCOCC CCCCTICOGG TEINICCGIT CITIOGAATG	720
45	GAGGAAGOOC AGGCTTGNOC COCAATACNC GCCCTCCGGG AAGNGTCCTC CTTNGCCTTN	780
	CCCANTEGEN INCITEGETT NEWNOCAAAN CNACHNENGS COCTCCTINEN C	831
	(2) INFORMATION FOR SEQ ID NO:376:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 802 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1286RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:	
	GATCOCACCT ATAATGAAGA CCOGFTTTTT TITTATGAGAA ATAGCAGCCC TCCAGOGGTT	60
10	ACTIVATIONA TAGCIACAGI AAGATTAGGI TATIGGITIG CAAATTCATT GGIAGATCAA	120
10	CITGEACACT TCAAATAATG CTTCCCTCCC ACCGTCATAA AACATGTTAT GCCCCGGTGTT	180
	GACAACTACT CTGAAGCTAT AGTCAGGGTA GTGCGTGGCA TTAGCTGGAC ACACCTTATC	240
15	TICACIOCCE ACCAAGACAT GOOCTGIGCA COCCCIGICG ACCAAAGGIG GOCCGITIAAT	300
75	TAGGICTICC CAGCCTAGAA GATACTCAGT GATGGATTIG GICGAAACTG CIACACOGTC	360
	GIAGAAGIGA TITIAGCITCC TGIACTIGIT OCCCATGITG GAGAAAAAGA ACTTAATTOC	420
20	GGAGCIGITC AACCCITCAT CIGGROGAAA TIGGROCITA TGAATTIGAG AAGCAIGATC	480
20	AAGAAGOOCT TGAAGAATGT TAGTGAAAGC TTTAGATATG OCTOCACCAT ATOCAACTIT	540
	CATTIGAÇÃO TICTAGGIGO COGCOGCOC AATAGAATGA TCTTTCTGCG TTCAATTGTT	600
0.5	GACOCCGTAT OCTGAAGOCT AATOCCAAGC CAAATCCACC CCATCNATTG CCCAAAACTC	660
25	CCACNGACAT TATTATGGTT GGCNCGTAGA CCATGAATCT AAACCCCCTA TCACNCACCC	720
	CCCCCACANG GITACCATICG CCCATGTCCC TTCCCCCANCC TGAGNTCNAC CCCATTINICC	780
	CCCTATTING CACATATONT CC	802
30	(2) INFORMATION FOR SEQ ID NO:377:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 835 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) CRGANISM: PAG1286UP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:377:	
45	GATCTICGCA GOCAGOGGT AGIOCACOGG CGICAGIOCC TOGCAGAACG CCCCGCCGIG	60
	CACGTACAGC ACCACCOGGT CGTCTGGGTIC CCGCTTGTCG GGCCGCCACA CATACACCGC	120
	GOSCOCAGTIC COCTOCOCCG COCCAGCOCCC COCCCCCCG AGCTOSAACA GGTGGCTATC	180
50	CLECACAVCE LYCCLICACT CCACCACCIC CCCCCCCCC LCCAVCCACC CCCCCCCCCCC	240
	CCACCACGEC ACGCACGTCC CGACGGACGC CCGCAGGGGC GCCGCCGCC CCGGGTCCGC	300
	GLEGOGGGG COCLCLYCOC CONTOCNELOC CYCCHCOLLE COCCECCOC COCCCCCC	360
	CACTURATION ACTOCHEST CUNCESTATE CONTINUES CONTINUES ACCUSADOS ACTURADOS	420

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	AAACOCCAGT ACCCTCCACG TITTGTTTGG ACATCCCATG ATGCCCGCCCC CAGGGCACGTC	480
	GACOCCCCCC ACCTGACCOG CCCCCTACTT ATACACCACA ACATTCTATA GAAAACGAAT	540
5	OCCACCAACG ACGAACOGIG TATCGITTOG GAAAAAAAAGG AGICCCCCAA CTAAACCTIG	600
	CTIOCIOSCY ACCACITICI GITICAGGIT TCTTCATAGC ATCCCAGTIG TITTGTFTGT	660
	TIGOCAAATC OCATATGAAC CATAAAANAT CAAANNITGT ACAATTGCTG COGACOGITG	720
10	COCCATICONO COGOGAAANA TOCAGAAATO GAGANAATTT CAGACGOOGG GTTTGOCAAA	780
	NICCOGAAAC CCCAAANICC CAACATTOCT GNCACATTIG ATTCIGNING NINCA	835
	(2) INFORMATION FOR SEQ ID NO:378:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 799 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1287RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:	
	GATCCCACTG GTATTAGGTG TCTGAACACG GCCAAATAAA ATACGCAAAA TGAAGGGCAT	60
30	TAATAATCTT TCATCAGTGT TGACAATAAC CCTTGACTCA TTCTGAGCAA ATAACTTTGT	120
	TACTTOGICG TIGAATAACG TGICATCTAA TAAGITCITC AGATTGICCC TATATTTCAC	180
	AGCIACIGGA TUCTIGIATG CTAACAACGC ATCTAGGGCC AGTTTCIGCA CTTGCAGGGT	240
35	TOGACTACCC AATAATICCA TCAACCTTTG GCGGACATCT TCGGATTTGT AAATAGCTTT	300
	GATATICTIC AACTICCCCA ATAATITCAA AATTAGATIC CTATCCGICT CAGACCATGI	360
	ATCCOCAGAG TOCACTOCTA ACTCACOCAG ATGGTCTTCA TCTTGGTTGG CATGGAATTG	420
10	ATCATTOCGT TITTAAGACAA AAGGTACAAT GAATCTOCTA TITTOCTOCC GOCAGCTGIN	480
	GCAGCOGGAT TAATATCTIC AATOCTIGIT TCTAATCATA COGCATATOC GAGTGAACCG	540
15	CGANCCCCTT TAAGGTTTTC CAACCAAGGA TITTTCGAAA NCAACAINCN TTINGAACNI	600
	TCCNAANNCA AATAATINAT CCTAAAAAAT TINTGCCCNA NIOCAAAAAN TCCCCNAGGG	660
	GINNAAAGAG TGOCCCCAAA TICNAAATNA GNGNITITIN GOGNITINCC NAAAAAAAAT	720
50	CCCNCCONAC CNCGNNTTTA ANAATTTTTIG GGAANCCCAT TCCCCCCCCA AGGGGAAAAA	780
	AGNOTIONNOC CNATITINA	799
	(2) INFORMATION FOR SEQ ID NO:379:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 817 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1287UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:	
	GATCAGGIGG TGTTGGCCGA TACCGTGACG GAAATGCATG TCCTGGCCAT GCCCGAGATA	60
	GATTTUCTUG ACACAACGTU CTUCTUGAAG GOOCTGATGC GGOCGAGAGGG CTCAATGGAG	120
15	AGGCACGTAC AGGGCGCGAA CACGGTCACA GACCCATGGG ACATGTCTTT GGAAGTGGGG	180
	AGAAGATACG CCCCTGACGA CGACCTGGAG CAACAGACGT CGCTACTGGA CCTCAACTTT	240
	GAACTCAGTG ACATGCAGAA CTCCAAATCT TGGGGTGAAG GGACGCACAA TTCCGAAGAG	300
20	ATCAGTGCCA ATGTGCTTGC AGAGTGCCAA GGCCAGGAGC TGCCCGGGAA GGAGGCATT	360
	GASOSTGAAG AGGATCTTCA TIGGAATICTG GGATTCACGG AACCAGCAAT TGTAGTCCCT	420
	TCAAGCGATT TIGAACACGA TAACAGCATA GAAGTGGGCC GGAGAGCAGT CCCCGAATGC	480
25	OGACCTICAG GAAACTGIOG ATTIGOGATT OGACTIOGAT ATTOCCAGOG TIGACATIGA	540
	GOCTACAGOC GOOGAGCAGA TOCTGOCAGT TTOCATCTGA GCTTTCCGGA AGTATAGTAC	600
	GTCTTCCTGG AACACTGTNC ACANCCAAAA CAAGAAAGGC ACCTGGTTAT CAATTCTACA	660
30	TICACCOCCA COCCATTACT GAAACCTONI CHAAAACCCC COCNACANTC CTCONTGANT	720
	ACCCATCOON NOCCCATTON NOCCNAAAAC GOVINIOGAC COTTINAAAT GATOOINCAA	780
	TITTOCNIGA CATOCTOCTIC NITTOCAACG ACNOCCA	817
35	(2) INFORMATION FOR SEQ ID NO:380:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 787 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1289RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:	
50	GATCOSGATT GACCGIAATA TYTCASCTTT TTGATGTGAA TTGCCAAGAG GACCACCGAT	60
	TIGAATCICG CIGACICIGI TGIGAGIAAT TAGTACAAGA ACCIGIGGCC TGICACAATT	120
	AAGCCCTGGG AATWGGACTT CAACTTCAGA AGCCCAOGAT CGTCAAGCGA TGATACAAGT	180
55	GCCTACCAAC ATTGACTTAA CATGAAAATT GATAGCATTT TTATAACAAT GGAAGCAAAG	240

ARGATGICAA CCITICCAAAA ATATICCICA GAGCATTAAT TATCATTACA CAAGCC GIGIGAGACA GAATCITIGA AGGIGCIGGG ATAAAACTCA AAATCGCAGT GCITIGG TAGGCCITAT ATACTGATIT AAGTGGIGGT GGITATCTAT TCAGGGITGT ATAAACT ATATCACAGT GGGTATACTC TTACACACTA ATTATAATCA CGIGATATIT GACTAT TACACCAGA CACCTCCCTA TGAAAATACC AACAGCCGA TGGTATTAAC ATCGCA ACCCCAACA TTAGAACACA CTACTGACAC AACGCCCAC CATTGGAGAC TATGGC ACTACTGCAN TACTGICATG CITATCTGAC NCCTGACCAC CATTGGAGAC TATGGC ACCTTG (2) INFORMATION FOR SEQ ID NO:381: (i) SEQUENCE CHARACTERISTICS: (A) LEINTH: 788 base pairs (B) TYPE: Incleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1289UP 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATCCCAGGC TGCCCAGGA TGACGGAAGA TTGCATGTTC TTTTCGGGC TACAGC CATATATICA TTGAAGTCAA ATGCATGATC AAAAAACTCG AAGACATTTA TGGTTC CATATATICA TTGAAGTCAT ATTAACTCAA GCCGCTGGCC AATTCTTTGC TAATAA CCCAAGAAGA AGAACCTTTA CGTGTCTACC GAACCAACC CATTCTCAAA CTCCGG CACCAGGGA AACTTCCAAC AGAACAACTC AGACGCATCC TACACTGCGG TACACC CACCAGGGA AACTCTCTA CGTGTCTACC GAACCAACC CATTCTCCAAA CTCCGGT CACCAGGGA AACTTCCAAC AGAACAACTC AGACGCACA GCAGATCTC TCCAACTCC CCCAAGATCA CCCCAGGTTG GCGCGCCCAC ACCAACGCCA GCAGATCTC TCCAACTCC CCCAAGATCC CCTGCAGTTG GCGCGCCCAC ACCAACGCCA GCAGATCTC TCCAACTCC CCCCAATACCC CCTGCAGTTG GCGCGCCCCAC ACCAACGCCA GCAGATCTC TCCAACTCC CCCCAATACCC CCTGCAGTTG GCGCGCCCCAC ACCAACGCCA GCAGATCTC TCCAACTCC CCCCAATACCC CCTGCAGTTG GCGCGCCCCAC ACCAACGCCA GCAGATCTCTC TCCAACTCC CCCCAATACCC CCTGCAGTTG GCGCGCCCCAC ACCAACGCCA GCAGATCTCTC TCCAACTCC CCCCAATACCC CCTGCAGTTG GCGCCCCCAC ACCAACGCCA GCAGATCTC TCCACCACACCA		50
TAGGOCTEAT ATACTGATET AAGTGGTGGT GGTTATCTAT TOAGGGTGT ATAAAAT ATATCACAGT CGGTATACTC TTACACACTA ATTATAATCA CGTGATATTT GACTAT TACACCAGA CACCTCOCTA TGAAAATACC AACAGCTGA TGGTATTTAC ATCTGA ATCCCCAACA TTAGAACACA CTACTGACAC AACAGCCTGA TGGTATTAAC ATCTGA ACTACTGCAN TACTGTCATG CTTATCTGAC ACCGCCACC CATTGGAGC TATGGC ACTACTGCAN TACTGTCATG CTTATCTGAC NCCTGACCNC TGATTGTTCC GGAAAT TTGATCAGA AAATCATATC GNTGACCACA ANDTCTACTAN TATTAACCCC CCCACC ACCTTG (2) INFORMATION FOR SEQ ID NO:381: (1) SEQUENCE CHARACTGTISTICS: (A) LENGTH: 788 base pairs (B) TYPE: INCleic acid (C) STRAIDENESS: single (D) TOROLOGY: linear 25 (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) CRCANISM: PAG1289UP 30 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATCCCAGGC TGCCCCAGGA TGACGGAAG TTGCATGTTC TTTTCGCCCC TACACC CATATATCCA TICAAGTCAT ATTAACTCAA GCCCCTCCC AATTCTTTCC TAATAA CCCCAAGAAGA AGAACCTTTA CGTGCTAGC GAAACAAACT CATTCTCAAA CTCCGC 40 CACCAGGGGA AACTTCCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATAACC CCCCAAGAAGA AGAACCTTTA CGTGCTTAGC GAAACAAACT CATTCTCCAAC CTCCGCCCCACCACAACCCCA CCCAAGACCA CCCCCCACCACCACCCCCCCC	TCA AAATCGCAGT GCTTGGATTA 42	30
ATAICACAGE COGTATACTC TEACACACTA ATTATAATCA COTGATATET GACTAT TACACCAGGA CACCTCCCTA TGAAAATAGC AACAGGCTGA TGGTATTAAC ATCTCA ATCGCCAACA TEAGAACACA CIACTGACAC AACGGCCAC CATTCGAGCA TATGGC ACTACTGCAN TACTGTCATG CITATCTGAC NCCTGACCNC TGATTGTTCC GGAAAT TIGATCNGA AAATCATNIC GNIGACCNCA ANTICTACTIN TATTAACCCC CCCACC ACCITTG (2) INFORMATION FOR SEQ ID NO:381: (i) SEQUENCE CHARACTERISTICS:		∠U
TACACCAGGA CACCTCCCTA TGAAAATAGC AACAGGCTGA TGGTATTAAC ATCTGA ATGGCCAACA TTAGAACACA CTACTGACAC AACAGGCTGA TGGTATTAAC ATCTGA ACTACTGCAN TACTGTCATG CTTATCTGAC NCCTGACCAC TGATTGTTGC GGAAAT TTGATCNGCA AAATCATNTC GNTGACCACA ANTTCTACTN TATTAACCCC CCCACC ACCTTG (2) INFORMATION FOR SEQ ID NO:381: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: INCleic acid (C) STRANDETNESS: Single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI289UP 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATCCCAGGC TGCCCAGGA TGACGGAAGG TTGCATGTTC TTTTCGGCCC TACACC CATATATCCA TTCAAGATTAA ATGCATGATC AAAAAACTG AAGAGATTTA TGGTTC CATATATCCA TTCAAGATCAT ATTAACTCAA GCCCTGCCC AATTCTTTCC TAATAA CCCAAGAAGA AGAACCTTTA CGTGTCTACC GAAACAAACT CATTCTCAAA CTCCGG 40 CACCAGGGGA AACTTCCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAAATC CTCCAATACC CCTGCAGTTG GGGGCGCAC ACCAAGGCCA GCNAATCTTC TCCAGC	PAT TCAGOGITGT ATAAATTAAA 48	80
ATCOCCAACA TTAGAACACA CTACTGACAC AACGGCCAGC CATTGGAGAC TATGGC ACTACTGCAN TACTGTCATG CTTATCTGAC NCCTGACCAC CATTGGAGAC TATGGC ACCTTTG (2) INFORMATION FOR SEQ ID NO:381: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI289UP 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATCCCAGG TGCCCCAGGA TGACGGAAAG TIGCATGTTC TITTCGGCCC TACAGC CATATATCCA TICAAGATTAA ATCGATGATC AAAAAACTCG AAGACATTTA TGGTTC CATATATCCA TICAAGACTTA CATGATCAAC GCCCTGCCC AATTCTTCCA TACAGAC CCCAAGAGA AGAACCTTTA CATGATCAAC GCACACACC TACACTCCAGAC TACACTCCACC GAACAAACT CATGATCAAAC CCCCAAGAGA AGAACCTTTA CATGATCTACC GAACAAACT CATGATCAAAC CTCCCACCACC CACCACCACC TACACTCCACC TACACTCCACC CACCACCACC TACACTCCCCC TACACTCCCCC TACACTCCCCCC TACACTCCCCC TACACTCCCCCC TACACTCCCCC TACACTCCCCCCC TACACTCCCCCC TACACTCCCCCCC TACACTCCCCCCCC	ICA CGIGATATIT GACTATITAT 54	4 0
ACTACTGCAN TACTGTCATG CITATCTGAC NCCTGACCNC TGATTGTTGC GGAAAT TTGATCNGCA AAATCAINTC GNTGACCNCA ANTTCTACTN TATTAACCCC CCCACC ACCITTG (2) INFORMATION FOR SEQ ID NO:381: (i) SEQUENCE CHARACTERISTICS:	IGA TOGTATTAAC ATCTGAAGAT 60	00
TIGATENERA ARATEMENTE GNIGACENCA ANITETACIN TATTRACCCE COCACC ACCITTG (2) INFORMATION FOR SEQ ID NO:381: (i) SEQUENCE CHARACTERISTICS:	AGC CATTOCAGAC TATGOCTOGT 66	60
ACCITIC (2) INFORMATION FOR SEQ ID NO:381: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: ENA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI289UP 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATCCCASC TECCCAGGA TGACGGAAGA TICCATGITC TITTCCCCCC TACACC CATATATICA TICAAGITAA ATGATGATC AAAAAACTCG AAGACTTTA TUGTTC CATATATICA TICAAGICAT ATTAACTCAA GCCCTCCCC AATTCTTTCC TATATAT CCCCAAGAAGA AGAACCTTTA CGTGTCTTACC GAAACAACT CATTCTCAAA CTCCGG 40 CACCAGGGA AACTTCCAAC AGAACAACTC AGACGCATCC TACACTGCCG TACACT CTCCAATACC CCTCCAGTTG GCCCCCCCA ACCAACCCCA GCAGATCTTC TCCACC	INC TGATTGITGC GGAAATCCNT 72	20
(2) INFORMATION FOR SEQ ID NO:381: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI289UP 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATOCCAGEC TECCCCAGEA TGACGGAAAG TIGCATGITC TITICGGCCC TACAGC CATATIATCCA TICAAGATTAA ATGCATGATC AAAAAACTGG AAGACATTTA TGGTTC CATATIATCCA TICAAGATTAA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG 40 CACCAGGGAA AGAACCTTTA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG 41 CCCCAAGAGA AGAACCTTTA CGTGTCTAGC GAAACAACT CATTCTCAAA CTCCGG 42 CCCCAAGAGA AGAACCTTTA CGTGTCTAGC GAAACAACT CATTCTCAAA CTCCGG 43 CCCCAAGAGA AGAACCTTTA CGTGTCTAGC GAAACAACT CATTCTCAAA CTCCGG	C'IN TATTAACCCC CCCACCGCCA 78	80
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1289UP 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATCCCAGGC TGCCCCAGGA TGACGGAAAG TIGCATGITC TITTCGGCGC TACAGG CATATATCCA TICCAGGTAT ATTAACTCAA GCCGCTGCGC AATTCTTTCC TAATAA CCCCAAGAGA AGAACCTTTA CGTGTCTAGC GAAACAACT CATTCTCAAA CTCCGG 40 CACCAGGGGA AACTTCCAAC AGAACAACTC AGACGCATCC TACACTGCGG TACAGT CTCCCAATACC CCTGCAGTTG GCGGCCGCAC ACCAACGCCA GCAGATCTTC TCCACG	78	87
(A) LENGTH: 788 base pairs (B) TYPE: moleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1289UP 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATOCCAGGO TECCCCAGGA TGACGGAAAG TICCATGTTC TITTCGGCCC TACAGG CATATATCCA TICAAGTCAT ATTAACTCAA GCCCCTGCCC AATTCTTTCC TAATAA CCCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG 40 CACCAGGGA AACTTCCAAC AGAACAACTC AGACGCATCC TACACTCGGG TAAATAA CTCCAATACC CCTCCAGTIG GCCCCCGCAC ACCAACCCCA GCACATCTTC TCCACC		
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1289UP (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATOCCAGGO TOCOCCAGGA TGACOGAAAG TIGCATGITC TITICOGCOC TACACC 35 CTITICCGTAC TGAAGATTAA ATCGATGATC AAAAAACTCG AAGACATTTA TGGITC CATATATCCA TICAAGTCAT ATTAACTCAA GCCGCTGCOC AATTCTTTCC TAATAA CCCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAACT CATTCTCAAA CTCCGG 40 CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATA CTCCAATACC CCTGCAGTTG GCCGCCCCAC ACCAACGCCA GCAGATCTTC TCCACC		
(A) ORGANISM: PAG1289UP (XI) SEQUENCE DESCRIPTION: SEQ ID NO:381; GATCCCAGGC TECCCCAGGA TGACGGAAAG TTGCATGTTC TTTTCGGCGC TACAGG 35 CTTTCCGTAC TGAAGATTAA ATCGATGATC AAAAAACTCG AAGAGATTTA TGGTTC CATATATCCA TTCAAGTCAT ATTAACTCAA GCCGCTGCGC AATTCTTTGC TAATAA CCCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG 40 CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATA CTCCAATACC CCTGCAGTTG GCCGCCGCAC ACCAACGCCA GCAGATCTTC TCCAGC		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381: GATCCCAGGC TGCCCCAGGA TGACGGAAAG TTGCATGTTC TTTTCGGCGC TACAGG 35 CTTTCCGTAC TGAAGATTAA ATCGATGATC AAAAAACTCG AAGACATTTA TGGTTC CATATATCCA TTCAAGTCAT ATTAACTCAA GCCGCTGCGC AATTCTTTGC TAATAA CCCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG 40 CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATA CTCCCAATACC CCTGCAGTTG GCCGCCGCAC ACCAACGCCA GCAGATCTTC TCCAGC		
GATCCCAGGC TGCCCCAGGA TGACGGAAAG TTGCATGITC TITTCGGCCC TACACC 35 CTTTCCGTAC TGAAGATTAA ATCGATGATC AAAAAACTCG AAGACATTTA TGGTTC CATATATCCA TTCAAGTCAT ATTAACTCAA GCCGCTGCCC AATTCTTTGC TAATAA CCCCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG 40 CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCCG TAAATA CTCCAATACC CCTGCAGTTG GCCCCCCAC ACCAAGGCCA GCAGATCTTC TCCACC		
CTTICCETAC TGAAGATTAA ATCGATGATC AAAAAACTCG AAGAGATTTA TGGITC CATATATCCA TICAAGTCAT ATTAACTCAA GCCGCTGCCC AATTCTTTGC TAATAA CCCCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATA CTCCAATACC CCTGCAGTTG GCCCCCCAC ACCAAGGCCA GCAGATCTTC TCCAAC	:381:	
CATATATOCA TICAAGTCAT ATTAACTCAA GCGGCTGCGC AATTCITTGC TAATAA CCCCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAAACT CATTCICAAA CTCCGG 40 CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATA CTCCAATACC CCTGCAGTTG GCGCGCGCAC ACCAAGGGCA GCAGATCTTC TCCAGC	TTC TTTTCGGCGC TACAGGCTCG	60
CCCAAGAAGA AGAACCTITIA CGTGTCTAGC GAAACAAACT CATTCTCAAA CTCCGG 40 CACCAGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATA CTCCAATACC CCTGCAGTTG GCCGCCGCAC ACCAAGGCCA GCAGATCTTC TCCAGC	TOG AAGAGATITIA TOGITOOGAC 1	20
CACCAGGGA AACTIGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATZ CTCCAATACC CCTGCAGTTG GCCCCCCAC ACCAACGCCA GCAGATCTTC TCCAGC	COC AATTCTTTGC TAATAAAAAC 1	80
CTCCAATACE CCTCCACTTG GCCCCCCAC ACCAACGCCA GCAGATCTTC TCCAC	ACT CATTCTCAAA CTCCGTGGCT 24	40
	TCC TACACTGOGG TAAATAGCGT 3	00
ACCOMMENTAL CONCENSION CONTRACTOR CONCENSION CONCENSION ACTOR ACTOR	OCA GCAGATCTTC TCCAGGGGGC 3	60
AGUGUCCAA GOUXGGOUT CUGGIUTAAG CUAGGGOGA GUIGUGCGA AGATIG	OCA OCTOCOGOGA AGATTGAGCT 4	20
45 CCCTCCACAC ATACAAGTCT GGACGGATCA AGACGAGTIGG GACGTIGTIGGA AGCAA	FIGG GACGIGIGGA AGCAAAGAAC 4	80
AGATOCOTAC TOCATATTGA ATTACOCAGG TOCOCGATAT CCTTGTCGTC GCGCC	VIAT CCTIGICGIC GCGCCACITA 5	40
COCCAATACA CTICCAAATT GCCCTGCCCC TIGITAAAAC CCGCGAACAT GITCN	AAC CCGCGAACAT GTTCNTCCGG 6	00
50 NATIONAACCA NETTETICCAAT TCTNCNCCCA NCOCRUTTINI GREVINTINA ACCCO	TTIN GVENINTINA ACCCCCCCCCC 6	60
	IGIG TITCACCNCC CANAAAANAG 7	720
TACCCCCCNA AAAANAANAA NAAAAACCCC GTINTCNGIG ITTCACCNCC CANAA		
TACCCCCCIA AAAANAANAA NAAAAACCCC GTINTCNGIG ITTCACCNCC CANAA GGINCCCCGG GAAAACGAAC TGGGGGGAGA GAGAGGNANN AAAITINCNAN AATCC	VANN AAATINCNAN AATOOTTITA 7	780

	(2) INFORMATION FOR SEQ ID NO:382:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 761 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1290RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:	
	GATCOCTAGA TOCCCAGGAT GAGACTOTIC AGGITAGOCA GGIGITGIAT GCGCCCCAG	60
	AGGGAAACCC AATGACTITG CATAGAACAA ACCCGCCATC ACCCATGTCT TGCGCTGTAT	120
20	AGAGACTAAG GTATCTGAGG ATCCCTTAGC GACTCTCTCC ACCGCTCGAC GAGGCCATTG	180
	ACCICITACG AACIGCACAA ACCIACICGA ACTCIGITIC CAGACITCIT TCTGITTGIC	240
	TICAACTOCT TTOSCATGAA GIACOCCCCA GOCTATTITT CITACCCCCC TGGTGTTTGT	300
25	CUATATACCE GGTTGTATTT TTGATAAAAA ACTCAGCTCT TCCTCTACGG CAGAAATATA	360
23	TATOCAGICC TTAGCGCCAT GCCAAAATCT GCCTTTTTAC GGCTGTTTCT CCCAGTCTTA	420
	AAAAAAAAA AAADOOCOO COOTCOCOOTAT ATGCOOTTAT AAAAAAAAA AAAAAAAAAAA	480
20	ATAGAAAAA AGAAAAAAA AAAGACGOO COOCCCCC COCAGAAAAAAA AGAAAAAAAAAA	540
30	GOCCCCACC CCTCCAACCA CACGACACOC CACACATAAT AAATCCCACA CCAAGGGAAG	600
	AAGTOTTGTG CACCOCTCCCG COTCATACCC CTCCCATTCT GTTCCATCCC GCTTGCAACC	660
	CAGTATGCAT GTCAAGCATG NTCCGAGCTC CGCTCCTTGG AGTCGAATCT CTTCCTACCC	720
35	AGCCGAATCC CATACTTGCC TTCACATACA TACCTTTCAT T	761
	(2) INFORMATION FOR SEQ ID NO:383:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 639 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) Original Source: (A) Organism: Pag1290up	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:	
50	GATCACACAT OCTOTTTTOC OCCCCTCCCT CCTTGTGGGT GOOGTCACCG CAGTTCACTG	60
	GOCCACCATC ACTITICATIC GOCCACAAA COCTIAGGAA TOTGACTITO TOTTGCCACE	
		120
55	AAGTGTTATA GCCTAAGGTT ATACTGCCAA CCGGGACTGA GGACTGCGGC TTCGGCCAAG	180

	GAIGCIGGCA TAATGGTTAA AIGCUGUUG TCTTGAAACA CGCACCAAGG AGTCTAACGT	240
	CTATECCAGI GITTECGGIGT AAAACCCCGIA CGCGTAATGA AAGTGAACGI AGGTGAQGGC	300
5	CICTITAÇÃO GIGCATCATO GACOGATOCT GATGICTICO GATGGATTIG AGTAAÇÃOCA	360
	TABCTICTICG GACCOGAAAG ATOGTGAACT ATGCCTGAAT AGGGTGAAGC CCDIANGAAAC	420
	TCTGGTGGAG GCTCGTAGGG GTTCTGAGGT GCAAAATCGAT CGTGGAATTT GGGTATAGGG	480
10	COGARAGACT ARTOGRACOR TOTAGTRAGOT CGTOCTCCCG RAGTROCCTC CAGRITACAGA	540
	ACTOCIATOA TITTATGAGT TAAACNAATG ATAAGTTACO GGGTTGAAAT GACCIGACTA	600
	TCCCCACTIT AATAGITAGA ATCCCTGTTG CITATTCAC	639
15	(2) INFORMATION FOR SEQ ID NO:384:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 813 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1291UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:	
30	GATCGTGCAC GGCAAGACGT COGAGCTGCG TCACCGACGGG CGCGGGCTCT TCCAGGGGGT	60
	ACCCCAGGOC GTGGCAGTGA CACGGTACCA CTCGCTGGCT GGACTGGCGT CAACGTTGCC	120
	GOCGGAGCTG GAGGTGACGG COCGCACGGA GACAGGCGTG GTTATGGGGCG TGCCGGCACGG	180
35	CAAGTACACC GTGCAGGGTG TGCAGTTCCA CCCGGAGTCG ATTCTGACGG ACCACGGGCA	240
	GCTAATGGTG CGCAACATGC TAGCGCTGGA AGGCGGTACG TGGGCTGAGA ACGACAAGCT	300
	CCAGCTGCGG GCAGGCGGG GCTCTGTGCT GAGCGAGATA TACGCTCAAC GACAGGAGGA	360
40	CATGGCAGCG CAGATGGCTA TGCCGGGAAC TGGTATGGCG GACCTGGAGG CGAGCTTTGG	420
	ATTGGGGGTT CTGCCGGGGG TGGTGGACTT CCATGAGCGG CTGGCGGGGG ACGCCGGGGG	480
	CIGGCIGIGG TAGCCGAGAT AAAAGIGOGT CICCGICGCG IGGCAATAIT AGCGAGGCGC	540
45	TIGGCNCCAN AANANGCGCT INCINITYITGC CGAAGGCGGA ATTITCCGCC ATCICCGGTG	600
	CTTTACCGAA CCCACTGTTC TAAAGGGACC CGCNAGANCN NAATTATTINC CCGACCCNCC	660
	CTTTGANAAA AACNANACTG COCAAANACC GCCGGGTTTG CTNCTTTANG ANATCTTTAT	720
50	TNICCNITCC AATMITTGAA GCCCGNITNE GGCCNACAAT TICCCITATT TINAAATTIT	780
	NAACCACOCC OCCCCAGACC NITITITIIN COC	813
55	(2) INFORMATION FOR SEQ ID NO:385:	
55	(i) SEQUENCE CHARACTERISTICS:	

	(A) LENGTH: 773 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1292RP	
10	DECENTION CENT ID NO. 385.	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:385: GAICCGIGIA TITTITATIT ACATTATITA ATTAAAAATA AICAITTAAA TAAATAITIT	60
		120
15	TTATAAAAAA TAATTAGTGC ATTGTTACAT GITCATTAAA GAATGATTAT TATCAAAACC	180
	ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTCAC TTAATTAAGA ATTAGGAACT	240
	TTATCTATTA GICIGOCCIG TTTCCCTTTT GATTATTAAC CITATCCCTA ATAATCTGAA	300
20	ATATTTAATT TTAGATTAAT AATATATTCT GAGATTTAAT ATTTTTAATA AAATAAATAA	
	TTATTCCCTA AATAATATTA ATAACTATAC CATATATAT	360
	TAACATATGT TICGIAGAAA ACCAGCTATT TOCAAATCAG ATTIGACITT CICTACITAC	420
25	CATTATICAT CAGATAATAT TOCTACATTA ACCTGITICAA TOGITITIAT ATTITATTAT	480
	ATTITAANIA TAATAAATAT ATATTITAAT CATTIGATAA TAGTAAGATC ATCTGCTFTC	540
	CGTTTAATTA ATATTAACTA AATTTAATTT ATTTTAATTA ATTTTACATN GTTAAANATT	600
30	TAAATTAATT TTAAAACCAN TITTATITTIN AAATTITICNC AAATTAATAC TOOGOODOCC	660
	CTTICCAAGG GOCCTIVIVIN NATTITTIINA AAAAAATAAA AAAGGOCIVIN ANAAACCTTT	720
	TAAAANITCC CCNOGOCCCC MAANANINA AANATTINAC CCNAAAGGIC CCN	<i>7</i> 73
35	(2) INFORMATION FOR SEQ ID NO:386:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1292UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:	
5 0	GATCCAGITA CITAGTAGAA TGATAAAATT AATAAATATT AITTATTAAT AITTGGITAA	60
	CARTAAAATI CAATAATITA TITAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
	TATAATGAGA TATATATITT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTTG	180
55	TOCCASCASC TGCGGTAAGA CAAAGGGGET TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240

	GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300
	GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA	360
5	TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GACTCGATAC CCGAGTAGIT	420
	TTAGCAGTAA ACAATGAATA CCTATTTATT TITTATTAAT TAAAGAATAA ATTAAATGAA	480
	AATTAAAGTA TYCCOCCTGA TGACTACGTT TGCAATAATA AAAATCAAAA CAATAGACGG	540
10	TTOOGACTTA AGCAGTOGAA CATGITTTIT AATTOGATAA OCIXOOGANAA ACCTTACCAN	600
	TTTTNGAATA TTTAATTATA ATAATTTNIA ATTATTACOG NGTGCATATT NICTTCCCTC	660
	CGGCCGGCNA GITTTINAAT TAICNINAAC GAACAAACNC CCATTITTTT TTINANAAAA	720
15	ATTATTTATT TTTTGAATAT TNAAAAAAA TAAANATOCT TIMICCTTIT TAATGANGA	780
	GINITITIT TINITON	798
	(2) INFORMATION FOR SEQ ID NO:387:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 762 base pairs (B) TYFE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1293RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	
	GATCACCEAG CACCTOSTITO COUTCOSCAT AACCOCCCTT OCTUTOTOCC CACTOTICTC	60
35	CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT	120
	GITTGIACAC CICTGGGTGG GGGCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC	180
	TCATCTCCCC CCAGIATGCC TCTAGTTCGA TCCCATCATC GCCGTCTACA CCCGTCCCCA	240
40	TATOGOCACO CAATGAGGOO TOCAAAGOOG TAATGGAGGG CTGGGACGTT AAGCCAGACA	300
	TCCAGITGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCGCATTGG ACCAITGATG	360
	CCACACCTOT CCCTCCACAA TCATGTGTAT CCACATGAAT TGGGAGGTCT GGATACTTTG	420
45	CONTGATICEA GOCAATCAGT AGUITTOUTE CACOGGGCTT CATGGTGCOG GOCATATOTT	480
	TAATACCCAA GATATGTGTG CCCCATGCCA ACAATCTTTT CAGTCAATCC AGTAGTAATC	540
	AAGGTIGTAC TICTIGCCIG CIGTAGCATA TCACCIGAGI TACAGATAGI GCICAACCAC	600
50	CCTCCCCCTT TCTTCACCGC TNNAAACCCA CTTCACTGTT CTAGTCNTCA CCCNTCNAAN	660
	CICIGAAAIN TCANNCATOC CCTTGCTGTT TGACAAATGT CATCCCNFTT CCGCNAAAGA	720
	ATTAACACCC GTGGCCCCAA CNCCCTGAAN GATTTTGCCCC NG	762
5 <i>5</i>	(2) INFORMATION FOR SEQ ID NO:388:	

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 805 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1293UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:	
15	GATCTTACAT CTGACAACAA TACOCTGOOG GCAGATGAGC TGCATTGATG GAAATTTTAA	60
	CACAGCTOGG GCAACCAGCT ACACGGGATA TATAAACTCA ATGCACGCCG CTCTTTACTG	120
	ACACAGICCA TCAGCATCAG CACCACCCC AAAAATGAAG ACTACACACA TCCTATCCCT	180
20	ACCAACACTT GCCCCCTGCG CACCTGTTCA GCCCCCACCT GTTCAGCCCA CGGACCTCGC	240
	CGCAGCGGCA AACGTCCCCCG AGAAAGCTGT TCTCGGGCTTC TTCCAACTGT ACAATGTGGG	300
	CGATGICGAG CTCCICCCAG TCGACCGACGG CCCACACTCC CCGATCCTTT TCGTGAACCG	360
25	CACACTAGOG GACGIGGACT ACTOCTOGGA GCATGIGGIT CAAAAATGGI TOOGTCTGIC	420
	TCTCCACCAT COCCAAAGTA TGTAAGGCCG GACCAGAGAC AGTTTGCGTT GAGATATGTA	480
	AGITTACTIG GIGICCTACA CCATGCATTA TGACACGGGC TTACGTACCT GCTTCTATAA	540
30	GCTAGTITAA ATGTTTTCTA TOCGTATTAT ATGGTTTACC CGCGCCCATA GTTCGCAGAG	600
	GCTGCTGTNT TAAGGCCNAA CTTTATTCCT AANANGGTGG ATTACCCGGT NGAAANAATG	660
	AATCTGAATT GOOGAAATTC COOCTGGACT ATTANCTCCC CWACCOGTCC MAATAAATGG	720
35	AANATGGIGG GGITTAATAC AAAANGGNCC GVIGCCGGCA ATGNACIGGA TTAATTICAA	780
	AAACCTCCAA NIACCCCCAA NIGGN	805
	(2) INFORMATION FOR SEQ ID NO:389:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 764 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1294RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:	
	GATOCOGAAT GTOOCTCAAG CTCCOCTOCT TTCGGCTGGC CTCGCTGTTC TCTGTGCAAT	60
55	CONTICTOST GOTCICCTIC TOCCATOTIC ACCTIGOSTI CAGOGICTIC ACCTIGOTACA	120
-	OCTOGAGAAG CTTOGAGTTA TOGAATQCAA ATOGGTTTAG CATCTOGACC ATATTCGCTG	180

	COCCACCIOC CTOCCCCTTT GOCCTTACAT COOGAGTICCA ACTTCAACGT AATOCTATAG	240
5	AAAACGCCAT 1680C1C6CC GICTTATCAC GTGACTGTTC ATTCAGCTGG ACAGCTACTC	300
	CACTAGGACT OCTOCTOCTT TAACTGGGCT ATACACTITA TATCGTTACA TTACTTTUTC	360
	CETEGRECOC OSALICOSTOS TOCHOSCTIC TETOCACACT CACTCTICAA CACACCACC	420
10	TTCTTAAACA TGTCTGGTAC GACAAAGAAC CTTACGTGCG AGCCTCCGCA CGAATACATG	480
	GICCATATGT GICACCIOSC CGITCCGIOC CGTCCCTGIC ACGICICITIA GCTGCCAGIC	540
	ATGITGICCT COCTOCCAC CAACTTOCCC CGATAGTITC GOOGGICGIT ACTOCAGCAN	600
15	ACCORGINGO TINGGOTTOC TICACACITA CAGGAATOOG GAANIGOCAG ATOVIACTIT	660
,,,	TROSTITICOC COTTICCINIT CCTCACANAA ANTOCTITIAT ATTITICOCOG AAAACMITTA	720
	ATTITIACATT TICNAAACAA CATANGITGC NITTITIACNN AACC	764
20	(2) INFORMATION FOR SEQ ID NO:390:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 800 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1294UP	
30	(A) ORGANISM: PAGI294UP	
30	(xi) Sequence description: seq id no:390:	
30		60
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:390:	60 120
	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:390: GATCTOGAAC TOCAAGTICC TGATGTCCTG CTTACGCTTC TCTCGCTGCT CATGAATCGA	
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:390: GATCTOGRAC TOCARGITOC TGATGTCCTG CTTACCCTTC TCTCCCTCCT CATGRATCGA CTGCTCCTTC CACCGRATGA ACGRACUSCTT GTCCACATTA GGATGTACCT CGATGTCCCA	120
	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:390: GATCTOGRAC TOCARGITOC TGATGTCCTG CTTACCCTTC TCTCCCTGCT CATGRATCGA CTGCTGCTTC CACCGRATGA ACGRCCCCTT GTCCACATTA GGATGTACCT CGATGTCCCA GTCATCCCAC ATTTCTATCT TGTCCCACTT TGAGTAATCG ATTCCCATTG CACTACCTTG	120 180
35	(XI) SEQUENCE DESCRIPTION: SEQ 1D NO:390: GATCTOGAAC TOCAAGTICC TGATGICCTG CITACOCTTC TCTCOCTOCT CATGAATOGA CTGCTGCTTC CACOGAATGA ACGACOCTT GTCCACATTA GGATGIACCT CGATGICCGA GTCATCOGAG ATTTCTATCT TGTCCCACTT TGAGTAATCG ATTCCATTG CACTACCTTG TTTCGTTCTC GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT	120 180 240
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:390: GATCTOGAAC TOCAAGITOC TGATGICCTG CTTACGCTTC TCTCGCTCCT CATGAATOGA CTGCTGCTTC CACCGAATGA ACGACCGCTT GTCCACATTA GGATGIACCT CGATGICCGA GTCATCCCGAC ATTTCTATCT TGTCCCACTT TGAGTAATCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGTCCAACTA AATAATGTTA CACATAAGGA AGGACCAAGG	120 180 240 300
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:390: GATCTOGAAC TOCAAGITOC TGATGICCTG CTTACGCTTC TCTCOCTOCT CATGAATOGA CTGCTGCTTC CACOGAATGA ACGACOGCTT GTCCACATTA GGATGIACCT CGATGICCGA GTCATCOGAG ATTTCTATCT TGTCCCACTT TGAGTAATOG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA OGTCCAACTA AATAATGTTA CACATAAGGA AGGACCAAGG CAACGCCTGC CCAGTTCTAG CAACTTCTGT GTGTCACTCT CAACGATAGA AGTCTGGTCT	120 180 240 300 360
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:390: GATCTOGRAC TOCARGITIC TGATGICCTG CITACOCTTC TCTCOCTGCT CATGRATICGA CIGCTOCTTC CACCGRATICA ACGRACUSCTT GICCACATTA GGATGIACCT CGATGICCGA GICATCOGRAG ATTICITATCT TGICCCCACTT TGAGTRATICG MITOCCATTG CACTRACCTTG TTTCGITTCTG GCTTCACTTAC TGITGICCTT AGATCTTCTG GATCCACCAA TRACTGATTAT CARAGRITICA TATATGCARA CGICCARCTA RATRATGITTA CACATRAGGA AGGACCARGG CARCGCCTGC CCAGTTCTAG CARCTTCTGT GTGTCACTCT CARCGATAGA AGTCTGGTCT CGAGATGTTG AGRCCGTACT CGCCCACACC CCTGCTGAGG TOGTTGACCG TCARCGTGAC	120 180 240 300 360 420
35 40	(XI) SEQUENCE DESCRIPTION: SEQ 1D NO:390: GATCTOGAAC TOCAAGTICC TGATGICCTG CITACOCTIC TCTOOCTOCT CATGAATOGA CIGCTOCTIC CACOGAATGA ACGACOCTIT GICCACAITIA GGATGIACCT CGATGICOGA GICATCOGAG ATTICTATCT TGICCOCACTIT TGAGTAATOG ATTOCCATIG CACTACCTIG TTTOGITCTG GCTTCACTIAC TGITGICCTT AGATCTICTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGICCAACTIA AATAATGITTA CACATAAGGA AGGACCAAGG CAACGCOTGC CCAGTTCTAG CAACTTCTGT GIGTCACTCT CAACGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT COCCCACACC GCTGCTGAGG TCGAGGTGAC CTTGTTCGCA TTGGTCTTTT CGTTTTGTTG GIGCCGCTGC TGGCTGATCT GCTGTGCCC	120 180 240 300 360 420 480
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:390: GATCTOGAAC TOCAAGITOC TGATGICCTG CTTACGCTTC TGTGGCTGCT CATGAATOGA CTGCTGCTTC CACCGAATGA ACGACCGCTT GTGCACATTA GGATGIACCT CGATGICCGA GTCATCOGAG ATTTCTATCT TGTCCCACTT TGAGTAATCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGTCCAACTA AATAATGTTA CACATAAGGA AGGACCAACG CAACGCCTGC CCAGTTCTAG CAACTTCTGT GTGTCACTCT CAACGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT CGCCCACACG CCTGCTGAGG TCGTTGACGG TCAACGTGAC CTTGTTCCCA TTCGTCTTTT CGTTTTGTTG GTGCTGCTCC TGGCTGATCT GCTGTGTGCC GGGCTGCTCC TGACCGACCA TCAGTTGTCG GCCCCCCCCC TGGCCGTTGT TGGAGTTATG	120 180 240 300 360 420 480 540
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ 1D NO:390: GATCTOGRAC TOCARGITOC TGATGTCCTG CITACGCTTC TCTOGCTGCT CATGRATOGA CITCCTGCTTC CACCGRATGA ACGACCOCTT GTOCACATTA GGATGTACCT CGATGTCCGA GTCATCOGAG ATTTCTATCT TGTCCCACTT TGAGTARTCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TRACTGATAT CARAGATTCA TATATGCARA CGTCCARCTA ARTRATGTTA CACATARGA AGGACCARGG CARCGCCTCC CCAGTTCTAG CARCTTCTGT GTGTCACTCT CARCGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT CGCCCACAGC GCTGCTGAGG TCGTTGACGG TCARGGTGAC CTTGTTCGCA TTGGTCTTTT CGTTTTGTTG GTGCTGCTGC TGGCTGATCT GCTGTGTCCC GGCCTGCTGC TGACCGACCA TCAGTTGTGG GCCCCCCACT TGGCCGTTGT TGGAGTTATGG GACCCGANTG AGGACCGAT ACGCAATACT CGTAGGCGTT CCGCCGCNAT GTCGCTAACG	120 180 240 300 360 420 480 540
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:390: GATCTOGAAC TCCAAGITIC TGATGICCTG CITACOCTIC TCTOOCTOCT CATGAATICA CITCCTOCTIC CACCGAATGA ACGACCOCTT GICCACATTA GCATGIACCT CCATGACCTG GICATCOGAG ATTICTATCT TGICCCACTT TGAGTAATCG ATTOCCATTG CACTACCTTG TTTOGITCTG GCTTCACTAC TGITGICCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGICCAACTA AATAATGTTA CACATAAGGA AGGACCAACG CAACGCCTGC CCACTTCTAG CAACTTCTGT GIGTCACTCT CAACGATAGA AGICTGGICT CGAGATGTTG AGACCGTACT CCOCCACAGC GCTGCTGAGG TCGTTGACGG TCAACGICAC CTTGTTCGCA TTCGTCTTTT CGTTTTGTTG GIGCTGCTGC TGGCTGATCT GCTGTGTGCC GGCCTGCTGC TGACCGAGCA TCAGTTGTGG GCGCGGGGC TGGCCGCTAT GCCAGTTATG GACCCGAATG AGGACCGGAT ACGCAATACT CGTAGGCGTT CCGCCGCTAT GTCGCTAACG AACTCTGGTT GCCAACGCGA AGAACGCCTT GACCCGANAT CAGTGCACAC CGAACCGTCC	120 180 240 300 360 420 480 540 600

(2) INFORMATION FOR SEQ ID NO:391:

5	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 796 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1295RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:	
	GATICTITICCT TCAAATTOOG ACCAGGTOCT TAAGTCATCC TGATCCTGCA CAATCACGTC	60
	CATATTOGOG GAGATCAGTG CCOGTTTGGC ACCAGAATCG CTGCCCCGCCC AGGTGACTAG	120
20	CAATCCCACC TCGTTCACAG TTTCCACCTT TACCTTACAC CAAACCACAG GAAAGTCCCG	180
	CGACAGCTGC TCGTGCAACC GTTTGAACTG CTTGTATGTC TCCGTGTCGG ACTTCACCGC	240
	TGTGCAGCAG TCCGCTGCAT CCACCACCCA TGCCGAGGG ATCTGCACTG CACGCTGTAG	300
25	CITCICGACA GIGAGATTOC IGAGCGICGA GITGIOCAGA MITTOCTOGA GGIOGICTCC	360
	AAAGCCCCCC TGAGGTTTGG ACACGTCCCA GCACGATGGC AGTGACGCCC CAGTCACCTC	420
	OGRAGARACA ACAGCACTOC GOGCTGTCTG AGCAGAAAAG CAGGCCAGCA ACGCCAGCGC	480
30	CGITGCAAAG GATATCOGIT GCCCCAAAGG CCAAGCIGCA AACATCATTC TOGTGGICAG	540
	CGACTGCTTT TCCCACGAGA TCCGTGGGGGA CCATGGGGCCA GATGGCGCCC TTAATATAAG	600
0.5	CCCCTCCTCG CCAGCATGAC TICTGCCAAC TCCCGAACAT TCTAAATGGC CAGCTGCTGC	660
35	TITGATGGTA CCINCCOCNG CINCCCCAA AATINATATA CCATAATCCC CVICCTAAAT	720
	ATINCITIACAT ACCACGOCCC AAAGCCCCCC CCGNAGCNCN CCCGAGCCCC CACITTICNCC	780
40	MAYANCC GALAR	796
,	(2) INFORMATION FOR SEQ ID NO:392:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 808 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1295UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:	
55	CATCAACTIC ACTICIOCOC CITTGICOCA TOCACOCCOC CCAACOCCAG ATACCTICIC	60

	ANCIGIBUS SIACCIOCA COSCICCAC GALOCIGIS CASIOSPAL SCISSIANI	120
	GITCTTGGTG TAGTGCTTGA AGTACTCCAA AGACCACACG AATGCGAGGC CTGCGAGGAT	180
5	ATAGAAAACC AGCGTCCCGT ACCTACCGAT TOCCATOGTT GAAGCAAGGA TTCCACTGCC	240
	GTAAGTACTC AATTATTGAG TOCTAGCAAG CTGATGTTGA TTGTGTGATA TCAACGGTAA	300
	TOGOTOGTTA AGGAACCTTT TCAAGAAAGG CAAAAGAAAT GOGTGOGTAG GTOGAGCAGG	360
10	TGACAACCTC ATATTACTCA TAACAGTTAT CTATCTAAGA AGOGGCACTA TOGATATACT	420
	ATCASCITCS TATACACATA TATATOGGAS GITTATAATC GCAAGITAGC TATAATTGCC	480
	ATCGAGGIGT AATACATOGA AGATTGICTA OGAAACTACT CTGTCACCAA CACATCAGCG	540
15	TATGAACAAT AACAGCAATA TTATGACAGG CAATTGCATA AAAGTATTCA AAGAGGGTTA	600
	AACAGITAAA TICCGIAAAG GITCACNGAN TAITCCCTGA CACCCCATAC CGAATCCCCC	660
	TOCACCAATT GTICACATGT TCANAGATTC TCCCCCCACTT CATATCNACC ATGITCCCCC	720
20	COCNAACTON CATTATGINA ATOCTIGINI TOCTGACTOC CCCCCTTGIC CCAAATGCCA	780
	TCCCAGGGTG ANAGGTGCTC GTGATCTC	808
25	(2) INFORMATION FOR SEQ ID NO:393:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 779 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pag1296RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:	
	GATOCATTICT COCHTTCCAG GICACCCCAC CCACCTOCAC AIGHACCTICA TGACCTTCCA	60
40	COGOCASCIC TICATICOTO COGCACOCAA GAAGCITGAG TICCCCACGT CICCOCCOCA	120
	CACTICOCC TACCTICCT ATTACACCC ATACAAATTC CACCCCATCC COCTCCTGCA	180
	CCGTCCGGTG GCCGAAACTC CGCGCGAGGT TCTGGAGAGC CGCGGCAAAC AGGTCGTCCG	240
45	CAACGGTCCG CAATACAGGA CTGTGATGAG AACCGGCGGTC GGGGAGCACA AGCTGGTGCT	300
	COCCACCIGAG ATCCACOCCA TCATTGACTT CCGCCAGCCT ACGGGGGACA ACCTGAAGCA	360
	CTACCTOGAG CTGAAGGTGT GTCAGAAGAA CCGGAACTTC TCAGAGAAAC TTTTCTCTTC	420
50	THOSCHOCAA TOCTPTCTOG TOCCCATAAA CACOCHTATT ATTGCATTCC GOGATGAGAA	480
	ATTOCTOCTG AAGAGOGTOG AGGAGTTCAG TAOGTCAGAG ATCCCACACO TGTTTAAAAG	540
	CCACCCAATA TICCATGIAT GITGIGGACG CCATAGATIG TATOGTOCTC CTTACAAATT	600
55	OCTAINIGAC TOOCCOGGGC CCTGAAAANA NITCAACTGT TACAGTCTCC TOCHNCATGG	660

	TECTTACTIT TECCCOCACTE COCAACAAAA ACCCCCAATE GEANAAATIN TECCTINETTE	720
	GTCCCCAATT GGNGNCCC CCANATANAA AATTCCCANAT TATTCCCTTG TTTCCTTAN	779
5	(2) INFORMATION FOR SEQ ID NO:394:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 815 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1296UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394;	
20	CATCCTIACOG TICOCCIOCTE COGTITIACOG ATATOCATOG GITGITTIOCA GITICOCCACA	60
20	GCACGGTGGT COGTGTCTCT GGGGACGTCT CGGACATGCA ATACCTACAG CGCCTGCTCC	120
	AGGACATOGA GATOGAGAAC AACTIACGACA ACAGOCACGO AGACOGOGG GAAGOGOTGA	180
25	AGCCCAGCTA TATTITICAG TACCITOCCT COCTCATUTA CCAGCOCCGC TCAAAGCTGA	240
	ACCOSCICIG GAACGCCATC ATCGTCCCCG GCGTCGAGGA CCGCCAGGCC TITCCTGCGTT	300
	AUGUGACCU CAAGGGCGIC AAGUACTOOG CCCCAAGCUT GGCTACTGGC TITIGGCGCCC	360
30	ATATOCCCAT TOCTOTCATG COTAAAGTOG CAGATOCCCA AAAAGACTOG COGCOGTICGA	420
	CCTCTCAATT GCGCGAGCCA CTATCCTGCA GTCCATGAAG GTGFTATTCT ACCGCGATGC	480
	GOGTAGTICC CGTCGCTTCT CGCTTGCCAT CATCGACAAT GATGCCGGTG TTCAGCATGG	540
35	AGCAACTOGA AGTOGAAAAC ATGACCTOOG GTTTCOCCCA AGGATATTCC GGGCTATGGC	600
	NCCCAAAINT TITGAATIAC CN3GGCCGCA ACGCCGCACC CIGITTACIA TCTIGITCGC	660
	CONTESTENCE CARCESCING GNIATECCEAT ACNITICARAR NECHIARICA TESTOCOCTIGA	720
40	ACCOUNTIEF TITINGINGAN ACCTICNOCO CITITICONGA TITICOCOGAT TICNOAAAAAC	780
	CCTTTGAAAA AACATTNCCC NTTGGNAAAT CGATG	815
	(2) INFORMATION FOR SEQ ID NO:395:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 766 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1297RP	

(XL) SEQUENCE DESCRIPTION: SEQ ID NO:395:

	GATCHOCTOG ACOCTOGTGA CCTTGCCGGC CTTCACAAGA CGGCCCAACT TGGTCACTGG	60
5	CACCCAGCCC TICTCCTGGA CCTCTCTTCT GCCCTTGCGG CCCTGACGGC CCTTGTTTCT	120
3	GOCGCCGAAG CCCCCTCTTC TTTGTTCTCG ACCTGACATC TTGCTATCGT CCGAATGGAA	180
	CACCIGADAGO TOCOGRACTA ACTITICISATO CACCOCTOCTIC ATGITACTITAC GATACACCTO	240
10	COCCOCCCC CTTCCCTCCT GAAAACCTCC CCACCGTCTC CCTCACCACA AAGGACCTCT	300
	GOSTICCTACO OCTICTITICOS GOCTICACIGAC GTIGTICTICOGTI TITCACACTICA AACOCACACA	360.
	TCAGACAAAC GCAGTCCCGG ACGGCTCGAA AGCAAAACCC GCGTGAAGGA GCAACGCGGA	420
15	ACCIOCOGO TOCGIOCOSA ATOTOGICAA AAACAGOGGI CACAAAGOGA TIGOCOCIOC	480
	COCCACCACT CCTACCCCCC CATTOSCCCC GCCCCCCACCAATC CACCAACCCC	540
	CTITOCCEAGE TACGGCTICAC ACTGCGGTIAT AAAGGCCGGC AGAGCGGTGG AAGCAGACAG	600
20	TCACACACAG GAGAGGACAG ATGTCOGAGN NCAAAATGAC AATCCTATCA ANAGGNOCGT	660
20	COCCCCAAA CEATCAANAG NITICGAAGIT CCAAACINGC CACATCAAAA GCCCCCAAAG	720
	GCAAAAAACT TOOCCCCCAC GACCCTTTCN CATITITIAAC CCCCNG	766
25	(2) INFORMATION FOR SEQ ID NO:396:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 795 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pagl297UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:	
	GATOCAAAAA CAATGAACTG TTITACAATGT GGAAGCCGTG ACACAAGTGA ATGGCGCTCA	60
40	GGACCOCTAG GAAGGAAGTC TATGTGCAAT GCATGCGGTA TCTGGTACAT GAAATTAAAG	120
	CAGCOGTITIC COGAGGAGGA TOCTICOGGIG ATTATOGAAT ACCOGAGATT AACTAATAGG	180
	CACGATGATC GCAGGGTGCC CAAGAAATTT GAGGTCCCAT TGCCTGAGGT CGAAAAAAGTG	240
45	AAGAGAGCCA TAAGAGCTOG TGTTGTGGAG TATTTGAATG ATGTTGAAAT CCCCGGTTAAA	300
	ACGAGGAGOC GOGOGITATT ACATAAAGOC AAGCCGGGCA GTGOGTTAAA AACAGAGATG	360
	AAAACCCCTG CCCCATGAAG CACTGGAAGG ATGAAACCAG TTTGTCAGCC GGAAGGACAA	420
50	TACCGGCGGG TACCAACGTA GACACTATCC TGTGGCATGT AACGAACGTA CTTTTATTTA	480
	TCEAACATAA CTAGGGITCT TITICACCION TACCITTIGIA TTATCCTTIG AANAACIGAA	540
	COCCOCNOCTY TYAAAAANIT TYCHNNYTICN AAATAAATOC CCTYTAAAGA ACCCCCCCOCN	600
55	NAANCAAACC CITIVINCCCI TIVOCCCAAAC CCACCCAGAA ATTITICCCINC CIVITINCCGAN	660

720

ACANCIGITIN OGAGATICCC CONTINCOC CIMAAAAANC ICCCCCCGAN INININCCAN

5	AGASCOCTITI INCNCTOCOC NOCNANASTO COCAAATTAG AAGGGGINTT CNCCONNOCT	780
	CCCCCGAGATIC CAAAA	795
	(2) INFORMATION FOR SEQ ID NO:397:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 601 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pag1298UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:	
	GATCTTCCTA CTGGACTGGC TOCTAGACGA TAAACGATTA TGGCTACGTC AACTGCGGAA	60
	CTCGTGGGCC GCCTTGGAGG AAGCGCAGGT GGCACCCTTT CCAGGTGGCG CTGTGGTGGT	120
25	GGICCICAAC CCCAGICACG TGACACAACT GGAGCGAAAC ACGAIGGITT GGAACICCCG	180
	COGICIGGAC CIGGIACACO AGACACIGOG AGCIGCAIGO CICAACACOG GCIGGGCCCI	240
30	AGITACACTT GATCCTAATA CTGCCCCCCA AGACGTCATG CACATATGTG COCTOCTTCC	300
30	GGGGCTGCCT ACATCCCGTC CCGTCGCCAT GCTAAGCCTG CAAAGTCTAT TCATCCCCCA	360
	COGTOCAGAT TOCATOGGCA AGATCTGCAC CATCGCGCCC GAGTTCCCTG TTTGCTACGG	420
35	TGITCGACAA CGATTTIGIT GAGCTOGACA TICGAGGOOG CAATTOCICC AGAACTTACT	480
33	CCAAGAACAC TIGIGCCAIC TGACCACCCC ATGGCTAACA GACCTACCAA CCCCCCTTCN	540
	GAACCAACCC CTICNATTIC NATCIOONAG GICNCTCCCT ACCTATACCG CTCTTGTGAN	600
40	A	601
	(2) INFORMATION FOR SEQ ID NO:398:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 753 base pairs (B) TYPE: nucleic acid	
45	(C) STRANDFINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1299RP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:398:	
55	CATCTCCCAC ATTGACACGG TAGCAGCCCA CATATTGCCC TTGAACGCCA TTAAACGGCG	60

	CCATTOCTCC CATAGAGCTT TCAGATTTCC TGTTAGGCTC CAACTCAACG TCATACTGGA	120
5	GIPTAAATOG AGTOOGTOCT GITGATATOC AACTTOGAGG CSTTCTITIT GTCCTCGTAT	180
<i>3</i>	COCTIGAATA OCCOCCCAGG TCCCGTOGCG AAAATCCATA TATATCCATA TTGGCCACCC	240
	ACCTRICTCAL ACATAGAGGC AATAGTGCCA GTAATGCCTC GAGCCGAAAAC CATGCAGCTC	300
	CCCCCCCAACC ACCCCCCCC CACCCTCCCC TTCCATAGAC CCCAACCCCC CCCAACTCCCC	360
10	CSCACOCTCA GCACOCAGITI CCTCCCTTGTC ACOCTATIGTC CCCAGCCGGC GGTGCGCACA	420
	CCCAGATACT AACACAGCAC AGACOCTGTA TCAGCTGATT GTCCAACCGG CGTACTATTT	480
	CACGITICIG GCGAATGIGC TAGTOCACGC GTTCCCCCCAG GCCCCCCAG TCCCCATAGC	540
15	AGIGGCGTTC TEGATGTCGA COGTGGGCCT GGGCATTCCC GCCCGCGCTG CCATTTGTGC	600
	TGCCCCACCC GGTGTGCCAG GGTTGTCTGG TGGGTGCGGT GTGCTGCCGC AACTACCACC	660
	TOGAGTACAT GCAGACCTAC ATTOCGAGCC TOCTOGTGAC GGGAGAGGGG GAGTCCTGTT	720
20	THENCOTAGE CONTROLLED STREEDS TOO	753
	(2) INFORMATION FOR SEQ ID NO: 399:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 751 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1299UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:	
	ACCCITITIGG TITTICCGCGI GATGGTGGGT GGTGGTATAG ACGATGTGAT CICCGGCTGC	60
	AATTIGTAAGC CTTCTCCTCC GGAGATATCC CGCACGGAGA AGTICGTCTAA ATTITAACATT	120
40	ACGITCATGT AATCACAGGG CACCITTICA AAGACACAGA CGATCATGCC ATTCTTACGC	180
	THICCCCACA TOGACOCCCA AATGAATHIC TGTGHATOCG AGGAHOCTGA CGATGCAGCT	240
	GAAGCAGGAG ACGACAGCGA TGTGACGCCT GGTTGTATGA CGCCTACTAT TTCACCTGTG	300
45	AATACTIGIT CITICOCCCTC IGTAGACATA AICTIGITAA GGACAAAGCT CCTGCTGTCG	360
	GTGTGTATCA GGTCAAGTAA AGTAAGOGCC TTAAATGCCA ATTTGGAGAT ACCGAAGATT	420
	AAGCATGCCN AATOGTTAGC COCCCTAAAC TGCCATGGGT GATGCTGGGA ACAGGTAAAT	480
50	ATGOCCTGAG GTOCTGTGTA CTTACCTGAT ATAAAAGTAT GCAGTATOCG GGGCGCTTCG	540
	TACGITICTIC TIGINGTICTIAT COCATOCTICG ATACATIGTTA GITICATOGGI AAATGGITIGG	600
	AGATAATITT CONCCIOCGA COCCIGIATA GIAGITTCIG TOTIGAATAT TCATGAAAIG	660
55	GITOGOCTAA GCTTTCAAGC AGCTGCTTCT TTAGTTCTTG CTCATTACTG ACTTTCTTCG	720

	CAGGATCTAC GUCATCOOKS TTGGTGCTGA C	75 1
	(2) INFORMATION FOR SEQ ID NO:400;	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 777 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1300RP	
15		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:400:	
	GATCTCTCTG COCCGCTGCAC AAATGACGCA GAAACAGGCA TTCACGGAAT TGAAGAGGCC	60
20	TCAACTGCCC CCCATCCCTA CAGGCCCAGT GCGACGACAT CCTTTCTTTG GTGCGTIATGA	120
	GGATACCTAA ATAAGCACAT ACAAAACGTT AAATATGCAT AAGGAGATAT ATGCGAAAGT	180
	TAAASTOTTT TTAGTOOCCC TOOGCCACAG TTGCGTGTTT CAGCGATAAT GGGAGACCAG	240
25	CCCCCCCCCCC GATCAGATAC GGITGTAGIG GCCATACCCC CTTGCCCCACG AATCTACCCC	300
	GINIGGIGG TGACGCIGGG CCGGGGGCGI CITIACGCIGA GITICCCCACA GCGGITICCIC	360
	GIACIGATIC ACCICTICAT COTOCACACO COCTOGITIC COCIACOSCO COCCACIOCO	420
30	CCCCCCCTTC TGCCCCTCGA GATCGTAAGA CTCGTTGCTG CTGCTCGAAA AGCCCTTCTT	480
	SCICTOSCIG TASTACTOST COTTISCOSTA GIACOSCIGO SCICTOSSIGIS TIACTACISGIS	540
	CTGGTATACC ACTIGTOGCG CGGAGCATAT ACTIGTGCAC GCTGCTICTC CTCGCGCCCCG	600
35	CCCCTGCCCC TOCCCTCTAT ACCASCACCA CCCCCACCAC AACAGTCCCA CATTCCNCTC	660
	ACCCCCCCAT AAACNCCGAN TTACACCCCC TATOCNATAC CCAATTGACG CTACNCATCC	720
	CNCTATACCC CATCNITICA CNCGGIACCT ACTITITOCCN AANIGACCCC CACNINC	777
40	(2) INFORMATION FOR SEQ ID NO:401:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 812 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1300UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEO ID NO:401:	
	GATOGAGGA TITOCACTOG AGGTGGCGCG CTACATGAGG CTGCTGCGCG AGATAGACGC	60
55	CAACTOCGTG CACACCGTGC CGGACCTTAA CGCGCAGATA GGGCGCTTCC TGCCTGCTTC	120

	COCCACCO GRADUCTOC ARTICALES CATCARCOS CICITICAS ACTIGITAC	180
_	GICOCTOGAG GAGAAGATOC ACGICTOGTIC CATTOCGTTIC GAGACOCTOG ACCOGCTOGT	240
5	COCCCCCCTC GACCTCCCCT ACGACCTCCC CCTCAACAAC CACGACATCC CCCACAACCT	300
	GCGCCTGGGC AACGACAACC ACCCTGCCAT GCACCTGCAC CAGGAGCTTA TGAAGAAGAT	360
	CGAGTCCAAG CAGCAGAGCA AGTCGCAGCA GGCGCTGCGC TCCGAGTCCC GCCGCGAGGC	420
10	GATIGGOGGCC AAGAAAATOC ACGTIGGACCC GCCGGCGCCG CGCCTGCTCT CAAAGGCCCCC	480
	COCCIOCOCANI GOCCOCCOCOC COCCCCTICO COCCCANACCO COCCCCANAA CITITOCOCCC	540
	COCCCGCCCC GCNACCGCAA GAAGCCCAGG AACAANTACT CCGCCCCCCC CCNAAACAAC	600
15	AATTICGGGA AGGCCTCTTA CTGCTACTGC AACCATTCNC CCTACGGGAA AATGTCGGTT	660
	COGAANGOGA AAAATOCCINC TCNATGGTOC CTCCCCTGGA TCACTCNAAA CCTTACCGAN	720
	GOCAAATGIT CTGCAANAAT GCAAAAAAAC OCTACATACA GNCCGGTTAC TANNIOCCCC	780
20	COUNCEINON TOCCTINGAA TOCCTIOCNO NI	812
	(2) INFORMATION FOR SEQ ID NO: 402:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 786 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1301RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:	
	GATCCGCGAG ATTICATCGTG GACCCGCCAC AGGCAATTAC TATAACAACA TCCTGCGGTG	60
	THARAGGACC TRACTICACOC TICARGUATUT CAGGATGATA TOCTAGATGA AGAGCIGOGC	120
40	CACACGCIGG TICGGFIACA ATATTOCICT CITCCGCAAA ATTTAAACAT GICTGTACTA	180
	CACCGACCTG GTCAACCACA ACACATTTTG TOCTGTATTT TTGCCCGTAA CTCACACTAA	240
	GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGCATTC ATCGAAACGT	300
45	TOCTOCCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACCC CTCTGTTTCC ACTGCTACAA	360
	CACCGATAGA GICTOCCAAA CCATGITICT CCAGCCCATA TACAATCCCA TIATAIAACC	420
	CCCCGCCACC TALCOCTGCAG ACCATALCTT TCACGCTCTC CAATTGCACG CCTTGGAGAT	480
50	OCAGIOCITE TACTACTICA TETACEATIG TIOCATOCCE TICCEAGATG AGTOGITGIC	540
	GAATGGATGT GCATATATCG GAGCGACTTT TTCTAATTCA CATTCCCCAT CAACTCCCGA	600
	COGIAAGITA TCATCOCTCT CTTTCAATAC ACTTCCCATT GANATCACAT CNOCCCCCGT	66
55	יירוותונגלא הבדותיאוים תאוחיותים מגירבורותים ויירובורותים מיורבבותוגים	720

	MILINACELLEY COCREGERACE LICCHTCOCKLIE CALOCKYOCKY CICCONYWAY WILLIOCALICE	780
_	GNGAAG	786
5	(2) INFORMATION FOR SEQ ID NO: 403:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 782 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1301UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:	
20	GATCATCTOC GTGCGATACT GGCAAAAAAT GAGAGACAGC ATCATGAAAA TATAGTTAAT	60
	AACATATTOC ATCATATAAG CACAGGOGG TTTCGTCCAA CAGCAAAGGG TGCACTTGAT	120
	CTOGAAATGA GTGAAAATGA AGACCAAGAG TIACAACAGT TTAGACAGAA AAGACGAGAA	180
25	CTITIGAAAC AAAAGATATI GGAAAATGGT GATACTAGCA AGCTOGTATIC TAACCCCAAG	240
	TCATACGCCT TTTTTCAGAC GATGTGGAC GATGTTACTG AAGCATCATT TGGAAATACA	300
	TTTGATGCCA ATATAGATGA AAAAACAGAT CCATCTGCTG CAGGTCGGAA AATTGTCATA	360
30	TCAGAACAAT TTGIAAAGGA AACOCTGTCA TTCTTGTOGA GCAAGAGTGG CGACTCAGAA	420
	ATCCCTGCAG AAACTAAATC TATTICATCC AGCACAGTTG AACGTGAAGA AATTCAAGAC	480
25	TTCATACATT GAAGCAAAAT AGTAACATTA ACATTIGAAA GGAGTCTAGA CTTCCTGCTC	540
35	AGATGOCTGA CTCAGCAGTG AGATAGAGGT GATTACNOCT TTCTTTANAT ANATTOCNON	600
	GOOGONAAAT TITTATATGA ACTACTICAC AANANITITA AAGTIGGOOG CAGGGGGGON	660
40	ATCITAAGGG AATAAANATN GOGTOCAAGC CCAATACTIT TNINGGAAAN NGINGNGGIC	720
40	CCCCCIDAAG GATTIAAATT CNACCAACIT NICCNCCANN ACCCCCCCC TINITITICNG	780
	NG	782
45	(2) INFORMATION FOR SEQ ID NO: 404:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 785 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM- PAG1302PP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:	
	CATCGAAGAG CTTCTCGCTG ACTTCGAAGG GCACAAGGTA CCCAAGCTCC TGTAAAGAGT	60
5	TATGAAACTC CGTAGCGGAA AGCGTGAACG AACCGTTAAT ATCATTGTCC ACATATATCA	120
	TOCCCCACTT CTTCACGCGC TTGTATAACG AAGTAAACTC AGACAAGTTT ACGGTACCAA	180
	ACCCCTTCCC CCCAAACACC CTAATTIACCC CGTCCACCCA ACTCATGCAG AACTGCCAAT	240
10	TGICATCATT CTGTAGCAGA TGCTGTAGCT CCTCTGCTGT GAGACGCTCC ATCTTCCGGA	300
	CGICGICATT CATGAATAAT TICTTTOCTG TTATACCATC GOOGICTICA TTACCAACOC	360
	TRECORDETT COCUTTOCCTA TREFTCOCCT CARRECTECTE ASCTECCTEC COCCUTTOCAG	420
15	GCAAATTATA GCTCTGTGCG CTCGGTGGTA TTGGCTTCCC GTGGCCCGGC AGGCCAGGCG	480
	GOCCTGTGGA ACGCGAGGAG GATTTCCCTG AAGCTGCCCA ACGCCATGGG CAGGCAACTA	540
20	CTATGIGTAC AAAAATTGCC GIGNICCTGC AAAACCTFTG GICTGIACAG AACCCANCCC	600
20	ATGCCCCATG CAACCCONIG CIVITTITICCC CCAAATTAAN CCCTGGANAA NICCCNAATT	660
	TITICOCCATIN TITITICONATT AAAAANOONG COGINNAACT CONACCIONOC CCATININGGG	720
25	GOGNAAANIC CGCGCCTTTT TNITTINCAT AANGGNCONC NITGANNINCC GCCCCNNINC	780
	CCCAC	785
	(2) INFORMATION FOR SEQ ID NO:405:	
3 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 803 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1302UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:	
	GATCAACAAC ATACTTCTAA AGACATCAAT ATACGCCCGC ATGTCTCCGG ATGAAAAAACA	60
	TGAATTGGTT GAGAGGTTGC AGTCCAFTGG ATACCAGGTT GGCTTCTGCG GCGATGGTGC	120
45	GAATGACTGT GGTGCCCTTA AAGCGGCCGA CATTGGTATA TCTCTATCCG AAGCGCAGGC	180
	ATCTGTTGCT GCGCCATTTA CATCCCGCTT GTTTGAAATC AGCTGTGTTT TGGACGTAAT	240
	GAAAGAAGSC CGTGCCGCGT TGGTCACGTC CTTCGCCTGT TTCCAATACA TGAGCTTATA	300
50	TICIGOCACA CAGITIGITA CAATATIGAT CITGIACAGO COIGGATOTA ACTTAGOGGA	360
	CTICCAGITT TIGIACATCG ACCICITICIT GATCGIOCCG CIAGCGGIGT TCAIGICCIG	420
	GICGAAGCCC TATGAAGTAT TOOCCAAAAA GCGGCCAACG CCAATTIGGT TICICCCAAG	480
55	ATATICATIC CHIRCICGI CCACATCGIG ATTIGITGGI GTTICAGCIT GICCOGIGGC	540

	TOCCACTOCA CCATATGAAG TOCTIACCOCC ACCCACTOCT COCCACCACG AACATGTTOC	600
5	TTCCCANGAN NACNCAACCC TTTCTTNGTC TCCACTTCCA TAAACCCTGG TCCCAATCNT	660
•	OCTICOGGIN GICONOCCON NOCONONACO NAANITIOGAA AATTITOGIT TATOOCANIT	720
	CCCCCTTCCC TGNCCCTCCC GGTGGANNAT TTCCCCCCCC CGAAACAACT TGGCNNCTTT	780
10	CNCTCCCGAA GITNCTCCAT MTC	803
,,	(2) INFORMATION FOR SEQ ID NO: 406:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 773 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1303RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:	
25	GATCAGGICG CCTITATIGGC CATACTIGIT GGACTCATAG TATATCTCGG CGACTGCACT	60
	ATTACTOGAC TOCTTOTICAA GATCTTOCOC ACCCATCACO COGACTATAC TACATOTICTC	120
	GITGGCCTTT CCGTCCCTAA CCCCCAGAAA AGATACCTTT ATACTITATA ATACCAGTGA	180
30	COCCOCCATA CCACCEDANC CANCELLETT CCCAAATAAT TACAATATE CITTERCETA	240
	CTGGAATTGG GCTTATCCFT ACAGIGTCAC ATCAATTTTC TATCGTAATT CGCTATCTCC	300
	OCTOGCAATO ACTOCACTOC AAACCATTAT COTOCTGATA GATAAAGATT ATAGGGTAGC	360
35	CATCAATAGT ACCOGTAAAG OCGTGACCAA TATTCTGCTG GOCGTGTTTA GATOGCCGAG	420
	ACCCTAGAAT GTGGGAGCAT CCTGGTTTAG CGATATGGGA AGCCTTCACT AGAACCCTGC	480
	CACTAGTAGA GCACAGAAGG TIGAGACTTA CAGCTGTTOG AAGTATAAGT TGTAAATTTC	540
40	CAAGGGTGGC AAGTAATATC AATTGATTCN AAATGACTTA CCCCTACGTT GAACTGCTTA	600
	CTTTAANTIG GGTOGGGCCC ATCAAGCCCT GACACTCTIG ACTITCCCCC ATGAAAAAAC	660
	TCCCGGGIGG GITTCNANCCC CAITINCCCAA ATACANTOCA TANGTCCTGG CCCTTAACCA	720
45	CTICNICCOG AGGATITTITI TINCCAANAAG ANNINACTIT TINAATTINGC CAC	773
	(2) INFORMATION FOR SEQ ID NO:407:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 807 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1303UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:	
5	GATICTAAGTIC CTICTCCCCCA AGCOGTIGACG CAAGTIGGACT GTICTIGTCOGCT COGTTAATAA	60
	AGITATOGAG ATOGICCACA ACCICATOCA COTOGGATAT AUGIOGOCTO TGAGTAGOCG	120
	CACACTCACG TOCOCTUTOG AACUTGACAT CACACTTTOG OGACOGOCTT OCTAGCTCAG	180
10	OGTOCAAATC AATOGACACC TTTTCCAOCT CTOCCAGCGA GOGCAAGAAC TTTTTGTCTA	240
	ATATATAGIC GITAGITIGG ACCACGCAAG AAACCGGICG TICGIGGCCT CCTGACGCTC	300
	TCCCGTGTAC CTCGGCTGCG CTGATGACTT TGCCAGTGCA TGGGTCAGCG CTCTTGGAGA	360
15	TGACTTGATC GOOCGACTOC CACTITIOCCA ATOGAGGATC GICTACAGTT GTAAACGGGC	420
	SCACITICIT TICIGIASGI SCICSOSCIG CISSIACIOS ACICCICCIG GACIGICIOS	480
	OCCUTAÇÃOS ACCUSCUSCU OCUSCUSTA CUOSAACOSA AAAAGAAAAA UGACUUCCC	540
20	TOTTITICATA TGACATTCCC NGITGIGANA CNIACTATIG GCCCCNAGAA AATAANITAG	600
	GENGARATAC ACTONOTATG TITGOCTATA TITCOCNIAC CATATACAGO CTGCTGATTO	660
	CCAGITTTAN AANIFTAAGT GCGTTACCTT ATATGTTGAA NCCCGTTATA TGAAGAATAA	720
25	CCCCCCAANT TIGCAANGAA CCCCCANACGC ATTGNCTCCT TCANCANNAT TAAGNACATT	780
	TIGICCTUTC AACNACUTTA TAACNCC	807
	(2) INFORMATION FOR SEQ ID NO:408:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 778 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1304RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:	
	GATCAATGAG COTOCCTACT ACTGATCCTT ACTGCAGTCC TGTGTCAATA TTACATATCG	60
45	GIGGATAGCT AGATAAAAAT GCTATACATA TATCIGICGC CATIGIGCCA ATCIATATCT	120
	ATTIGIGCCG ACGITGCCGA CCAGTAGGAG GTTGTGTTCC GCGCGGTGCG CAAATTCCGC	180
	TGAGATCAAG CCATTGCCTG TGCTCTTGCC CTCCCCTAGA TGGTAGGTGC CACTTGTAAT	240
50	AAAACCGACG ACATCTTGTA COCGCGCACA ACOCTGATCG GCGTCATGGG TCCGTTTGCC	300
	COCAGCATTE TATTICCTES AAGCGACTEC CTGCCAATGG GCGAGATGCT TGACAGGCAC	360
	TOCATACAAG COOGCATTOT CCCTGAAATG GCCGCGTTCG AGGGCTGTAC AGACAACGGC	420
5 <i>5</i>	GATCACOGGA AGTTGGGTGG TCACAACAGC CAGTTGGACG GGCAAGCCTG TGTCCATAGG	480

	AGGITITIGGA AAAAGAGACA ACTGOCTTAT TGINAAGGIC CCGGGGANCT NCNAAAANAA	540
	TCTTGGTGGC AATACCAACN CCTAAGGATT TCANCENGIT CCCCAACTIN ATININITIIN	600
5	TNOCNCCCGT TTCAAATTCA TATNOGTOOG TTOCNGCCON GAATNITCTT TTCNAITTCA	660
	AACCAACGNG GGGGNGCCNI TIGACATTIG GANACNCCCC TCIVAAANANA MITGTCCCCT	720
	TICNOCNNAA AACAAAATIN NOGAGGAAGA GGITITIANOO CNNIATATNO COOCNOON	778
10	(2) INFORMATION FOR SEQ ID NO:409:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 792 base pairs (B) TYPE: rucleic acid (C) STRANDFINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
2 0	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1305RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:	
25	GATCAATGTA TCCATTATAC CCACCITTCG CACCGACATA ATATATTGAC TIGATTITAA	60
	AGCOGTAGAA CTTTACCCCC CTACCCCCC TAGGTATCCA ACCTTTACCA TCACGATCCA	120
	CGICTOCAAA GCACTTCTGC AAGGCTGGAA TGGGCTGGAG TACTTCGAGC TCACCCGCGA	180
3 0	ASITTOCACG AGGIGCTTIC ATGGGGTCTT CAATCGATAT AGACGCAACT GAGAAAGACA	240
	CONTRIBUTATE GITTITACCO TITACTICIT GIAGIGICGI GICCACCATO AAAAAAAAIGG	300
	GCTGGCCGTC ATGCTCTACT CCCTCACATC TGTCGGGAGA AATATAGTAC ATTCTAATAC	360
35	CATATOGAGT ACCOTTTIGA TIGATIGITG TCAACTOGAA AGAACTITCG TCTTTAATTA	420
	ATTICCTORG TICCACTOCT OCTIGITIGIT CCTCCTOCGA COCTIGORGG ARAGCCGAAG	480
	TAACTAGTOC CAAAAAACAT GTAACTAATG AAAAAATOCA CITCATTGTT OCTATTGAGT	540
10	GCCAATAGOC GAGACTCATC CATATGINAT GAAAGCGTFT ATANATCNIT GITNIGOCTT	600
	GAAAGAATTA TTATACTTTT CONGGOGGTT ACATTATCTT CCAACCAAAT TGTTTCCTTT	660
	TIVSANAGGNA ATCCCCAAAA TITTINAAAT TAATINGICN NOGCANOGGI TITTITCCCCG	720
15	GNGGGAAAA NAAAGCNGGN NACCCCGCCAA ANCCGAATAA AGGATTTCCA TNAAAACCCA	780
	ATINICCIVAA AC	792
50	(2) INFORMATION FOR SEQ ID NO:410:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 812 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: TNA (genomic)	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1305UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:	
	GATCCCCAAG AAGAACATCA AGATCCACOG GTTCTAGOCG CTATGTACTT TGTGTAACTC	60
10	AATACATATC CICCICCICC TCCACCACCA CCACCICCIC CTCCACGICC CTCIGGGCCT	120
	CCGCATAGTA CCTCACACAG TACGGGAACA GCTCCTCGCT GAACAGCCTG GCCAGCTCGT	180
	COCCUTTURC AAACTCCTCG CCCCCCCCCT COCCTGTCCA CCCCAACCAC GCAAACAACC	240
15	TOCOGTOGTA GOGOTTOGGO CACITOCATOT COACOGCOGO GOTTOGGCACT TOCCOGTOGT	300
	COCCCACOGT GAACTOCTTC CTCACGCTCT GCGCCCGCAG CCTGCCCTCC ACCTGCCCGA	360
	ACTICIACION GATICOCAAAG TOCCACOCCO COGCOCOCOC CCACTICCACC TOCCACCOCOC	420
20	GCATCGCCTC CACGTACCGC CAGTCCGCCG CCCGCACGTA GTTCGCGAAA ATCCCCGTGC	480
	TOCGTCAGCA CGAATCCCCCC ACAACCCCGC CATCCCCTCG ATCCCCTTGC TGCCCCCCCC	540
	GIATACCISCO CCCAGCISCOS CIBCOSCTICO ACCTICCASCIS CCCGGTTCCTIC CCGGTTCCCGC	600
25	NCCGCTNGGA NTCCGGGAAGN GCTCCACGNG CGGGCCTGCN CCCGTTAGTC CCCTGGCCCGC	660
	CATTITACING GOGNIGODOC TINNITIGITT NINGAAGGNA GNGTCCCGNT TCCNGGGCCG	720
	GVINNETTT TOGGINGGAG NACOGNITIT TTOGANCNOC CANICNOGGA NICCTOGNOC	780
30	GAANCONGT INCONCONN TIGAGOCCCC CT	812
	(2) INFORMATION FOR SEQ ID NO:411:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 778 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1306RP	
45	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:411:	
	GATCTGATAT TGOGTAATTG CAACCTTTGC ACCOCTTTGA AAAGTACTTT ACGAAGTGGT	60
	ATTIOCAATA TAGTICATCA TIGIAGIOGA AGCACGAGGA TACCITACAC TIGGTACCOC	120
50	ANACOGISCA SCAGAAGIGI TOOTOGICAT ATAGCTINOC ANATGIATIG TAATACAOSC	180
	COCTCAGIGG CTTATTOCAC ACATAACACA ATAGCTIGIT CCGCGTGAAA TAATCCTGCT	240

300

360

GOCATAGCAG TACCACTITCA GACGUATCOG GGACCTCATA AGGCAAGAAC TICCOCCGAC

ACAAAOCTOC ACAATOGTGA CAAAOCAGAC AGTTTTCATG GTAGTAATCA CCAAGOGCCT

	TCAGGGAGIT CTGCGTCATA ACCCCUTIGC ATTGTTTACA GATTTTGGCC GTTTTTTGAG	420
	ATGAGGTGGC GGTTTATGCT CCGCAGACGT TCGCATTACT TGCTCCGACG CACIGIGICT	480
5	ATOGTTGATA TOGTCACTAT ACGICCACCA ATACCTGTGC TTCTGTATAT TAGTCATGAA	540
	AAACAGTAGC ACTOCCTATO TTACOCCTIGO NGATOGTATT GGTACOGCCA AATNGTTAAC	600
	CCATTITICCA AGAACATION ACCNOTICGG TITTITIGCCCA AAGAGAGGIN TOCTATATIT	660
10	OCCAACAAA OCCCAACIGA AATINAANAA ACCCTITTIT CCCCCTITIN ITTCICCCGA	720
	GCAACCITTT CGGCAANITT CNCCCTAAAT TGINTGGGGG NIGANANCCN AGAAAANC	778
	(2) INFORMATION FOR SEQ ID NO:412:	
15	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 806 base pairs (8) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1306UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:	50
	GATCATTICA GIGGATGOCG ACATTCATAT GGATATCAGT TOGACTITIG TITICCAGTCT	60
30	TATTCCACTG ATTITICAGGT TACAAGAATT GOGAAGGGGT CTCCATTITG TAGGGACGAA	120
	CAATTGTAAG ATGTCTCAGG AATTCAAGAC TCAGGTTGAA ACGAAAACTA TTATCTTATC	180
	CCTTCCTGIA GOGGACGATA CCCTACAGAT GATTATCCAA CCCATCTCTT ACGAACTGTC	240
35	ACTACATACA GITTTCACTG ATTTTATTTC CATATCTAAG GTACAAAGCT COGAAACTAG	300
	OCATATOGCA ATTATTOGGG AAATTAAAAT TOGATATOAA ACAGCCAATT TTCAAGTGAA	360
	ATOGIACAAC TIGAAATIGI COGAGACOCT OCTAACATCA AAOCTAOGGG GGAGTIGITC	420
40	TOGAGCOGIT GAACTITATT GITCIGATAG TGACATCAAG TIGCITITIG AGGAATGICC	480
	CCCCCCCCA AATGAATACC COCNATIVING ATTCCTINAAC CGAATTCCCA AAACCCNTIN	540 600
	TNAANTAATC CCTTTAAAAA TINATTITTC CCNAACNITT ACNCCCGCNA ATTITTTTCC	660
45	CAAATGGGCC CCTTANATGA AAAAANACTN CACCCCCCN NOGAAAANAA ATTTCNCTTT	720
	GGAAANINNN AAACGAATIA TICNCNCCCT TINICCCCCC CCCGAAANAC ANINITICCT	
	CCCCCCTTT AGGAAAANIG TFTICCCCNA TTINANANIN TCCNCCCNCC CCCNNAACNA	780
50	AAATMITAAA NCACCCCININ TINING	806
	(2) INFORMATION FOR SEQ ID NO:413:	
E.E.	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 753 base pairs (B) TYPE: nucleic acid	
55	(C) STRANDEINESS: single	

J	(V1) CRIGINAL SOURCE: (A) ORGANISM: PAG1307RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:	
	GATCCCTTTA TCTCATATTA TAGTCCATAG TACCCCGTGG ATGCCTACCA CACAGAGGTC	60
	CCTCTTCTGG ACCTGAGACC TAGATATCTT GCGATATCAT TGAAAATATC GTTCAATTGC	120
15	TOUTOGGIGA GOOGOTTAAC TROCOCCIOG ATAICAGCAT COOGTGITTIC CGAGATGTOG	180
	AAGTICICAA CITTOCCCIC CAAAAACTCC TCAAACTICT CITGTICICT CAGTGTCGGT	240
	OGCAACAACT CATAAAATTT OGCAAGCTTA TACAGCTTCA CATTGTCTAG ACTTTOGAAG	300
20	TOOCOCCAACG TGAGAGGGAA TACGOOGTOC TTCACGTOCG GAATCTCACC GTCCCCCGTTTC	360
	GECANTIGGAG CCAAGAAGTC CTTCTCCTCC GACTTCGTCG AATTCACTAA GCGCCGCACC	420
	CACCOCTICIT CCATCGTGTC AAGCTGGCCC TGAAGCTCCC CCACTAGCTG CACTAAGTCC	480
25	TCATTOGTOG CGAAATCOGT TGTATCAAAC TTGCCGGGGG CCCCTTTAGG AAGGAACTTT	540
	TOGICTAAGT TIGOCATGIC ATOCTITIOC TIGOTGACCT GTAGCTOCAG CACOGACTGT	600
	CCTGTCTTGG TGATTAGGAC GCTCTGCCGT TTAACTAGCG CCTGTAGCTC CTCAACTGTT	660
30	TOTICAATGO CICGICIGAO ATAACGOACT TOAAATTTAG TAGAACGOOT CIGAATATTO	720
	CTACACCAAA CGCCGCAGAG AGAATGGTAA AGA	753
	(2) INFORMATION FOR SEQ ID NO:414:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 811 base pairs (B) TYFE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
40	(ii) MCLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1307UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:	
	GATCCACCAA AGGSTATTIT ACTATATGGG CCTCCGGGGA CAGGTAAGAC ACTTTGTGCC	60
	OSTIGOCOTIGG CCAACAGGAC CGATICCTIACA TITTATICAGAG TCATTIGOCTIC CGAATTAGTA	120
50	CAGAAGTACG TOSCIGAAGG TOCTAGAATG GTTAGAGAGT TGTTTGAAAT GOCCAGAACA	180
	AAAAAGCAT GTATTATTTT CITICGACGAA GTGGACGCAA TTGGCGGTGC TCGTTTTGAC	240
	GATGGAGCGG GTGGTGACAA TGAGGTGCAA AGAACTATGT TGGAACTCAT TACGCAACTA	300
5 5	GACGGATTCG ATCCACGTOG TAATATCAAG GTGATGTTTG CTACCAATAG GCCGAACACC	360

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

	TIMECOS CATOTICOS ACCOSTAM AMARCOSTA ADSTRAMA TELECOTOC	420
5	GCATTIGGAA GOCCGTGCCA ATATTITICCC GCATTCACAC AAAGTCCATG AGTGTTGAGC	480
3	GTOGTATTAG ATOGAATTGA TTCCCAGTTG GTGTCCAACT CCACCGOCGC TGACTANATC	540
	INSTITIOSCC CGAGGCTOGC ATTITTOCAA TCCAATTCCC GACCCAGGIT ACCTACAGAA	600
10	ANGACTICCT TAAACCINGIG GATAGGICCT CCACGGCTAT AAAAATICAC NCCCCTTCCC	660
10	CGTTTINIGC AAACCCIVAAN CINVICNOCCC CCTTGNGGCG TITITTTIAAA GGNITAITTIA	720
	TCCCAAANNG TNITCCITIT ACNATACTAN TGTTCCAATT TCTATNAAAT NITMICCCCC	780
15	CCGIGAAANC CINCCCCGIT NOCACCCCTA T	811
73	(2) INFORMATION FOR SEQ ID NO:415:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1308RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:	
30	CATCTGTCTG CTGGTACACC CATGAACCAA ATAATTGTGA CCGTCACGCA CTTCCACAAT	60
	GCACTICGGA AGATAAAGCC TICCGGICAGC GATAAAGATA GAATGAAATA CAATAAGCTA	120
	AACAAAAAAA TOOOCTOGAA TGACGAAGCA GOOGTOCAAG TCGAAGAAGA AGCATAGAGC	180
35	AGCAAGTTAA ATAGGCACAG CTATGTACAA ATAACCAATT TCAACTTGTT CAAAGTCGTC	240
	COCGICTIAC AGAITTCACA CATOGAGACG GOOGAATTTA CTIGITIATAA TOCCCICTOC	300
40	TOCCAACGIT TITTICGAATC TICCAGACAT ATTCCGTATT TCTTCCTTTT CCAGAAACAA	360
40	ACATATOGIA TITICICIATI CCIGIAACIT GAGCITAGCA ATTICIGIGG ATATAGTICC	420
	GCAAAGAGGT AGATCCGTGG CACCTCTGAC AAGAACGAAG TTATTCTTCA GAGAATGAAC	480
45	ACGCCCCCAT ACATOCCCAG AATGTATATG TTCATAAACT TOCGCTCCAA CATCAATGGA	540
45	ATGGATAAGA GOCAGOGTAA CAAGTOOCAT ACTAGTATAG TOCAGOGGAA TGCTTCAACA	600
	TTGGAATACC CGCACATGTC ATATCCGGAG CTCTTTGATT GATATAACAA CCCCCNCCCT	660
· •	NITINIGOCNO AAAATTOCOC CTGATGGTAC COCTAANGGT TCTTGCAAAA GCGCAACCCT	720
50	ATCCCCTGGG AGCCNAAACC CTTTACGACN AACNNATTAT GGCCCGGTMT TTNACGTCCC	780
	TNNCCIGION N	791
e e	(2) INFORMATION FOR SEQ ID NO:416:	
55	(i) SEQUENCE CHARACTERISTICS:	

5	(A) LENGTH: 817 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(11) MOLECULE TYPE: DNA (genomic)	
10	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1308UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:	
15	GATCACGTGG GCCGTAAGTC GCAGAGAAAC TTGCAACTGA ACTGCCACTG GGGCTCATGC	60
	ACCACCAAGA COSTTAAGOS CGACCATATIC ACCTOCCACC TGCGTGTGCA TGTTCCCCTG	120
	AAACCCTTCA GCTGCTCCAC ATGCAGCCGT AAGTTTAAAC GCCCGCAAGA CTTGAAGAAA	180
20	CACCTGAAAG TOCACATOGA OGACACCATG AAAGAGCOTT COCCTOCOGC OCCOCCTCG	240
	CGTOGTGTTC GCAACACAGG CGTTAACAAG GGCTCTGCCC TACAAGAGAA GGCGCCCACG	300
	TTACOCAACC TGACTGTGGA GAGCTTTGTC AGCCAGGAGA TGCAAAATTA CTACCCCTAC	360
25	TACAAAAGCA GACAGCACCT AGACGAAACA CTGTOGCACA TTATTCTCCC GCCCCCCAGC	420
	COCTCTAGGT TOGTACTITIG GOGTCOCGAAC COCCAAGCTA CACACOGGAAA OCAGTGTCTT	480
	CTTCACGACG CTGTCGCAGG ACATGTCTCG TCGCTTGCCT TCTCTTGCTC CTTGCAACAG	540
30	CCCCCCCCCC GCGGTTAAGA TGGTAATGCT TCCCCCGCCC CAGAACAGCA ATATGCACCC	600
30	COTOCCCIAG ATATCCCASC GATGCCCCGSA CTCCCTCCCT TTGGTGACTC TCCNGGANCG	660
	AATCCCANCC TITTOCCCGAG ANACACTITCC GACCCNCTCC ATATCCCTGC TCTANCTGCC	720
25	CNCCTCACCG CITTCTCATA AAATOOCATT GITGCCGCAN CCTATCCTCA TCAAGCCCCC	780
35	TEATANACCE TENAAAAGAC TEANTECCECE CCAAACC	817
	(2) INFORMATION FOR SEQ ID NO:417:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 795 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SCURCE: (A) ORGANISM: PAG1309RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:	
	GATCAATTAT TAGAGGCAAT ATCAAAGAAG TOOCATATTA CTGAGGAGAA CAGGGAACAG	60
	CCTGGAGAAA GAATGCCGCA GACGTACAGA TACACGCTGG AAAATCAGCT TGCCCAGTGA	120
55	GTOCTOGAAC AGCCGATAAG AGTATTGACA GTGGTAGCGT GCAAGAGTCA ACGACAAAAT	180

GAACAGAACA TCATACTTOG GGCGCGAGAT GTTGAAGCTC GACTTGGTCC GCCCGTGGAC	240
CTTTTTTGAA GAAGITGCGC CAGGATCCCA CGGCGGCCTT GCGCGACGCA GCAGGGACTG	300
GICTOCAGOG COCCAGCAGO AGGGAGOTTG TCACCACGOT CACAGAGOTC ATCCCCATAC	360
CCCCCCCCCC ASCCATGOCC GCCAATTIGTA TOCCCCACCG AATGAGGACG CCCATGCTGA	420
CTTOGGAGCC ATGAGAGAAT TGTACAGGAC TGCCCAGAAA ATGTTCAGCT TGACGCGGTT	480
AACGTGGCGC GCGCGAGATT CGATGGCATA CAGAATGCGG TTTAGCGGCG GCGCCCGAGG	540
AATGTCCCAA ACCACGATTC CCGCGCGTTC CCCACGAAGT CACTGTTGCC GCACAGGGAA	600
ATACCCAGIT CNCTITCACA ATTOCCACAA TTTCTTTGAN GCOGTCTCCC GATAAGGCAC	660
ATATINGTIN TITTIGCCGC ACIGCCGCAA NGINCCACTT GCCCCCCTGG TACTITCCCT	720
GAACATTTIG ACCGATNOCC AANCEIGCAA ACTCICCCNC CCCGIGTINN CCCATACCAT	780
CCANTITITIG GCCNC	795
(2) INFORMATION FOR SEQ ID NO:418:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 797 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:	
GATCAGGACC GOGGICACIG ATTOGATIGG CCATGAGITT AAGTATGACC CAGAGGCCC	60
CCCTGGTGTA TCTAATCTGA TTAACATCGT AGCTGCCATC CAGAAGAAGA CTATCGCGGC	120
GETEGROCA GATATECTG GATTARGGA CCACECARCT TITARARACT ATGITACAGA	180
CATCCTAGTA GCTGAGCTGA GGGGGCCCAG AGAGGAGTTT GCCCCCTATA TGAATGATAA	240
ATCATACATA TACGAGGITIG AGCGCAATGG GOCTGAGCGA GCAGGIGCCA TAGCIGCIAA	300
AACCCTGGCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTCAGATT CCAACTTTGT	360
CTATAGACTA GCAATAATTA TAAAGATACA TCAAGAAGAC CAAGAGCAGA TGCGTAACTG	420
GITGICACIC TTIGGACCIG CCGGATATCA GCACATGCAA CCAATATCIG CITCAGCAGI	480
CCTCCCCCTT CTCGTTAGCT ATTGTGCCAC CTTGTATTCT CCATCCGTTA TACAGCCAGC	540
TCAGCACATC ATOCATCTAT TITIGAGCCCA TICTGCTAGG CIGATGCAAT AGACTTCCAT	600
ATTROGRAT CATEGOCCO TEATRITITE GOVEACCACC ATCINITITE CNATCAAAAN	660
CGTGACAATC CNCCNGTTTT TONACCCTCC CTCCATNAAA TMTCTTTCAT CGTGGGTTTC	720
GEATCAANCC CINNOGNICH TOCCCTINCOC CTCCATCCNG GNATTIACAC CONTINITIT	780

797

CTCCCCCCCTC ATNAANC

	(2) INFORMATION FOR SEQ ID NO:419:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 830 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1310UP	
15	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:419:	
	GATCCAAAAA AATTTTAATA CTGAAAAAGA AATGCCACAA CTAAGCTCAG CTACCTTAAA	60
20	GAATCOOGAC CAAAGCIGIA AGGCAACAGC TCTTCCAATG TTCGCTGCAG AACCTTGGAC	120
20	COGTOGOCCT TOATCATAAT CACOGTOAGO TICTTOGGAT CAACGAACTO GOOCAGGACO	180
	TOCOCCAAA TOCCACACOG GETCACCACG TOCCACCAET COCCACTCAA TOCCATCCAG	240
25	ACCCAATTCS TATGCCCGGC TGTTACCGCC TTTACGACCG CTGTGCGTTC CGCGCAAATA	300
25	CCGGCTGGGT AACTGGCATT CTCGACGTTA GCGCCGACAA TATACTCGCC TGACGCTGTC	360
	AAGATOCAGC AGCCCACOCG GAACTITOGAG TUATOGOCTG TACGAGAGCT CCTTCGCGGC	420
30	TAGTOCTOCA GCAACOGOOC COTGATATOG CHOTOCOTGT GTGCTTGGCA TTGGCTTCGG	480
50	TOPOGICOCC TOCIAGGIAT TOGOGITCOC CITAGGIACTG GCTGOGAACC CITAGGITTT	540
	TIGCACCOCA ACCAATIOCC COCCAACCOC GICAATCCCG GCAACAINCA ANIACCONCT	600
25	TITIEGVINNC GEENAAAGGG NNANNITCCN NNCTINGCNC COOCNEGAAN AAANAATGIT	660
35	AACCATGIGG ANTAAACCIT TAANAIGANN OCTATGGCCN GITTIAACTIT ATOCCCCCNC	720
	CCCCCCTTT AAANGINNNA NCCCCGCCNT TNTACCTCTA NNCCNGCGG GGNGCNNANC	780
	CCACAAAINN INTGITIGNOC GONENOOGIN NCTAATATOG ACCCINGGON	830
40	(2) INFORMATION FOR SEQ ID NO: 420:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 799 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(v1) ORIGINAL SOURCE: (A) ORGANISM: PAG1311RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:	
5 5	GATCITATOS TICASOSTAC OSTOTISCAAS AATOTISASAC ATAAACITISC SCIISOSACSA	60

CTICTICSIA AATICTICSI ASTACISICC STIGICCCCT TCCAACGCIT CCTICCCCCG	120
CITIGITACAGO AGOTICOACOT TITIOGGIOGA GAGOGGOTOT TOCTICOCGAG AAGOCTOOGO	180
GTCTAGCGGC ACCTCGTGCC AGGGCATGTC CGCAGGCACC AGAAGGTTGC CGCTGCGAAC	240
CGAGCGCAGG TCATCGACCA TGCCGCGCGC AGETTCCTCC CCGGGGGACT CGGCATGGAA	300
COCCOCATION CALTOCOCCO CCTICTOCOCC GGALTOGOCG GCATOSCTGT CCTTCCTCGCC	360
THECHCIPE CONTROLLOR CONCURRENCE CHOOSETTICE TECHCIPETT CONCURRENCE	420
TIGOTOCTOC ACCGAATOCT COOGCITOCT COTOTOTOCT COTOCCCCTC COCCITOCTCC	480
COCCOSCAGO COATOTTOGO AGCAGOCCOO TGACGTOGIT CTGCAGOCCO GCATCGCOGT	540
CICCTICGIC COCCCICAAT COCTGTTCCC TGACCTCGIC TGCGTTCCCT CAGCCCTTCC	600
ACAGGGCAA GIIGIICIIT CINAACCCCC CANNOCCAAT NGIIGINGGG CNICATCCCC	660
CALIMITACO CACCALLACO CALLOCANAN COCCACANAN VOLLALACO ACCALLACAN	720
CAATTOCTTT TICATTIGGT TITCCCCCCA AAATTTINAN ANNGGGTTAN CINNICANNN	780
NGCCNGNINA GAGAAACCT	799
(2) INFORMATION FOR SEQ ID NO: 421:	
(A) LENGTH: 790 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1311UP	
(xd) SEQUENCE DESCRIPTION: SEQ ID NO:421:	
GATCTICIGA TOCATATTIC COCTCTCACC TICOCCGITA AGTITTICCA TGIAGATACC	60
TCAAAGICAT CATCCCCGIC ATCTTTTICA GIGIATAGAT TCIGIGATAC TICICCTICT	120
TOCTOTTOCT CITCTTCCTC TICTTCCTCG TCTATATGAT CPTCGCCTGT CAGTTCATTG	180
TOTATIOCAT AATTGOGTIC AACTTTOOOC TIGGGCTOCT TITGCTOOCT ATGATCTTCC	240
TOGATACCIT TCTGTCCATC TCCCAATCCC GITTTCTCAT CAGTACCTTG CGAACCCCCC	300
ACAGTATOGA TITIGITTIGA OCTAATIOCA TIACTACOGT CACGATOTIC AAGAGGICCT	360
THEOCASCAT CACTITICOGA AGAITTICGAG CETTIACCIG CAGSCECACT CITACCCOGT	420
TTATCTGCAG GAATGTAGTC CTCATCGTCT TCATCTTCCT GTATCGTCTG TATGCCTCTC	480
CTCACGATOC CGCCCTTACG CTGTCCCTAC ACTCTTCATC ATCCTCCTCC TCATATCTAC	5 4 0
CTCTTTCCA GTCTTCTCCA CTCATACTAT CTCTACCACA TATCAGGATA ACGTATAATG	600
GIGIGACITT TTIOGATAGO ATONOTOSCO CTACGAANGO INSCGITOGG AATATAATIT	660

	AACATCTTCC CAATCACAAA TINCTCAGTA ACNGTGGTAA ATTNAAACGN AANTTTTTAA	720
5	CTITICCATAC GGTTTANGNC CCATGGCTCT TGAAANCGGA AAAATCCGGG GCCCCCCTTN	780
	GAACTIGITT	790
	(2) INFORMATION FOR SEQ ID NO:422:	
10	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1312RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:	•
	GATCATTCTC ACCAGTACAA ATGTATATT ATATGTAATT GTCTCTCTCT GCTTTTGCCA	60
25	TATTTTTTTA TTTTTTGTGG TGACAGGGTG CACTGAGGCT GACGCGCAAG CCGCAGGCGC	120
	GATTOTTOGO AACTITTOGT CAACGOCGGA CAGACAGTCA GAAAGTAATA GGAAACAATT	180
	AAATACGIIG TTAIGITATA IGAAGITATA CATAAGIGGC IGCCATCAGG TTATATATIG	240
30	CITTAAATAA COCATIOGIC TOGAAAOCIC CICIGIGAAT GOCTOGCICA AACOGGGAIG	300
	GITCTGITCG ATCTCCCCCA AATATTACTG ATAATTGATC TACACCGTCT TTTGTCTCTT	360
	GAGTCCGTGC TCTATCACGG ACOCGTCGTA ACTGTAGCGG ATAACATGTT TAAAGAAGTT	420
35	TAGTTCCTTC TGTGAAGGAG CAGCAGCTTT GAGTGCCTTT TCATCATAAT ATTGTTCAAG	480
	GTAGGAGAGG AGGTAATGTT TGTCTCTGGG TTCTTTGAAG QGCTGGATAA TAATGACTTG	540
	ATTGTGACTC CTGGTGATGG TACATTTAAC ATGCCAATCC CAGTTCCCAA GTTAGATTCT	600
40	TACCGGTTTT GITATACCTT GTTTNATAAG GGTTACTTTG CNCCCCNACT TGCCAAGAAA	660
	TOATCTIATO COTTIGANAG GICACOIGIO COTTAATIGT AAACCIACNO COTTIACAAT	720
	CTATGCTTAT ACCONSOCAT TGTCCCTGAA GGATTTTWIT ATTAACCCTG CNCACATCCC	780
45	TROCTOG	788
	(2) INFORMATION FOR SEQ ID NO:423:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 769 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1312UP	

	(XL) SEQUENCE DESCRIPTION: SEQ ID NO:423:	
	GATCAGGCAA AGGATTTCTA CTCGTATGTT GGCAAGAACC TGTCACAGAA ATCCGACAGC	60
5	AAGPTOCTIC CTCOGAGGAT TCAATTTGAA CTTCAGAGGT TTGACTATTT TCACTCTCTA	120
	CTCCAGTATG TIGTAGGATG TAACGCTCGT GATTTTGCTG TGTCACTTGC GAGGTTTCAA	180
10	TCTTCGATCG ACCCTAATAA TAAAAATACA AACATGCACC TCGTGAAGAA GTATCGTTCC	240
10	CATTICTIAC CATTIAACAA GATAAAGAGC CAACAGCGCA TAAGGCTITC TAAAGIGTCC	300
	AACTATTCTG ACTTGAATGA CTTCTACCAA CTTGCATCAG CTACCTCAGA ACCAAATAAG	360
15	CCCCTCAAAG AAGGACTCTT ATGGTCCTAC AGGAATAATG GATGGCATAA ACAGTGGGTG	420
,,,	GTACTACAAG GATCACAGCT CICAGAATAT TCCGATTGGA AGACGAAAGC TAAGGTGCTC	480
	AGCCGACCGG CCATTAATTT GACGITTIGTG TGTGTTAAAC GTTCGGAGAA AAACCCTAAC	540
20	GGATTIGATA TCATAACTAC CGACGGGGAG GCTCGTTCTT TCCAAGCAGA GTCAGAGGAT	600
	GAAATGAAGC AGTGGCTGTA TGCGCTTCAC TCTGCTGTCG GGATAATAGC CATTGAGGAG	660
	ACAGATGAGA ACAAAGATCC ATTGTCTATT GTCCGTAATG CGGATCCGTC AAATAGTCCA	720
25	TOCIGICACT GICGGAGGGA TAAGCAAGTG AATGGATATC TCIGAATAT	769
	(2) INFORMATION FOR SEQ ID NO: 424:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 799 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1313RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:	
10	GATCGIGTCT TOCTGACTIG CATGICIAGC TCAGITCTTT ATTACCCGCC TCATGITGAA	60
	ATTITICCAGE AACCATCOCA CCAAATGIAC CGATGATATA GATTACATCI ACCCTTICCGC	120
15	AAGCCTGGAA GGAAGCTAGA CCTCTAATCT AGTAGCTTGC CATGTACATC CCGCCATCCG	180
•	ACCOCCAAG ACCAGCCAAG CTCACCCCCG GCCAGCTCTG CCAGCTGTGC CACGCGCGCA	240
	AGGCGCTGGT AAAGCGCCCC AAGAACTTGC AGAAAGTCTG TAAACTGTGC TTCTTCCATG	3 0 0
o	TATTOGAAAC CGAAATCCAC AATACCATTA TOGAGAACAA GCTATTCCAG CGCGGGGAGC	360
	GGGTGGCAGT TGGCGCGTCC GGTGGGAAAG ACTCCACGGT GCTTGCGTAC ATATTGAAGC	420
	TOCTCAACGA AAGACACGAC TATOGTCTOG AGATTGTOCT TOCTGAGCAT OGACGAAGGG	480
	CATIGIOGET ACCGAGACGA TITOCOCTAGE TACTIGIGAAG COMAACCAG AGCAATTACOG	540

	TITOCCCCIG AGAITIGIGIT CCTACAGGAC CTCTACGAAC TOCACGAATG ACGAATAGIG	600
	CCTGCGCCCN GGAATGONCA ACACTGCNCC TEACTGCGGG TTTTTTCGAC CCAGCGCCTG	660
5	ATTICOGOGG GGNAATOCTT GAATOCACON NITTIGITAAN GOCCATACCO GAAAAAATGC	720
	CHAAACHOCC CANAAATCCT GOCCGGGAAA TITGGCNAAT CNAAATAACN CTTTTCCCCA	780
	AANAGGICCC GNTAANNIT	799
10	(2) INFORMATION FOR SEQ ID NO:425:	
15	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 819 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1313UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:	
25	GATCAAAAAA GATACOGATG TTATOCTTGT TAAAATATTA TATOCTATAG TACAACGTAT	60
	COCGTCAAAC ATAACOCATG AGGACTATAT TTTTAATTCA CTAACTTCGG CGAAGCATCT	1.20
	CCGGAAGAAA TAGCCTCCTG TATGGGGGTTA AGTCCATAGG CGTCGGTTGG GCTCATCTCT	180
30	GCACACTITA AACAATTAAC TOOCAACOOT ACOOTOCCAT ACCOCAAACC CCACTGGGCA	240
	CTITICTICCA CACATCCTIC TCACATACCC TTICTIACTC ACACTGGCGC AACATGGGCG	300
	COGGRAGGRA TACTITIGICC GIGCARIGRA COCTOGGRIA ARGCCCIACT TRECCCGITT	360
35	TIGAAAAAIG IGACAGICTI GITCITGATA ICTAGCITGI ACCICGITGG AGIGGGITCC	420
	TITICCAACAC CAGTOGGITT TICCGAAAAG CITOGCGTCT TOCCOCAATG AATTCTCAGT	480
	CCTGGTAGGG AACATCCGAG ACTTCCCAAA AACCNTTTCN CINICCATT TCNAAAAAAA	540
40	GEARATCHNE COGGCEATTA INCATCIETT COCARATTIAE INCINCINCE TEACITTICIG	600
	ACTIGOGRAT ANAGANCOCC NICHNACOCC TOCAAANAAA AAAAATICTC NINGIGCCCC	660
	MINATTOCCO COCGGGGCON MUTTITAATT CHCCCCAATT AAATTTTGTA TOCKNGCNCG	720
45	THISAAGCANG TEATHGCCCC CCCTTGACCC ATMITTMACT THITTAATITT TCCCCNNACG	780
	CIVITGGAAACT TITGCCNAAAG GCANGCTTTT TGAACCAGT	819
	(2) INFORMATION FOR SEQ ID NO: 426:	
5 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 791 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: HNA (genomic)	

(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1314RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:	
	GATOCATAAA CTATCTTCTC ACTOGOOGGA TOCAAAGTAT CAAGGAATAG GOGACAATOG	60
10	GEARTGATTG OCTOGRACTO ACCICAGATAT TGGCGCACTT CIGATATCCG TGGGTTGTTC	120
	GATOCATGAT GCACATGAAT AAAAGGAAGA AGCTTOGAAA GAGGTTACAOG GCCCGGGTTAG	180
	CONGRANGA GAGCTIGTTAG TICCOCCTICA ACATCAOCAA GITTICTICTIAT ACCOGACOCA	240
15	GOGTOGTCAA CATCATTTAT TAGACACTCC AGCAGTTTGT CTGAAAAAAA GGTGTGCATG	300
	CACAACTOCA CCTCATOCTT TGAGATGOCG COGATAACGT CCCTCAGCGA CGCCAGTCTC	360
	ATCOTOCAAC TOCOTICAGAA AACTICTTGAT TGATAOOGTA ATOCAGTICAG AAGAAGTOGT	420
20	TAAAAGCACT TICGATGCCC CAGTGAAACC TAATCCTCGT COGATATAAA ATCGAACGTG	480
	TEACCAACAA TOTECCATAT COCCAAAGEG TETEACAAGC TECHTACGAT TETECCACTOC	540
	TOGATIGNAT ACTICOGROCIN ANTICITITIA CONTATACAC CONVINCING COTTITIGOAC	60 0
25	GAATTONITA TITGITGAAG AACTGGACAC TITGAAACTT TOCACATTOC NGANICCGAA	660
	ACNOTTITON CNOCCAACTA ATMINAACCO CAATCCIGAC CCAATACACT CCCCCCCAAA	720
	CATGACCCCG CACANGATIN TITTITICCCN AGAATTINIT NAACINITIG CCCCCTNANA	780
30	CATTNIAAAT C	791
	(2) INFORMATION FOR SEQ ID NO:427:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 833 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1314UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:	
45	GATCHTOCHE CAGACAGATE CCGCGGAGCT ACCCTTTCGA ATCCTTATAT AAACCCTTTT	60
	CCASCIGIAC COCAGIAAAC TCCCCITOCT TCAGGACCIC CAGGCTGCCA COCACACICG	120
	ACCOCTACAC COCTICACTOC ATTOCCTTCT CTOCOCACAC CCAAGTCTTA AACCAACCTC	180
50	ANTOCCATCO AACCAGITOT GOTAACGTAG CTACTICTIGG CCAATCGCTC AGCCCCATAC	240
	OGTOGAGOCA ATCTTTOCCAA GOCCACATAAA OGAAACCTIAC ACAGTTACTG COCCAAGOCAA	300
	CTCCCAAAAG ACCACAGGTT CCGCAGTACC AGACCAAAAA GCTTACCTGT CAACACTTCG	360

420

AACATTOOCG TOGOCTTTAAC CATATOOCAC ATGAAGCAAT ACACOOCTAA AATAGAAAGC

GARTGGCCCC GAACAGACAT TCCTGGTGTT GTACTTGGAA CTCACATAGG GGCTGCACAC	480
TGCTTAAGT CCTCGCTTGC AGCTGAGGCC ATGTGCCCCT CATTAGTGAC CCACGTTGAT	540
CTCGAGCCCG CAAATGATCG TCAGCGTGCA TCCGACTTGG CATTGCAAGG GATGTTGATC	600
CCCTGANGGG AGGCTTGCAA CAGCGCCNCC CTTGTTTCNC ATCCATAGGC TGTCGAGGCC	660
GGAATGATCC NCTCTCCAGG GGAACNCCCT CCCCAACGCC CCATAGGGCC CNCCCTGGGN	720
THITGCCCGG ANACTCCHAA NCHINGGTITA AANHTTITTI TIAAAHGNCC CAGTGGTHTC	780
AAGGCCCCCN NGCCTTTTTC CANCCCGCAN TERCTNAATT TTTGNCNGCG GNA	833
(2) IMPORMATION FOR SEQ ID NO:428:	
(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 839 base pairs (B) TYPE: nucleic scid (C) STRANDEDNESS: singls (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DEA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1315RP	
(xi) SEQUENCE DESCRIPTION: 68Q ID NO:428:	
GCGGCCGCTC NNCCAACTAG TGGATCTTCA TTTGTGGCCC GGCCGACAGG TTACCACCGC	60
TTTTCTCCC CGTCAGCATC TCAACTAGCT GCTGTAGCTG GTACTCCCTG TCGCCGCGGA	120
ACACCITICA CITGICIATI CCTCTOCATG AAAGATCOTG CAOCTGAACT ACATTACCGT	180
ANGTONICAG CCCANCANGC GCGTTGGGGG GCAGCANCGN CAGAGAGGTG ATGATCGANT	240
COTTCAGCGO CTGGAGGTTC TOCTCCTCCG COOTTACGTC CACGACGTAG AAGAAGATCG	300
GEGERACETG CACEGGEEGA TITGTGATGT ACTEAACEGT CGTGGAGTTE AGTTCEGEGG	3 6 0
GENTEGEETE ETGAGACATG TTESCATAGT GETGEGGAAG ATGOTTEEGE GTEEEGGAC	420
AGAGGGCACG CCCACACGTT CGACCGCACG TCGATCTCGC AGTACGGGTT CAGCACCCGC	480
CTTACAGTGT TGGCCCCACC CACACCAC CCGGTTTGTT ACGAAAACCA CCGCCCAGCT	540
CCCTCCAATC TCCTTCCACC CCGTTGTTAC AGCATCCCCM CCGGCNCCAC GTTCCTTGTT	600
CHCGTTCCCG TCCGGGAAGC CCGGGAAAAC ATTCCCACGA MAACCGCACC CCHTTTAGTT	€60
CTTCCTTCCT ETTTCGAANC CACCCTTGAA CCGNGANCCA CTTTTANNCC CCTTTACCCC	720
CTTTGATCCC CHCCGAACCC CCHAAATGGA ACCAAHNAGC CCHTAACHBN TGCHAAAACC	780
CANTIGUES TITCARGUES CERTOSTITE OCCCCONGA ANARAMINE NOCCCCONA	839
(2) INFORMATION FOR SEQ ID NO:425:	
(i) BEQUENCE CHARACTERISTICS: (A) LENGTH: 818 base pairs (B) TYPE: nucleic acid	

(C) STRANDEINESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1315UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:	
	CATCTTOCGC AATATCCCCT CCCAATCCCT ACCCATCCAC TTCGACACTA CCGACTGCAC	60
	COCCAGOGTIC TITCATICOGCA CAAGCTIGCTIC TICCTAGGCTIC AGCACCGGGG GCACCAGAAA	120
15	GTAGAACCGC CGCGTGGTCT CCAGCTGCTC CCGCTGGTTG CGGAACGACA CGTAGTAGCA	180
	ATACCACCC GCTACCTACA CATCCACATC CACCCACCTG TCCTCCAAGA AACCTGCCCT	240
	CAGCAGATGC TTGTAAAACT TGTTCCCCTG GAACTTCGTA TTCCTTTCCG GCCCCAGTT	300
2 0	GOOCACACT AGOCCOTOCC GTGTCACAGG GGATOCGGCG GCTACCACCA ACCGCACCG	360
	CAGOCCOCTG TOCTCCCCAG CGTCTCGGCC AACAGGTAAA CATGGCAAGG TGAGCACACC	420
	CITICCAACC TCTCCTCTCA CCGCCTCCCC GITGTCGTCT AATCTCAACA GCACGGITTT	480
25	CATOGCTGTT TGCGCCCTTT GCTGCGATCT AAAGGAAGCT TGCCTTGTCA TGCAGCTGCT	540
	AGCCTIGGGA ACTGCCATAG TCCTTTGACC TIGACGCCGT GITAAATAGT GCATTTCAGT	600
	ATACACAATT TGACTTAOGN NCTCCCNCNG TGCTAACTGA GGGANATTAC CCNAAACCCG	660
30	GANGGGANNA TAACNGNINA NAATTINCCC GGINGCACNC MIGCCNIAIG NITCCNITIT	720
	TOGAAANAAA COCTNOOGNU OGINOGITIGN NAAAAATTIGA AAACOCNOGU TNAATACTINC	780
	NITINACINITIN TOGGAAAACA AAANINOGGC COCCCCGN	818
35	(2) INFORMATION FOR SEQ ID NO:430:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1316RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:	
io	CATCCAATAT ATCCCATGGT CTGAAGGGTT GTCCACGTGA GTAGCTTAGC GAATACTTTG	60
	CCAMBOCGIC TOCCACATCA AGANCAGTCT CAAGATAATA ATAGTOCTTT TTGGGCAGTA	120
	AGCGAAGATT GTTCCTCGCC TTTGTCATTT CTGGCCGGTC CCTGGACCCA TTTGGTGCGC	180
5	TGTTGAAAAA GCGCCAAAAG TACTTCAAAA TGACCGATTT TTCGACCTCG AAACCTCCCT	240

	OGAGAGAGAA GIOGIOCASO AACGIAAATT CACTGAGAGA CAGCAGTGIT TOGATAATTG	300
	CAGATTCTTG ATTCTCCTTC GTTAATTTTG GGTACAATTT AGATGAGCTT AATAAAAATT	360
5	GTAGTGTCTG GACAGATGGC GATTCAGCCA ATAAATAATG GCTGATGGAT TAAATGATGC	420
	CASCIGOSCO AACTCATCIG CATTOSCIAA GGAAOSCATT GATTICAGAC TATAGITATT	480
	OSCASCATOC ATGIACTITIS TIGIACTOGA TOAGGTCCTT CACTGAGACA COGTCAGAAA	540
10	GOSTCACOST CTCGTCAATG AGTTAGAGCC ATCCATAGAT TTCCCCGAGG CAGTTCCCGC	600
	CATGAATTTC CACCCACTTC CCCCCCGGTC CATACCGCAA TTTGAACATT CCCGGTCAAT	650
	ACCITICITICE TECCECOGNI NITICENCAAN AGGGAAGITA NATICETGNE CITTITITIN	720
15	AAAACCCAAT TCNCACCTTT TCNCGCAANT TTTCCCGGTT GAGNAAAANT CCNACNCCCG	780
	GINGCOGGIT TRATINCO	798
	(2) INFORMATION FOR SEQ ID NO:431:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 820 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1316UP	
30	(A) ORGANISM: PAG1316UP	
30	(A) ORGANISM: PAG1316UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:	
30		60
30 35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:	60 120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC	_
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA OCCACATGAT GGTTTTCTTG GCGGGTGGGC GGTGCTGGGC	120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431: GATCAACACT COTACAAACE AATATAGTCA CATGACCAGA TAATCOTCOT GACTOGCACC CATACATCOG CACCCATGCA COCCACATGAT GOTTTTCTTG GOGGGTGGGC COTGCTGGGC GGGCTCCCCCC GTCTACGCTG GOCGGTGTAG GCGGCCCCCCAG GCGGAGCAAT	120 180
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA OCCACATGAT GGTTTTCTTG GCGGGTGGGC GGTGCTGGGC GGGCTCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGGCT GGGCGGCCAGCAAT GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGCAGCAGC TGGAGGGTCC GGCATGTGTG	120 180 240
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGGGCC GGTGCTGGGC GGGCTCCCCG GTCTACGCTG GCCGGTGTAG GCGGCCGCCAG GCGGAGCAAT GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGGCAGC TGGAGCGTCC GGCATGTGTG GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT	120 180 240 300
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC GGTGCTGGGC GGGCTCCCCG GTCTACGCTG GCCGGTGTAG GCGGCCGGCT GGGCGGCCAGC GCGGAGCAAT GGGCGGAGGA ACAGCGAGGG CGCCAGCAGC GGTGCGCAGC TGGAGCGTCC GGCATGTGTG GAAAATTTGT ACAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT AGGTTTGAAC ATACTATACA AGCTCCCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA	120 180 240 300 360
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC GGGCTCCCCG GTCTACGCTG GCCGGTGTAG GCGGCCGCTT GGGCCGCCAG GCGGAGCAAT GGGCGGAGGA ACAGCGAGGG CGCCAGCAGC GGTGCCCAGC TGGAGCGTCC GGCATGTGTG GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT AGGTTTGAAC ATACTATACA AGCTCCCCAAT CATUCACGAT GGCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTCGT TGACCCCATTC ACCACAAAGG	120 180 240 300 360 420
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATOGG CACCCATGCA OCCACATGAT GGTTTTCTTIG GCGGGTGGGC CGTGCTGGGC GGGCTCCCCCG GTCTACGCTG GCCGGTGTAG GCGGCCGCCTG GGGCGGCCAGCAAT GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGCAGC TGCAGGGTCC GGCATGTGTG GAAAATTTIGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT AGGTTTGAAC ATACTATACA AGCTCCCAAT CATCCACGAT GGCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTCGT TGACCCCATTC ACCAGAAAGG AATGGTACGA CATTAAGGCC CATCCACCTT CGAGAACAGA AACGTCGGTA AGAACCTTGTC	120 180 240 300 360 420 480
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA OCCACATGAT GGTTTTCTTIG GCGGGTGGGC GGTGCTGGGC GGGCTCCCCG GTCTACOCTG GCCGGTGTAG GCGGCCGCCT GGCCGGCCAG GCGGAGCAAT GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGCAGC TGGAGGGTCC GGCATGTGTG GAAAATTTIGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT AGGTTTGAAC ATACTATACA ACCTCCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTCGT TGACCCATTC ACCAGAAAGG AATGGTACGA CATTAAGGCC CATCCACCTT CGAGAACAGA AACGTCGGTA AGACCTTGTC AACAGTCCAC CGTTTGAAGA ACGCAGCTNA CTTCTTGGAA GGGCNNTTTC TTCAAGGTNT	120 180 240 300 360 420 480 540
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431: GATCAACACT CGTACAAACG AATATAGICA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC OGTGCTGGGC GGGCTCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGGCT GGGCGGCCAG GCGGAGCAAT GGGCGGAGGA ACAGCGAGGG CGCCAGCAGC GGTGCCGCACC TGGAGGCTCC GGCATGTGTG GAAAATTTGT ACAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT ACGTTTGAAC ATACTATACA ACCTCCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTCGT TGACCCATTC ACCACAAAGG AATGGTACGA CATTAAGGCC CATCCACCTT CGAGAACAGA AACGTCGGTA AGACCTTGTC AACAGTCCAC CGTTTGAAGA ACGCACCTNA CTTCTTGGAA GGGCNNTTTC TTCAAGGTNT NGCNTTGGCC AACCANCNGG TTCNTACGAT TNNCNCTTCC NAAAGGTTCA ATTANAAATT	120 180 240 300 360 420 480 540 600
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGCC CGGCTCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGCT GGGCGGCCAG GCGGAGCAAT GGGCGGAGCAA ACAGCGAGCG CGCCAGCAGC GGTGCGGCAGC TGGAGCGTCC GGCATGTGTG GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT ACGTTTGAAC ATACTATACA ACCTCCCAAT CATCCACCAT GGCTGTTGGT AAGAACAACA GATTGTCAAA GGGCAAGAAG GGTTTGAACA AGAAGGTCGT TGACCCATTC ACCACAAACG AATGGTACGA CATTAAGGCC CATCCACCTT CGAGAACAGA AACGTCGGTA AGACCTTGTC AACAGTCCAC CGTTTGAAGA ACGCACCTNA CTTCTTGGAA GGGCNNTTTC TTCAAGGTNT NOCNTTGGCC AACCANCNGG TTCNTAGGAT TNNCNCTTCC NAAAGGTTCA ATTANAAATT TACAGGTCCC NGGGCAAAAAC CCTTUCCCCGG TTTGGGATTC CCCCCCCCNA	120 180 240 300 360 420 480 540 600

(2) INFORMATION FOR SEQ ID NO:432:

s	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 807 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1317RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:	
15	CATCITIATO TITOCATGAT ATCITITOCTG AAGAATOGAC AAACACCTGG TOCAGCAAAT	60
	TOGANOCIAN GICTOTOCAN TOGGATOCAN ANTAGITIGAC ATRACOGOGON TITANCTITON	120
	CTAACOGGC GGCACCAATA TOCTCCAGAA CTGTATTTAT TTOGCTAGGC TGAACGATTT	180
20	GITCAATCAG OGTAATATTIC GICAATACAA AGAACCCAAT TCTCTGCATC TGAGGTATCC	240
	TTTTATGTGG ACCTCCGACT TCCGCCTCTA ACTTTGGATT TAGAATCTTT TGGCCCTTGC	300
	OCTICIAGAGA TATOGITIAAG TAATICIATAG CATOOCTIGAA GAAGCAAGAG AGCAATTOCT	360
25	GIGCATTOIT COGIGICATA GATATOGICO AAACATTIIT TGATTCATIG GOCAGCCATG	420
	ATTCCCCACT CATCCATTGT ATACTACCAA CCCAACCACA CTTCTATTCA CTAAACTTCC	480
	GINGICIGGA CATAACATCA ACTIGIGGCCT CCAGTTACAC CATTATCAGT GGTAACTICAG	540
30	COCACACAAG COCTITITICA COCATCIACT TGINICNATO TITTICAACA NOCACNOCCA	600
	AATTTCATTT CANGTONGOC THOROCOTCC CAAAACHGIT CONIGGITCT NGIAAAGGIT	660
	TNIVOCCTABA BATIVOGOVIT COCNIGINAG MITOCOCCOC BATICHABON NABNACOONA	720
35	TITTINIAAT TOOCOCNOCA AAATTCAATT ATACOCCOCN TITINGGIAT INTAAATTIN	780
	GCCCCVLTCN NITICCAAAAA GCCVCCNG	807
	(2) INFORMATION FOR SEQ ID NO: 433:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 835 base pairs (B) TYPE: nucleic acid (C) STRANDERNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1317UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:	
	GATCGITCIT ATATTIGITA AAGAAGAGIT TICITCAAGC ACTTIGAGCT GAATAATCIT	60
55	GTCAAACATA TIGICAGGOC TCCGCTGGTC GTTAACCGGG CGAAACCTCT TGAGGAACCC	120

	ATCTAAGATC ATAATTOCCT TTTCTGOCTC OGATAAAGCT TTAATAGATT GATGGTTGTC	180
5	GCCTCTTTCT GCAACGCGGG ATTTAGTTAT TICTCTAACG GATTCCACAT CCTTGTAAGT	240
	CAAAAATGAT AAACACACCA CITTGACTOC ACTOTTOTAC OGAATATAAT TCTCCTTCAT	300
	CITITICCAAC CATTOGAAAA GITGITICOG CTOGAACOOC ATATGATTIGT TICTIGICCAC	360
10	AATTACAGCT CTTGAAGTAT CCTTTTGTAG AAACTCTAGC GCGTCACGCA TCAATTTGCT	420
, -	CITATCCITA GIAACAATAT TATCATICIG TAIGIGGCCC CAGGACICIC CAAAAATATI	480
	CTTCAATGCC ACCOCGACTG TOGTCTTTCC ACAACCAACC GTGGCCACAG GGAATGAAAA	540
15	TGAACTTOGT ATCTCGTCCT ACCTTATOGA GCTCCAGATG CATACTGGTC CCCCCNAGCT	600
	CCTTTATATC CTCCGAATTT CCATAATATC CAATCCCAAA ATCCCCAAAT CNITCCTAGG	660
	AANATTITOO NNAACINGAA ATCCCCTTAC CITGINIATA CCCCCTGNAA ATTINGGAIN	720
20	TIGATICONG CCACOGANIA CNATICOCNA TITTINITIG IGANNAACAA NOCTITIGAA	780
	TITITGICCC CNCCCNCTGT GNANTACCON CCCTCCTCCC CCCCINITIN TIACN	835
	(2) INFORMATION FOR SEQ ID NO:434:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 748 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1318RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:	
	GATCOCCTCG TCGTTCGCCC GGCTCGTCAG GCTCTGCGCA AGGAACTGCC GGAACCGACC	60
	AACCAAATCT GOCATGTCCT TCGCGTAGAT GAAACCCTGC TGCTTGCTGT CCACCGCATC	120
40	CCACACGITG TTCAGAATAC CCTCTGCCTC CGTCATGACT CCTGAGCCGT GAGTGCAGTT	180
	CCCAAGGCTT TIGTIGIGCT TGGCAGTTGA AACGACGCTC GCAGCGGCAA AACAACACCG	240
	GCCCCGCCCC AATTOCTCAC GTGCCTCCTC GCGCCACATA AGCACGCACA CCCTGACCGC	300
45	ACACGCACCC TOCAAAGIAG GICATCACCA AAGGGGGCACC CCGCCTGACC GITGCCTGCG	360
	TOGASCASOC OCCOSCOAGS COCCAACOSC CACCASCATG COCSTTCTCC GTACCCGCCG	420
	COCCCTTGG CCATCGCCCA AAATACCICG GTTTGGCCCA CTCATGCCGT CTGCCGTCCG	480
50	COCCECCOCC COCCCCCCC COCCCCCCC COCCCCCCCC	540
	GETCACETET GCGETTACCC GGGCETCETT TAGATCGAAG GITCTAGGTC TETGCCETGC	600
55	GETICACETET GOGETTACCO GOGOGICETT TAGATOGRAG GITICTAGGIC TETICCOGTIGO TECCCCTTET TETICCTACOG CCAACAGTIGG GOGOGGOGTA COCOGCAGGIC ACCACGTIGOC	600 660

	CTATITIACAG GOCACTITAGG NGTTGACC	748
	(2) INFORMATION FOR SEQ ID NO:435:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 758 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1318UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:	
	GCAAAAAATG AGGTCCGCCA TOCGCCGCCGG CTCGCGGCCCG TCCGCGACCA AGCTCCGCCG	60
20	CCCGTCCCCCG CCCCACAGOC ACCAGCTCGC GCCTGCCGCGG TAGCTCGCGC CCATCGCGCA	120
	GICCOCCACC GCCCCCCCC CCCCCAACGT CCACAIGICG CCCACCACCT TCTCGICGAG	180
	CACACOCCC COSCACSTOG CCOSCOCCIOG COCCOCCOSC GOCACCTOGC GCTOSTIGOSC	240
25	AGCCAACTOG CCTGTCATGA ACAACGCTGT AGGAATGCCC ATCTTTGCCC TTTCCGCTCG	300
	CIGCOGCIGI GIGIGIGCTA TACOCIGCCT TATATACCIG CCAGGAGAAA TGTCIGCTAC	360
	TATCCCCCCC AAAATATCCA TCCGATGCGA ACGGCGGAAC TCGCCGGAAA CCTGCAGCCC	420
30	COCCICIGIC GATCGIATGS AGAAACAGCT AAAATCGCIC AGCIACTCAT CTCTGGCGCT	480
	GIGGITICACG GICOCCOCAA TOCCOCCACAT OCCCAAGICC GITTITITICIC TGIGOCCOCG	540
35	CCACGGACAG CGGGGGCAG ACGGCCAGAT TTTGTGCACG GCAGACGGC TTGGCTGTGG	600
33	TAACOCCTAT GAAATACGOC GAAGOGOCGA TTACCAGTOG GTTTCOCTGT CAGGGGTGCC	660
	TOOOCCOCG GAACCCCGTT ATGGTCTATA TTACAGAATG TGTACAAAGG AGTCACGTGG	720
40	GOOGGETOGC GOOCNOGACA GCTGCCTCTG TTTCTTCC	758
	(2) INFORMATION FOR SEQ ID NO:436:	
4 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 801 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
5 0	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1319RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:	
55	GATCHICCTG CONTINGACO TOTACATTAA TOTACIOCIT TAACHTCITH TOOGRETICAA	60

	GAATGICIGI TAGCAGITCC TOTICCIGIT TCGGTTICIT CCIGITCCIC CIGCCAAGAT	120
	GCAGCATCGA GITTTGCTGG ATGGGCAAGA AATTAGAATT GATATCGCCG ATCCCTACGA	180
5	AGAAATOGTA COOCACAACO TIAATGAGAT TCTCOCACCA GITOCAGACA TCACCTCTAT	240
	COTCAATGAC TACGACCATC GACTOGTCCA TCGGGAACAG ACGCTGGAGT GATTTTTTGGG	300
	TCAGOGAACC GTTTTCATCG CGTGACAAAA TTCTATCGCC AAAGAGCTTC CCATCCGGGT	360
10	CAATTATCTT GGCAATCTCT AGCGCATAGG CTCGAGTAGC CATGGTGTAT ATATGCAGCT	420
	CGAAATOCOG CGCGATCITC GCAAAGAATT CCTTCAGGCC TGGCCGTAAT TTCACGTTAG	480
	TACCAACACT TOUGCOGFIG GITGOCFFTT GCCCCCCATA TAGAACOGCG GCAGCACAGC	540
15	TOCTOCATOC GANAGANAAA AACTGONCAT COTTAGOGOC COGTATTOGG GITTGTTING	600
	GITCCCITTG ACCACTCCCC CATGGTGGGT TCACACCCGC NATINGATTICN CCGTCTGGTT	660
	CAATTITIACC CCCAGCAING CITIGOGONON TOONNICAAC TITIGACTIGON CONCTGACCA	720
20	AAATOCAACT TOCVITOGAC CCGATTIGIT TITTIVITIG AAACGWANI TOCINGIOW	780
	CTTGGCNCCC CNCTTTCCCN A	801
	(2) INFORMATION FOR SEQ ID NO:437:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 834 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI319UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:	
	GATCATCOGC ATOCTOGAGA ACCCAATTITE CCAGTCTCAG ATGAACGAAA TOCTCAACAA	60
40	CCCGCAGATG ATCGACTTCT TGATACAGCA GCACCCGCAC CTGCAGGCAA TGGGCCCGGC	120
	GOOGOOGAA ATGCTCCAGA GCCCCTTTTT COGCCAGATG CTCACCAACC COGACATCAT	180
	TOSCCAGATG TOTOGOCTOC AGATOSOCAT GOGGGGTGCG GOGGCCCAGC AGGGCACCGA	240
45	CTTTCCASCC CCCGGCTCCG CCGCCACACC CGACGCCGCC GCCCCTGCGC CGAACCCGTT	300
	GOUTGOCATO CTAGGOTTGC AGCCCGGCGC TGCTAACCGG CTGGGCGCTG CGCCCGCAGA	360
	CCGCGGCCTT GCAATGCCCC CTCTAGACCC GGCTATGCTC TCTTCCCTCT TCGGCGCTGG	420
50	GCGCTGCCAG CCCTGCGCCC GCCGAATAAC AGGGCTNCCC AAGNANGNGN TANCAAACAA	480
	ANATTOGOCC ANGCINAATN AATTNOGGON TOTOCAACTT GAANAAANAT TICCGGOCTT	540
	ANATTOGOCC ANGCINAAIN AATINGGCN ICTCCAACIT GAANAAANAT TICCGGCTT NAAGCGCNCG AAGATGITCT NICHNGGGC CCCTTNIATT CTTINNIAAA GGNAAANIIN	540 600

	TTGINITCTC CNINCTONIT TOONACCOCA CNCAATTITT TTINGGTOOG GOCTNOONIN	720
	TITICAINN TINCNANNAC CNCGNIAATT ATANITGINI ATCACGICCT NITINITITT	780
5	NNCONACNON TROCGREGOCO CONTINANNE GACCINICIGIO TAGGGAAAGA AAAT	834
	(2) INFORMATION FOR SEQ ID NO:438:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	-
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1320RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:	
	GATCTTTCA AGAAGTTTAA CAATGACTT AAAGCTAGCA TTGATAAAGT ACTCAAGAAA	60
	CCTAACAGAG COGAGATGTA TGATOCTCTT TTGTCAATTA ACGTCCATTC TAACAATATC	120
25	ACCTOCOGEAT TGAATAGACC TATCTCCACT CCTAATTOGT CCTTAAACAG ATTTAACATG	180
	GAACGIGCIC GIGITACCCA IGICITGAGI AGGCITTCIT ATATTICIGC ICIGGGIAIG	240
	ATGACAAGAA TITICTTCGCA GTICGAAAAA TCTAGAAAGG TTTCTGGTCC TAGAGCTTTG	300
30	CAACCCTCOC AGTTCGGTAT GTTGTGTACA TCCCATACOC CGCAAGGTGA GGCCTGTGGT	360
	TOGITAAGAA CTTAGCATIG ATGACACATA TTACCAOGGA TGATGAAGAG GAGCCCAATA	420
	AGAATCTITG CTACTTACTG GOOGFTGGAG AACATTACAT TGOCTAAANA ANGGCNCCCT	480
35	TOCTTTTAAA TNINNOOCCIT TTTATTTOGA AAGGGTACTA COCCCOGINC ACAAAATCCC	540
	CCCCCONSTIT TIGHTCCCCC TITTAAACIN TANAAAAAAC GNSTAAATTI CCNNATTICI	600
	TTTCCCNVIN TCCCAANNAC CTCAAAACTT NITCTTTTGC AAGGAGGGG GAAATTIVIN	660
40	ACCCCTTINI TITNINGGAA GAGAATTITT GICCCGGNGG CCCCCAAAAA TTTTTAAGGG	720
	GAANTONITA NATTOOCNAN NOOGGNINNI AATTITIOGN TITTANAAAA AAANOOCOCC	780
45	CONCOGNIVAA A	791
45	(2) INFORMATION FOR SEQ ID NO: 439:	
5 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 844 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

	CATCATGAGG GAATCCTTGG AAGAGGATGA CAAGAAGTCC GACGATGAAG GTGACCTGTC	60
5	TATTCCAGAT GCGCCTTCCT CTGAGGAGGA TTAGGCATAT AATGGGTCGT TTATATGTAC	120
	ATTAATTAAC ATTOCGOTTT AGGTTTTTTA CICTTATCCT TAGGGTAGGT CAGCCATATC	180
	TUTAGOCCIG CTCAGITATC ACTAAAACGA GTGCCAGGCC CTAGTACTAT ATAATCCCGA	240
10	GTTCGAGCTG AGAAACAATG TCTGATTCGG CTGGTTTGCA TGGGAGTACC GCGATGCAAG	300
	ATCCAGATAG CACTITIAGTC GAGGAAAGGT TGGCGGCTAC GCCAAAAGTT ATCAACAAGG	360
	TCAGCAAGAA AGGITCAAGC CCCCTTTCAG TGTTTAAGTT TAAAGAGGGG AGCCTATCCT	420
15	OCCMAAANIG COCCAOOGIN CNIGAATTIN OGAGAAAAAA NIGCGITTIT TOCCGGAAAAAG	480
	COCCCCNTGA NACCAAAATT TATTAGGGAC CCNCNACACC NCGAGAAATT TANTTAAGN	540
	OCOCCCTTTA AAATNCCCAA TNICTTCNAA ANNATTIGAG GNOGAAAGAC ANITINITTIN	600
?0	AATINCOCOG GOOGINITIT TIGCCGCCCC GGNGNICNIC CCNCCICCAC NANITINAAA	660
	NATAGSAGEA ANDOGNOGNE OCCANATITIC CACCITTONN AGITINEANNG CONGNAAANA	720
	GNATGCATION CCACCAATING GGGTGNINGA AAANANIINGN NACTGCTTGT ACACAAATTT	780
25	TTTTGTGCCG CNCGTGACAG AAAAAAACAN GGATTTTTTN ACAACCNNAA AAANAAAAAA	840
	AAAA	844
30	(2) INFORMATION FOR SEQ ID NO:440:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 788 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1321RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:	
	GATCACGICG TICCIGGACT TICTATCGIC GACGGIGCIG TICIICAGCC GGGAGGGGAT	60
15	ACCICUTORCO ACCICTOCCICA TCAAGACOGG CGCCCACCACCGC GCCCACCATGTC	120
	TOCOCACCTG CAGACGCCCC TGAATTTTOC AAACATACCC ATGTGCATCG GGGCCCCCT	180
	GOCCGTGGTG CTGGCGGTGT GOCAGTACTC GAACCTCAAC AGCTACTTCA CGCAGCTGCC	240
60	GITCTTCTCG TOGTCCATCT ACCTTGTCCT CCTGTCCATC CTCCCCCACC TCCCCCACCCA	300
	OCCOCTIGIAC GIOGIGAACC AGTICATOCT GAACTACOOC AACOOGTOGC AGTICGAGGG	360
	TOCOCCOGTIA OCASCOTOCT OCCTOCTCAA CTTCOCCGGTG ATCTACTOCT ACCACAACTG	420
55	GITGAATGGG CGCCCCAGAC GITGCACGACA GCTACAGCCA GGAGGCATCG CGGTGCTTGC	480

	TITINCOCCE GEGAAGGIIG COCCONCCAA AACTIINOCT GECCCENTOT ACITGAANAA	540
	CTTOCONCTC TOOGOCCOCA AAAACTTTTT TCCCTTTNIT TNACAAGTTC CTTTTCCCGN	600
5	NATTITITAC GOGNI'INITO CNOCCONAAT TINITOCCCC TICCNAAGGT TITTTOCCCC	660
	INITINITIA NOCONOCTIN NCAAGGGGGA AANNITITIN CITOCOCCNC CCCGGGAGAA	720
	ANNOGGANT TICCTITITT TTAAAANGON NCCCCCCCON ANGNITITNN CCCCCAAGAA	780
10	NATUTU	788
	(2) INFORMATION FOR SEQ ID NO: 441:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 815 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1321UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:	
	GATCCAATTIC CATTTCCTTT COGTCCAAGG AAACAGAGCC TTCCTTAAAG TOGGATACGA	60
	AGACCGTGCC CAATTTTCGT COGCCCTTTC TACATACATC TCAAGCGAGG AACTTATCGG	120
30	CGTGCCATTA GTGGTCCATA TATTGCAAGA ATGTACAAAG TTAGAGAGGA TGAAGGTTGG	180
	OCACCACT CACCTATOCT TCAAAACCAC TITOCACCAA NAACTANOOC ATTCCACTIG	240
	TAATTAGCTA CAAAAGCOGA ACGOGTCACA CTAAAATTCC ATGCGCTAAC TTTTCCACTG	300
35	AAAGAAGOCA CATGAAGCTT TTATATCTTC TGGGGCTCCT CTGGGACGCT TACACGTCCA	360
	GAACTOTTIC CCAAAATICC TCGACGITTT CGACGITTTA ACAACCGATC GGTCTCCGTG	420
	CTTOCAGAGA GGTGCATTTG ATGGGGCGAA AAATGGTTTT TCAACCGCCG AGGGTCGTTG	480
40	TICAGGAGCT TIGHTAGTIC GAAGITIGGAG COCCATICCA TIGATIGCCC CITOCICTIC	540
	CTCCCTNGCA CTTGCCGCTT GCTGCTATGT TTACTTACTA NAAGCACCGA NCCACACTTA	600
	TOTOGRAPITY TYPICCIATO CIGANACIOS CITGAATTAT TOOCTOCTIT TGACTITOCO	660
45	CCTGFTCCAC GITNGTTACA CNITTCCTTT GAATAICTTT CCTTTCCGAA GCACCCATINT	720
	TTATAATTAG TOCTATTGAC COCCCCACC TOGTTTTTGT TTTCCTCCCA ACANGTTCTC	780
	TICICCACIN AGNITIGIAT ACNGAATGIC NACCC	815
50	(2) INFORMATION FOR SEQ ID NO:442:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 773 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1322RP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:442:	
10	GATCCAGGAA ATAGTACAAC OCCCTTOGAT AATGCCAGOG ATTCCTGACT CCTAACGAAA	60
	AGCCICICCT CITCTAATIT CTTATTAAAG TAGITAGCIG CAAACTGIAA CAAATCCCCC	120
	GOCCOTICTTT GCTCCACTTC TTTCTGGAAT GCGTCCAGTA GGTCACGGTG TTCCTGTGAT	180
15	AAAACCATCG AGTAGTTTGT TGTGTGATGC AGAAAACCTG CCTATAGCGG AACCAAAATG	240
	CTCTAGTAGT GTGAGGGCAC CGTTTTATCC AGTTTGCTAA GCAGCTGCCC TAGGTTAGGG	300
	ACAGIAGAAA GIGICATIOG ACCCGAATIT CCTICIGCGC GCGGCGAACG ACGITAAATG	360
20	TGATTCACGT GATCACCCTA CTGCCCCTAA CTACCAATTG AGACACCCTA GTTGTCCGAAG	420
	CCTGAGGAGG TCTCCGAAAA GCTTGATGTG AGGATACTCG TGTTCAGTTA TCTTGTATGC	480
	CTGTATTGAT CTGTCCGTGA GACCTCGAGC TCTTCGTCCG TCAATGCCCC GCCCCTAGAG	540
25	AGCTAGGTIG ACICCOGAGIT CIACAAAATT TONAAACNOC TIGAAAATIC NCAACATIGT	60 0
	THIOGACCAT CHANFICCCC NCCTTCGGAA NNAAGCCCTC CANCCTTTT THACGITCCT	660
	NACTINOCON CIGAAAAAAC GIIKNAITIA COCINIINIA CNOGGCAGGA AACCCCCCAN	720
30	TICTPITTOC AINAACCOGT ANCINAAAGA AITPITCNNOC CATGNOGITT ANG	773
	(2) INFORMATION FOR SEQ ID NO:443:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 817 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1322UP	
4 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:	
	GATCTTCACA ATGGACGCCA OGTGCATGGC GATGTTGGGC GGCACTGCGG TCACTGTGAG	60
	ATATICGIAC GGAGAGAGCC GGIAGGIGIT GATCATGAAG TIGGGCACAT CCITGTAGGC	120
50	TITIGGCCGTC TICAACCGCA CCCAGTCGTT GAAAAAGTCG GGCAACGCGC GACGCTCCAG	180
	CTCATGGATC TCGTTGAACT GGAACCAGGA GGCAAACGAC GGCACGATCA COGGGTGCGC	240
	CTGCTTCGCT AAGAAGCGCG CCGCCTTGTC CTCCAATTTT TGCGCCTCCT GCTCGTAATC	300
55	CATCHTOOGT TGHTCCTCCT CCTCCTCCTC CTGHTCCAGA TGTGGCAGCA CAGGHACAGA	360

TOGATICACG CIOCCOGTIGT TOCCOGACGA AAGOGTTCCA TOGCCAGOGT TGTCAATATT	420
GCCATCCTGG ACATCCATTG OCTOCCTCAT CGTTATAAAG AGTATCCCAC OCTACTTTCC	480
COGITTAATA COTTCAAAC COGTCTTOCC TOTOCTACCC COCTTAANTO CACACTOGTT	540
TIVICTITICC NOCATACOCA AANITITAAA ACCCATITITI CCACATCACC CCCATATCCT	600
COGITICGIN GNOCAAATTI GAAACCCANC CCICOCCICG COGAAAANNC INCITATOGA	660
COCCUTTOCC MICITICAAT COGTOCCCTT NACCAACANT TTAGCCCCCCC GGNANANGAC	720
CAATINGGIC CTICOGICNC TTICCCTINI TAAATIGAAA AAGGIINOOC TITGAAAATT	780
AACOUNSCOO NOVICCOCCO GANAAATOGI TITITTGI	817
(2) INFORMATION FOR SEQ ID NO:444:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 759 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: PAG1323RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:	
GATCAGTITIC CAGGGACCAT GAGCAGGGCG GGGGACGAAA GCAGCTCTCC TTGGTACACC	60
TOCCTICCAGE GOCTICAACAC GOCCTICOCAG GOOGACGACGA GGAACATICOG	120
SCACCETTIT ACATOCATOC AGATTIGAGG ACATCACAGO TOTACTITIGA GAAGATGATO	180
CATCAACACC COCTCCCOCC GOCTGTTAAG CCOCTGTTCT ACATTAATCC GTATGGACAG	240
GAAATTITOC CTGTCGCGAA CTCTCGGTCT ATCCACCAGC TGAAGCGATG CCATATCCTT	300
CIGIATICCA TCCGCTCCTT AATTACCACC TATTCCCCATC CICATCCTCC CCTACTTCCC	360
AGGTOGTOGT CCAAGGGAAG ATGAAAAAAT GCTACTGGTC NCNCCAATCA ATNNCNAACC	420
TCCGATTAGG GOGGGGGNT INTITITITA ATTITAACCC CCCTTTGGGG TGACCCGNC	480
NAAAAAAAAG GOGOCTITIGN NNWITITITIT INGNOCCCOC CNOCINITICG GNAGWITITIT	540
TITICIOGNE COCOCCCC CONNICOCAA AATNITINING AAAACGAAGN ATTINCCCON	600
NANOGOGANI TITTIINITA NNAAAINNAA AAAAAATINN TICCATICCC NNAAITINNN	660
NUTTININN CINUINCOGN TITICNAANIT NACCCCCCNC NANAANITIN NITTITICCC	720
CCCCCCCCC CCCCCCCNNN INCNITTITT TIMMCAIN	759
(2) INFORMATION FOR SEQ ID NO:445:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 834 base pairs (B) TYPE: nucleic acid (C) STRANGEINESS: sincle	

1000000 -- CD MACE10080 1 -

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: PAG1323UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445;	
10	GATCCGTTTT TCCAATATTT CACCGTCCTG TAAATCAACA GTTGAAAAAAC AATGGCGTGC	60
	TITAATOGAGG AACGCAGCAC AACCAGCAAT AGOCTITOGAA GCCGTITOCAG AGGTGATIATO	120
15	OCAAAGITOC TOGAGCACTA GAACOGACTG OGTCATTATA TAGGTOGTAG TAAGAAGTOG	180
15	GINGANGUAN GOOGACIATG GINCNOOGG GOOGIGGNGG CNGGCACGCC GCNGIGGGIG	240
	COGCTCATOG CCATGOCCAT ATCCCCCACT TGTACCACTT CGTTTACAAC CGCCCCCCC	300
20	TECCEACETA CACETITACT COOCCEACCTE COOCCEACCAGE GEACCOTTEA COOCCAGCAAT	360
20	GTTGTGTGCA COCTAGTGCA CCTGTACCAC TCCAVTTCCGG CCGACATCCC CCTGAYTAAG	420
	ACCCATTONA TOCOCCOCTOG GIGINICIGA NOVAAGITOG ACCCNOCAAC CTGATTGTTT	480
25	TETEGONAGA ACACATNOCC TIGTTOSTOG ACCCACCOGA NAATTAAACC GOCCCNOCAA	540
	GACNACCOCC CCTCCCCCCCN CNOCCTTTGG GTTNNNCCCA TINGTCCGGA CNTCCAAGAA	600
	MITTACINGC ACCORCAGNG GCACCACCOCO COSSOCACTI MITTCAACNC CMITCCCCCC	660
30	CMIGGGGGG NCCCCCCCTT TGAAAAANNG TGGGGGGGAC CGGTTCGGGT CCCMITCCCC	720
	CCATTCHATT TEINITTANA NANNACCAAC CCCCTCCCT TINICCCCACN CAAANNINGT	780
	THETTAANCT NOCCCNITAT TOTNOCCCCC CGNONCNIAT TOCKACCCCCN CNGT	834
35	(2) INFORMATION FOR SEQ ID NO:446:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 785 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1324RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:	
	GATOCTACOG OGATOCACGA COCATACAAG TATATCAGOG ACCTTGCCGA GGAAATGOGA	60
50	CATAAAATTG AAGGACCAGA TCACAATTOG TCGITCCTTA TCATAGCCAA GATATATATA	120
	TATATCIOCE ATAATTACAG COCTTOGTAT CTATACCTCC TACATACAAA TACTTACATA	180
	CACATAAATA TAATACAGCT ACTTGTAAGG CGAGAAAGGT TACTTCTGGA GAGCCATTAG	240
55	AGACOCAACG AATGTCAAAA TCAACCTCGG GCGGACTTCA TTGATATCTT CAGGAACCAA	300

360

CCAGATTAAA GCACCAAGTT TTCTCGCGAT AGAAATTGCC AATTTAGCGT TTGCATACTT

	CICTICCICI GITACGCCG GGAGTAACCA AGICATAATC CACATATOCT GGAGCTAATC	420
5	CGTTCAATAC ATCCAATAGG AAATGGGCAT TGCTCAACGA AGCATCCCTG GAAAGACATA	480
	TOCTOCTOCA TITIOCOACCO TITOSCACTIG COTTOCCCCC ACTITIAGATO TGACATOTGA	540
	ATNOTOTACO AAACAAACIN TGAGGANATN TGTTTGACAA GTTTTCTGCN CCTCACTGCC	600
10	AAACTAAACT AAGGTCACAC CINITIGCNI CCCCAATICG AACCCCCINN GCCCCCCAA	660
	AAAAACTINA ATTOOCAAAT TOANNOOCIN TITIGGITTOO COCCOCAATNA NONINAATTI	720
	CONCCONTINO CTOCOCCOG INGAAACCON TGAAATAACC CCCCGAATAC CTNONFTCCC	780
15	CCGAAC	78 5
	(2) INFORMATION FOR SEQ ID NO:447:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 866 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1324UP	
30 ·	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:	
	GATCITAAAG AGGCTCAGTA TGCAGAGGCA GTTTCCAGAA GAAGACAGGC TGGGCTTCGA	60
	AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGCCCA	120
35	GCAAACGCCG CTGCGCGCGCC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCACGCC	180
	GTCGTCCACT GGTGCAGGCC AAAAGCGCGA CTAGGACTAC TCCGTGTTCA ATGAGAGCAG	240
	GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA OGCACAAACG	300
10	OGIATICCAC COCCACOGIC COCACGACGA CAGCTACCGC COCGACTIGC AGCCGCTCIG	360
	CTGCGACAGC TCGGACGAAG GAAGGGAGAG CCCCCGGCGC CGCGCTCGAGA	420
	ACCCCCCTT TOCTOCCTCN ACCATCCCCC CCANAINCNI CCCACAAAAA ANINITTOCA	480
15	ACACOCCOCC CONCAGAACC TOOCNITAGC GAACNITINNA AGAAGAAINI	540
	THICCANTITIC CONCCCTINCT TOGANAATOG TOGGCCNECT THACHAAACG CTAGGTTGNC	600
	COCCCCAAAA NCACTITECT TNACCOCAIN CTCCCCNGAA AGANAGANAG NTCCCCCNCAC	660
50	TITINOSCAA TITINIOCOC OSOGANAAAG GITOOOGITN ANOOGANOOG NOOCGCANNA	720
	ANAAACCTAC NCANTTINAA CATTOCCCCC CNTTTTTINC AAAAAAGANA ATGMITTITT	780
	CACCNIGACA ANIGATINICI TITINIGAAGG GNOGNACIAC CCCCCCCTTG CCTNICCTCC	840
55	CCTTAGANCT NONATTITGT TITTINT	866

(2) INFORMATION FOR SEQ ID NO:448:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 749 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1325RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:	
	GATCAATGOG GGAGTGOCAA AAAGOGACTC AAGGTGAACG TGTFTCAGCA CTGTTCATGA	60
	TOCOCCETOG TCATTTTOCC OCAGCCATOG TATCTCACCA ACGCATAGAT ATCAGTGCCA	120
20	ATOCCAAGAG GCATGGAGAA TOGTTACAGG AACAGGCGT GCACTITICTT GAGCACAAAA	180
	CSTTTCACAG ATACACCAGE AGGCGGAAAC AAGGAGGTTC ACAATCGGTT ATGGATAACG	240
	CCANCESCAA ACCANATICC CENCECTICTA CECTACESTAG ATACANTENG CCCSCATTAC	300
25	GGAATGACGT TCAGGACCTG TTAAAGAAAT GGAGGCCATA CTTGGGAACGC TGCGAACACA	360
	TATTTATTAG GGCCAAAAAT GITGCGGACA GGAGCGTATT CITTACGGAA AATACCCCAT	420
	TGACCAAGGT TAGACCCGAG GATTCGGACA TTCCCATTCA CAACCCGTAG ACCTACCACA	480
30	AATGAOCTAA GOOGAGCATG GTGOCGAGATA ACATACTTGA AGAAGACATT GAACCCCACC	540
	CATCACATOG GAGOGGCATA CICCTAAAGC GACAATGATC CACTGCCAAT AAGCGACGTT	600
	GTACGCAACT TAACCCCGING GNAAACCTTA NCAGGAACGG CITCTTTICTT TOGATTICNAG	660
35	GCCCCININIT ATTOCCTIVIT CNAAAANCNI NITTOCCCAA CCTCTTTTTA AACCCCCCGA	720
	AAAANVITIN AAACOONONC COCCOOCOCA	749
	(2) INFORMATION FOR SEQ ID NO:449:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 801 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1325UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:	
	CATOGICOCA TGICICATET CGIATTICCA TCCCCCCCC GGICCCACIC CCACCICCAC	60
55	TACGAAATCA AGGACGAACG TGAATTTTCA GCCGCCCTAG ATACTGTCAA GGGTGCGCTA	120

COCCCCEARA AGRAGICOCC CTOCCGCACG ACCGIOCACC CIGGGCCTGG ACCAGGCGGG	180
AACAACACOC CGACACOCGT ACCICTOTCC AAGCTCTTTG TAGGTGCGAA AAACACCAAG	240
TICANGCCAG TGATGCGCTC TOCGGATGCC GCTATCGCGG CAGGCAGTGC CGCTTCGGGC	300
COCCACTOTO COCTATTOCA TAAGACACAG ATAGATGACC CACTOSTCAT GAACAAAGCC	360
OSTGACCACG AAGTOGAAGT TGTAGTOGAT CCTATTTTGT CAAAAAAGCT ACGCCAGCAT	420
CAGACAACAG GTGTTGAATT CATGTATGAC TOOGTCOOOG OOCTCOCAAG GTCCGAGAAG	480
GACGATCATA GAACAGTGAT GATCTTGGAA TATGATAGTG ATGTCAAGGG TTGTCTGTTG	540
GCGGACCACA TGGGATTAGG GAAAACATGC ATGACGATTG CTCTGATCTG GACGCTACTG	600
AAGCAGCATC COCAGGCCAT CGTCTGTTCC DATGCTCCGC AATTGGGGGG TTTGGTTTGC	660
AGGGPTTTTTT GOCANAAATT CTCNTGGTAT GCCCGGGTGA CTCTGATTGG CGACTGGGAA	720
AANCATTICN CONAINGON GOOGANGAAT AAATTIGGANC CINGAANCON ATTGONAANT	780
ACCCCCCAAA ANAAAAATG N	801
(2) INFORMATION FOR SEQ ID NO:450:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 774 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:	
GATCGAATTA AGTCAGATTT GATTGOGATG OCTACTAACG AACGTGCATT GTCAGACGGA	60
COGAATCAGG TACACATTGA AACTOGTGAG TOGCTAGTOC AGACAATCAT AAATGAAAGT	120
TGTGGCTGGA GCAAGGGAAC TGGGATGCCT TAACTTTCTC AAAACACTCA TGGGTGGTCA	180
AAAATCAATC TATTCAGTAT ATAGTATATC AAAACATTAA ACCAAACTAG GCGCCCAGAA	240
TATTOCCAAA ACATTOCACT GGAGTATTAG TATOCAGAGA AGTAGCAATG GGCGGCTAGC	300
TOGTTACGTG GCATTCACGG ATGACTTATA GAAGCCCATT AATCATCTTT TAGTGACAGT	360
AAGATCAGAC ATTAAATAAC GTATOGAATT TTAGGGGAGA AGTCATCACA CTTGCATTAG	420
TATACOGCAA TAATTCOCOG ACCACATCAG TTAATACTOG GCATOGITIC TAAAAAAGUGA	480
AACIGOGITC ACATTCAGIG TGITTTOCAA CATAGATGIC TCTCCTCAIG CIGCTTCTCG	540
GITGAATAAC CATGCTICAG TAGGCACCGT TCCCAGTATT TGGTAATTAG TTGCCAGACT	600
OCTITATAAA OGATGACCOG AATATGANCT TOCATTAACA TIOCCNOGAA AANANATTIG	66 0
SCANCOGIAN ATATTTTCCT GOCAATIGAN ACOGFICINI GAACOCCINC TIGGGGNOCN	720

	GCTTUUCAAA AAUGAANTTU CUCUGINGNI NITTITATAGG TNONAAGAAA AANA	774
	(2) INFORMATION FOR SEQ ID NO:451:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 779 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(11) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1326UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:	
	CATICAACAAG COCTITOCOCC ACCTICOCCCA CAACCTICOCC CTCAACCCCC TGACCCCCAG	60
20	CGOCAAGCOG CGOCTGTTTG TGTOOCACAC GTGCACGCGC GCGTTTGCGC GGCACGAGCA	120
	CCTGATCCCC CACAACCGCT CCCACACGAA CGAGAACCCG TATATCTCCG CGATCTCCCA	180
	CCCCCCCTTC ACCCCCCCC ACCTCCTCCT CCCCCACCCC CACAACCTCC ACCCCCACAC	240
25	CTGCGGGGCAC GCGCTGCTGA AGAAGGGCTC GCCGCCGCGG CAGCGGCTGA GCCGGGCGT	300
	GCGGCGGCCC AACAGCGCGC AGGGGCTGCC GGCGCCGCCC AAGGCACGGC GGCGCCTGTC	360
	GTTCTCTGCG CAGTCCGGGG AGAGCTACGC GTCGGTGCGG CCGGGCAGGG CGGGGGGGG	420
30	CGAAGAAGGT GCAGITCICG ACGCCGCAGC TGCTGCCGGT GGACCTGAGG CAGCAGCGGT	480
	CGACGITCAC GOCOCIOGAG GCGAACGGIG GITGCAGGAC GIGAACAGCC IGICCGCCCT	540
	GCACGCACGC CGCAGGCACGC CAGCTGCAGC CCGCGTCGGC GCTGTGGTGG CAGGCCACGC	600
35	ACACCCCCIC CCIGITICCC CACCCTICCC NGITGCCCGT CCTTACCCCA ACCIGCTICN	660
	COCTITITOCC COCCANTICACA CALIFOCAACA CALIFOCACA CANDOSCANON COCCCCCCC	720
	OSCATOCCCC COCCININOCC AAAAITTCAA GTTAACCCAA NAACAITCCC TITCIOCCT	779
40	(2) INFORMATION FOR SEQ ID NO: 452:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 763 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1327RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:	
**	GATICCAAGOG TOTGGAGTAT GOTAAACGAG OGTOTCATGC CAGGAACAAC GTAITTATCTC	60
55	GITGAACGCT GTCCTCGAGC CTCGAGCCAA ATCTGACCGT TTTTTTTGCTA GAGCATACCC	120

	AMMALAMAC ASCITIGATION GUTAMALAME ATGACANTIGA TIMBOGOGAG GATGOCTIVIO	180
5	ATGITICIAAA TICATGOCTC GAGGICCCAG TCGGIGCCCC ATGITAGICCT GCCGGCCGAT	240
	TATATTOCOG COTAGCTOTO GTGAAACATC GOCOCTAATT GACGGATAAG CAGCTGTGTA	300
	CCTTATTTTC ACTATTTCTT TTCACATACC AACGACTAAG GTTGATTCCA AGAGGTACTG	360
10	ACTGACCCAG TOGACAGCGT AGTTATCOGGA GIAACTGCGCC AATGTCGGTAC GGGFTCTCCGG	420
	GCAGGGGAGG AATGGGGCTGC TCAAGGGCGGA GCACGCGGGAGG GAGCTCAACA	480
	TOCCCAAGGA COTGGCGAGC GCCATGAGGA AGTCGCTGTC GTACGACTTC CTTAATGTGC	540
15	CTGGCGGGGA CGAGCAGGGG AGCCCCATCGG GACGCCCAGG ACAGCGACAG CTGAGGACGG	600
	COCCEACIGEA ACTUGAAAAC CAAACCOOCE AANOGOCCON AGGGCNONGG ANCAANIZYCG	660
	GAAAGGGGGA ANITIGCCCA MIACCNCIGT TOOCCCNCCC CCCCCGTTCC GAMITIGGGT	720
20	TENCARATC COCTOCTORC TINCARACCT NOTGRESINNA AGT	763
	(2) INFORMATION FOR SEQ ID NO:453:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 794 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MCLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL327UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:	
35	CATCOCARGO GIOGOTICAMO COTICOTOTIO TITOTOTICITO GOTTICOCTIAC GOCCOGACTITO	60
	GCAGCCGCG CGCTCCTGAG CGTCTCATAC TTGCTGCCTG CTACTTGCAT GGTTTCTATC	120
	GICACGGIGC AGCAACTGGG ACAACAGCAC CCAGCAACGG TIGCAITTAT ATAGIGICTA	180
40	CCTGTACGAT AGGGGACTGA TCGCTCTGCG ATGGGTATCT ATCTCATTGC GGAAGGTTCT	240
	CGAAACGAAA AGCGCCAGTC GCTGTCGAGC GACAATAGCG AACCACAATG ACACAATAGT	300
	GCGCGTCGGC GACCCGATCC CTGCATGAAG ACCGAATGCT CGAGCAGATT CTTGTGCGGG	360
45	CGICAGCGG TAGCGCGGCT CGTCGTGTGG CGCAGCCCGG ATATOCGATG GCACCGCATG	420
	COGATGICCT COCCCTCCC GATTAATCTA CCTCTTCCCA GATATCCTTC TGTACGACGA	480
	AGAGGGCGTA GGGAGAAGGC CTGGACGGGG GCTTGGGGAG CTCTGCAACG TTGGGGGGGC	540
50	GIGCOGCOGI AGGCGGCGC ACACCGGGGIA AAINCINCING GANCCINGIN COCTOCNITC	600
	CNCCCCCAA ACTTGCCCCC NITINCCCINC CGAATINICAA GCINIARCCC NAAATCCTINA	660
	ACCCCCCOUNA GGAAAGNVIT GOCCTIVITGA NCAAANNACN CGCCTIVIAAA MICCCCGGGG	720
55	TITICASACC CCCAAAAANGG GGATIAAACCN GOCKIACNACC TITTICAAAATC GCGTTTCVIT	780

	TINOCCCCAN ACMT	794
5	(2) INFORMATION FOR SEQ ID NO: 454:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 757 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1328RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:	
	GATCTCTTCT GCAAGITTCT TTATCGGAAG CCCAGGCTCT GGATTTCCTT TCTCAACACC	60
20	ANTOSTATIG TCTTCGATAT CAGAGAAGGA GCOCTTCGAA TTTTGCGCAC CACCATATGG	120
	ACICICITEA TEATFFECE TATFFECIOC ATCACTFECE CTICCCAAAG AAGAATCCAT	180
	COCACCCATT ACATCCAATT CITCATIATC AGCITCTCCA CCIGITGIAG TATTIOGITC	240
25	ACCATIATIA TOCTGTIGCT TATTGATTGC ATCACGGCCC ACACGGCTCA TITGTATCAT	300
	GCTAGATGIA TATGGGACAT AATGCACCTT TTGCAACAGA GGACGGAATG GCTGAACCAA	360
	GIATIGATIT AAAACCAGGA AGITCITTIGT ACIGACCTCG GCATATTCCT GATCTTGCCC	420
30	GAAACGIGOC GAAATTACCT TAAATAAGIC GAGCACGCAT GAGTIGGCCA TGITATCAAA	480
	GIAAAGATIT TCTTGIAGCA GCTGACAAAT TGGATCAAAA AGATCTTAGA TATGAGATAG	540
	TIGIGATAAA ATICATCATT TACAGCCAGG ATACCCTIGA TACCCGAACT GCAGCCAGCC	600
35	TIAACIGIAT AATATOGATG GITCCATTAG TITCCAATAG TCAATAGATG CCATTITCCA	660
	ATATNAACCC CCCTTGACAG CATAATATCA GTTCCNTGTT NINATAATCC CCCCATTTIA	720
	CCAAACCNEC NENGTIGATT NCCCNNCCTC CACCCCT	757
40	(2) INFORMATION FOR SEQ ID NO: 455:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 794 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1328UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:	
55	GATCGGAGGT ACATAAGTGC TCTACCGACC AACCCGCTC TCCATGCATC AACCAATGGA	60

	GTTGAAACAG TTGACTUSCG ASCAGOCCGC CGCACTAGAT GCGGAACTCA TGGGCCCAGA	120
	CGITGOCTAC TOOCTOCATO AATTGATOGA OCTAOCAGGT CTTOOCGIGG COCCAAGICGT	180
5	COTOCOCCAT TOOOOCOCC CACAGOCGAA GAAAAAGGTG CTTGTOCTAT GTGGGCCTGC	240
	CAATAACOOC GOOGATOOCT TOGITOCTOC ACGOCACITG COOCTICTIOG GCTATGACCC	300
	TGTGGTCTAC TTGCCGCGC TGTCGGCCAA ACAGCCCTTC TACGCACAGC TTGCCCAAGCA	360
10	GCTACACTIC GTCGGTGTCC CAGTGCTCTC CGAGGGCGAT GACTGGGGTG COCATCTTGA	420
	GCCACGICAC ACOCTCTOCG TIGIGGATOC OCTCTTTOCC TTTTCTTTTC GTCCCCCCCT	480
	GCGCGACCCC TTCGCTAGCA TTGTCGCAGA GCTCAAACGC CATGAGGATG ACATCCCAAT	540
15	TGTCGCTGTC GACATTCCCA GTGGTTGGGA CGTTTGACGC AGGACGCTCA CCCCTTCAGA	600
	CTTATOCACO TGTOCTGAIN TCTCNTGAAC GCCCCCCAAA AGCTGCTCCC NCNCACATTIC	660
	AAACTGGTTT TTTACCNCCC ATTANTTTCG CNCNNGTTTC ATCCCNAANC CCCNGCCCCN	720
20	CCTCCNTGTT TTTANICCNT CCCCGTATCC TGNNCCCATC CANANIGOGT TTTTGANITG	780
	CCATTGENIN ATCT	794
	(2) INFORMATION FOR SEQ ID NO: 456:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1329RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:	
	GATCCCCTAC GOSCIGCIGC ACTIONNET CITOSCOCTE COCTICHOCT TOCCCTION	60
40	GOCOGIGUAC GUOCAGUTCA AGAAGOCCOG CUUGUGAGUT AAGUAGAATA TAGUCTAAUG	120
	CTATICAGG CCCCCCCCC CCCCCCCCCCCC GCCCCCCCCC TCACCTCACC	176
	(2) INFORMATION FOR SEQ ID NO:457:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1329UP	
\$5	(xi) SECUENCE DESCRIPTION: SEC ID NO:457:	

	CATCCCCCTC ACCTGCCCCC GCCGCCCCCC GGCCGCCGCC CCCGCGCCCT GCATAGCATT	60
5	AGACTATATT CTACTTAACT CACAAGCOGG CCTTCTTGAA CTGCACGTAC ACCGCCACGA	120
	ACCIOCAACCA CAACCCCACC CCCAACAACC CCAACTIOCAC CACCCCCTAC COCATIC	176
	(2) INFORMATION FOR SEQ ID NO:458:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 767 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: INA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1330RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:	
	GATCTTOGAT TTGACATTGT CAATGGTGTC AGAGGACTCG ACCTCAAGCG TAATAGFTTT	60
25	CCCTGTCAAA GTCTTCACAA AAATCTGCAT ACCTCCCCTC AAGCCCAACA CCAAGTCCAA	120
	COTAGACTOC TTCTOGATAT TATAGTCOGA CAACOTGCOG CCATOCTCTA GITGCTTACC	180
	COCAAAGATC AAGCOCTOCT GGTCTGGGGG AATGCCCCTCC TTGTCCCTGGA TCTTCGATFT	240
30	GACGITGICA ATGGIGICAG AGGACTOGAC CTCAAGOGIA ATAGTITITCC CTGTCAAAGT	300
	CTTCACAAAA ATCTGCATAC CTCCCCTCAA GOGCAACACC AAGTGCAACG TAGACTCCTT	360
	CIUCATATTA TAGICOGACA ACGIGOGGCC ATCCTCTAGT TOCTTACCTG CAAAAATCAA	420
3 5	GOOCTOCTOG TCTGGGGGAA TGCCCTCCTT GTCCTGGATC TTGGACTTGA CGTTGTGGAT	480
	GETGTCAGAG GACTOGACTT OGAGTGTGAT TGTCTTTCCC GTCAAGGTCT TGACGAAAAT	540
	CTOCATACCA CCTCTCAAAC GCAACACCAA GTGTAAAGTA GACTCCTTCT GGATATTATA	600
40	GTOOGACACG TIGOGGCCAT CCICNINITIG CTTACCCTICC AAAAATCAAA COCTOCTINGT	660
	CCTGGGGGAA TGCCCTCCNF GTCCCTGATT CTTCNANITT GACATTGTCN ATGGGINCCN	720
	AAGANICONO TOAATTNITIG ANTITOTICO COGNOAGGIN TIGAANN	767
45	(2) INFORMATION FOR SEQ ID NO:459:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 794 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1330UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:	
	GATCAGATGT TTTGTGCTAG TACGTCGCGA TAGTACTAAA ATTACCATAT GCCCATCAGC	60
5	ATTATACTAA CTAGTGITGT TITGCAGTAA GCGGTAAACC ACCCATTACG CCTGITGTAT	120
	CACCAGAATC CAAATOCGIT TITIGAAAAGA GETTAATIGA GCAGTATATC GATGAGCATG	180
	GOGINGACCO AATOTOCAAG ACAAGOTTGA CTAAGCATGO GOTAATTGTO ATTGCCCAGA	240
10	CACCOCAGCA GTACGCGCTC GCAAACGCAG TTAACTCGGC TACGCTCAAC GCCAATTACA	300
	GCATCCCCAA CCTTCTGTCA ACACTACAAA ACGAATGGGA TGCCGTGAIG CTGGAGACAT	360
	TYCACCICC CACTCACCIC CATATGICCA AAAACCACCI ATOCICACOC CIGIACAACI	420
15	COCACOORSC TATCOSCOTIC GOOGCACOCG CGAAACAGCA GAATGATGAA CTCACACACA	480
	CGITICACOGA GCCTICACOGA GGCAGTICOGC GGGGCAGGCTIG CCGATIGCCCC GCCCCTTCCA	540
	GCGGAATTIGA TTACCGCGAT GGCAGAAACG CACAAGAATA TGTGCAGCAA ACGAAAGAAA	600
20	GAAGGAAATG AAAGCCAGGT AGTGACGGCA TTTGCTCCTG GAACAGCCGG TCCAAAACGG	660
	NICCOSACEIC AACCOSPITT TIGGITACCC GITINNITGS TICCOSAAAA ANAATTANCT	720
	INCTITITIAA CCCAAAGGCA GGGCCNINIT GCTGAACAAA AAGGGTTTTT GCTNCTNVAA	780
25	AATINGCONC TNAC	794
	(2) INFORMATION FOR SEQ ID NO:460:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 776 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1331RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:	
	CCATCATTCT CAGGTATUAG ACATUCCUGA TGGGCACGCG CTTTTTCTTC AAGGAATUCG	60
	ATUGGAGGOG COTOTAGAGT TGAAACGAGT TTATTATACT CAGCCATTGC TACAAGCATA	120
45	TAATCAATAG CCGCAGCGCA ACTCTGAAGA TGATCTAAAG AAGGAGCATC TGCCTTTTCT	180
	CCTAGAACAT TCAGAGCGGT TGCCTCTATA ACTTCATGCT TATAAGTGGA ACCACTGGAA	240
	ATAACATGTG ATAAACGTGG AGAGTTGCCC AATGTGTTCA AACCTTCTAA TTCTGAAACG	300
50	CANATTAGIG CATACCCAGC ASCIGCASCI TINTICIICA ANTGNICGAG AGAAGGIGAT	360
	TOGOCIACIG TICTCAAATC CAGAAGAACG TICGAATCAA GGATTICCAA GITTCTTICA	420
	GATOCATOTT TETTGAGGAA GCCTTCATCT GGGCTCTCCG TATATCTGCT TCAACTCATC	480
<i></i>	CATAGIAATC ACCAGAAATG ACAATCCATA TATGGITCIT GGCTTTCGIT TGIAGITAGI	549

	CCATOUTICG ATTITICCIAT GGTACAAACA ACAATATUGT GCTCTTTCTT TTCAAACAAC	600
	AAATATCATA TOCCCTTGGC TTTCTCCTGC CAAAATTCCA AAATTAGANA TTTCTNATCC	660
5	CCTTTAATAN TICCACATGT TCCCAATTCC TCCCAINANA TNACTGTCTA ACTGTTTGTT	720
	SCNNACCCAA AAANATTOCT TOCINICOCT TTTCCCCANA TOCTCCTTIN CCAGIC	776
	(2) INFORMATION FOR SEQ ID NO:461:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 808 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1331UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:	
	CATOSTOCOC CTOCTOCACO AGCOGCTOCC CAAGGOCCACG COCTOCGACG TOCCCTOCAT	60
25	CAAGAGCTAC GICTACCCCG ACCESCTICGA CGAAACCCCC TEGTICCCCCT CCCATECACG	120
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	180
	CCACCTOCCC ATCTTCACCC TCTCCCACCT CCTGCACCAC CACTCCCCCT CCCAACATGT	240
30	CATCCCCGAT AGCATGCATG CGGGCGACGC GGTCAGCCTG GGCTCCCCGC AGCCCCAGGC	300
	ASSOCIUTOS CASCACASCI TUTOCOCASA TICCACSCAC SOSTOSCOCO TIESCOSCOCO	360
	COOSTITAACC COCTIGACOC GCGCGCCCCC CICCCCACTC CCCGTCCCGG TGTACACCGC	420
35	OCCOSCUTOC COSCUTIGAÇU ACAUTICOCGA CAGCAAGSGA TGAACCCCTA OGTOCTOCAG	480
	GOCCCCAGCC AGGCCCGCAG CCCGCCCCTCC CTCNTTGAAG GTNNGAANGC CACCCTNCCA	540
	AAANTITAGG GGINGXXXXC CXXXXXXXXXX CAACCQNITG GCGTCCQXAA AANCCNNTGG	600
40	COCCETIVACE CONNCTITIAA GOCCOCONICG AACNONGOVI NITITOGOGNA GOGTITICCAN	660
	ACNCARACNG TIMINOCCCC CCTTTTTTCT TCNARNARAG GCCTNTTTGT GTCNNTTCCG	720
	CCNGGNAGAN AATITTINITIT TIGIIGGGGCTIG NACCCTINAGA AAACNCOCAC MGBGAVENNAG	780
45	GGGAAAAAA AANI'ITTITT CONINGGI	808
	(2) INFORMATION FOR SEQ ID NO: 462:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 762 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
5 5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1332RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:	
5	GATCTITTAT GTTCCTTTAG AGCAAGGTCA ATTTTCACAC CACTTCTATC ATCTTATATC	60
	CAGAATAATT TGAACAAGAA GGTACOGTCT AGTGAACGAC GTGATTTCAT GCCGGCGTCC	120
	AAGGITCATG AGTCATTACT GAAAATGAAG CAGCACTATA TOGAAAATAG GITGCTOGAA	180
10	CTACAAAAAC TICATCAGIT ATICIGTAAA GATAACGIGA ATITITICCAA AAAAATGATA	240
	AATGTCCAAG AAAGAAGAAT CGTAAATCTT CTAAATGACC TAGATGATGA TOCTAACTTT	300
	ACTITICAGA CIGICCATAC TAATTITGIG AATAATGAAC TATTCATGGA ACTACATGAT	360
15	CACAAGTCAG TGATATOGGG CGTTTGGACA TTAGATACTG CGGAGGATTG CAATCGCATG	420
	AAGAAAAGGT TACGACCATA TACACTCAGC TCCTCGACTA TTTCAGGCTC AAGTTGTCCA	480
	ATATTCATGT AGATCCAACC GCCACTATGA ATTINAGTTC CGAAACTCCN TTGANCAGTG	540
20	THACCICCIT ATTGIGITIG THACNOCAAT TGATCCCTCC ANTITICCGAT TCTGGAAAAT	600
	GCEVOGAAAAC CNNCCAAAANT GCNGAAAAAC CTAAAANAAG GAANACCGIT AACNGGGI'IN	660
	GGAATGTCTA TTCCCCCCCC GCCNNANCIT TTAAACNINC TITCCNCCCC AANANNCCNN	720
25	NCTCCCNINA AANITITTIC CCCNGGCNAA AAANITNICT GG	762
	(2) INFORMATION FOR SEQ ID NO:463:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 798 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1332UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:	
	GATCTTTTTC AGACGCAGTG TACTATCGAT GAAGCATATG ATTATTATAC AAAACTTCTG	60
	TCCCATACTA TTGCATTAAA CCCGCTTAAT AGAAACGAAT TTTTGGAAAG TTGCGACACA	120
15	TTAGAGATGT ATGGAGTGGC TTCTATTGAA AATGGCAAGC ATGGCAAAAA GGCCAAACAA	180
	TTOGTAAAAC TGATCAAGAG TACAGTTGAT GAAAAGGAGT TCCATGATGA AATATGTNAG	240
	ATOGACTIOC TTAAGAAATT GATAATATAA AAGOCTACGA OCTTCAATAT TATAATACOC	300
0	ATTOCATAAT TTATTACATT AAATTGATAT AGGTATATTT TTCTTCGAAG AATTAATTCT	360
	AATCATTTCC ATGTGAAGAT ATGGCCCTCT GTGTTACCTG GGGATATTTC GACTCTTAGT	420
	ATATCTACAT ATTITICOCGA GCCATTATIT AAACTCGCCA GCTTGACTCT GGACCCAAGA	480
	CONTRACTOR OF CONTRACTOR DESCRIPTION OF THE AMERICAN AND AMERICAN AND AMERICAN OF THE AMERICAN	E 4 (

	CCGCCCTTA ATTCCASCAC ATATAACASA CCGCCCGC CAATAACCCT AACACAATTA	600
5	TICCCTITCT TICCCATCAT GITTCCGATA CIGGACATIC CCIGAAATOC AANITTAACA	660
	ACCCITATAC CAGTGAAATC NIGOGITTIG AAANATGCON TGCCAATTIC AACCCGTGAG	720
	GIOCGIAACC TGAACTTTTT TIGAAATTIC AACCCCCCCA ATNANIMTIC NITTTIGNAA	780
10	CCCCATGCCT TGTTCNCT	798
	(2) INFORMATION FOR SEQ ID NO:464:	
15	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1333RP	
<i>25</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:	
	GATCACCOGG TGAATATGCT GCTTGGCATA GTTGATATAC ATTGTGAGAA AGTGCACCGG	60
	AAGGATGTCC GACTCGGACA CATGGGCCGG CTTGTCCTCT AGGTAGAGGC TGGTCAGGTG	120
30	CITOSCIAAT TCTCCATC	138
	(2) INFORMATION FOR SEQ ID NO:465:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 137 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1333UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:	
45	GATCGAGAAT AGCCAAGCAC CTGACCAGCC TCTACCTAGA GGACGAGGCC GCCCATGTGT	60
	COGAGICOGA CATCCTICOG GIGCACTTIC ICACAATGIA TATCAACTAT GOCAAGCAGC	120
50	ATATTCACCC GGTGATC	137
50	(2) INFORMATION FOR SEQ ID NO:466:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 766 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1334RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:	
10	GATCATAATC CAGTOGCTGT OGAGATACTC GACAGGAATG GACGTCAGCG ATTTCGTCGA	60
	AGAGCGCCGG AAAACCTTGT COGTTGGCTC CGGCGTTGGG GTGAGCGTGC CGGGCGCCGT	120
	GCCACCGCTC GACTGCAGCC GCGCACGCTT CCGCATTATC TGGTTCATGG AGAATAGCGA	180
15	CGATACTOGA COCTICATGA TOCACTITAA GOCCACAACC TCGGCCGTAF CATGCTGGCC	240
	COCCOCCAC COCCCCACCO CICOCCCCCC CACCACACIO COCAAACCCC CICGICCIIAA	300
	COCACCCTCC AGCATATACT GGITCACCTG CACGCTTTCC CGGCCCCCTA TCAGCCGTGT	360
20	CUTCTITICC ACCAGANCCA TCTCCACCAG CTTGTTATAC TCCTCAAATA ACCCTGCGTA	420
	TETTACTOCC TOCCOCCOC AACCOCTOCT COCCAACACC GTGTCCGTCA AACCACAGCT	480
	CCTACCCCTC GACATCCTCC CCACCAACAG AGAGTGTCTC CCTTCATTGA ATTGCACGAT	540
25	AGRAGOGRAC GAACTCATOC NOCCTATOCC CTACACCATG NANCTOGREE CTATTGENN	600
	TONOGCOCC NATIONCTGIT CCAACIMIIN TTANCIGGGC CACMITITIT TMIGGIIGCC	660
	CCCCCAACCT CCTTCCCTTA ACCAATCCTG GCCCTXCTTTC NCAACAGGAA ACCTINIGAA	720
30	CACTTICCCC NAAANGINGC GAANAAAAAN TITTITTINAT INCCCT	766
	(2) INFORMATION FOR SEQ ID NO:467:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 796 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1334UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:	
45	CATCCTGCGC GCCTCCGGCG AGCCGCACAG CGCCCCTTG GCCATTCTGG AAAGCGCGTC	60
	COCCOCCOCCOCCION COCCCCIACT COCCCCTACT CAACTUCCCC CCAACAAAAAC	120
	OCTITICGAC ATCACTICTCA ACOSOCTISCO COSSOCTISCO CASTACTACOS COTOGATICOS	180
50	COCCUCTOGI CATIGUCICO COCCOCCOCO CICCACCOCC COCCOCTICOC ACCIGUTICOA	240
	AGACGCCGTC GCGTGCCAGCC GCGCCAGCCC GCTCGGCGCT GACCTCTGCG CGGGCTCCGC	300
	CCIGILICALC GCCCCCICC CCCLCCACCC CCLCATCCC CCCCCCLICC LCCLCCCCCC	360
<i>\$5</i>	CCACCOCCOC CACCOCCTCU CCCOCCCCCC COCCCGTCCCC GTCCTCCCCCC GTACCCCCCCC	420

	The state of the s	400
5	CGGCTCCGCG CGCTCCGCGA ACATCGCAIG AACTGTATAC TACATACCTG CTACGTTGTG	540
_	CTCGCCCCC CCGCCAACCG CTNCCTCCAN CCGGGGGGGC CCGCGGGGGCC TTCCAACTCA	600
	CCGCCGGGGG GCCCGCGCGCAAAAC CCCCTTCCGGC AACGNCCAAN AANNCCANNC	660
10	CONTACNACN COCANTTANC CAACACNITIC NICAACOOST INNINOCCCC CCCCCOCNONC	720
70	TICICCOCIC TITITITITI CCOCANNAIT NCICAICCON COGINICCON COTIATITIG	780
	NIMPECCOCCC COCCCC	796
15	(2) INFORMATION FOR SEQ ID NO:468:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 791 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original source: (A) Organism: Pagi335RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:	
	CACCCAACCC ACCICCCCCI CCIATCAAAG GICIGGIAGT CCCTATCTCC TTTCCCCACCT	60
30	TITGGGGITT TGTGGTCTTG CTTTTGTTGG ACGCTAAGGT TGCGCGCCCC GAAATCACAT	120
	OCACTOCOCC CCATTOCACE TOCOCCAACT TAATGOCANA CACCOCCCC CTCAGCATAG	180
	TOCTGTOGGT CCTCCTATGT CATTGCGACC CAAACGTATG GTCCGCCCTT GGGTTGTCAT	240
35	TTTCTGACGT TGTTATTCCC TCCGGGCCAC TAAAACTGCG CCTACTCTGA TTCTCTGTCA	300
	GTAACGCAGA GTAAGACACA CGCTTGCTTC GTGTGAGCGA TAGTGTGCGA CATAAATTAC	360
	TATGCGGGGA NCCNINCCAA NITTAACCIN TGNNAANAAA ANACCCAAAC INITTCAAAA	420
40	CCCAAANITC NATTINGGEN NCDGAAAAAN CCCOTTINGGO AACCCCCGT NNGGGGTTT	480
	AAATOOOGIT TOCAAAAAAA ACCONCCANI TTTCCCCCCC CCCCCNAAAT TNITAAAAAN	540
	NCCTITIAAA AANVINVIIT WIGTGGNGNC CCCCCCCCCC CCCNAAAAAA AATCCCCCCCN	600
45	AAAAAANCNG GINITITCCC CIVINCOGGG AAACCCCCCC NAAAANXCNN ACNINCNANN	660
	NVEXECUCCC CNINCCCCCCN ANCHONIVING TNCCCCCCTT TIMANAAAANG GNCCCCCAAN	720
	CNITTITITN NUMNINIAA AACNOOCTITI TICNNOOCOC CCCCUNAAAA AATTITITINN	780
50	NIMWITTIN G	791
	(2) INFORMATION FOR SEQ ID NO:469;	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 807 base pairs (B) TYPE: nucleic acid	

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1335UP	
10		
ru	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:	
	GATCACATAA GAATTGAAGC TCAGCGGCTG ATGAGCGCAC TGCTTCCGAT ACGGTGGTCC	60
	TGTACCAGGC TGATAAAATG TGACACTATC ACCATAATGG GGTTGTAGCT GGATACGATG	120
15	TOCOGRATIGOS GATIGGACTIST TICTICAACAAG ACGTIGCAACG TIGCGAGGCCC ATAGTIGGGAA	180
	ATCTAATTAA CGIATTTACA TATCAGIOGC GATGTGTCTA GGTGCCGGCC ACCTCGATTT	240
	CCTGTCACTG GACAGCGCCG TCATATAAAC ATTATTGTTT AGGGTTTAAA GTTGCTTTGT	300
20	GOGGIOGAAA ACAACGICAC ACACTAACIA AATCIAACIC GAGOCAGCAA GCAACTAIGI	360
	TAAATAAGCC GAACAGTTTA CGATTCCAAG GGCACGGTGG AACCCCCCAA GGCCCCGCTC	420
	CNANICNTIC CCTTACAAAA AGGGAGGGGG GCCCTACCAC TACCGAAACC ATACNGGTIN	480
25	NAAACAACCC NAANCCCGTT TTTCCCCCCC CCAAAATTAA ANANTGGGCG CCCCCTGNNC	540
	NCNATTETT NUMBERADE GCANAGEACC COCCOCCOGG GAMAGENICC COCCNATIONA	600
	AAACCANNAC CCCCACCCCO ANAAAAANDG GGGGGGGGG GGAACNCCCC GATTTCTAAA	660
30	AAATTIAAAA ATTIMINGAA ACCGNAAAAC GGNGTGINON TINCCCNNING AAAAANGITTI	720
	TIGINONNA CANOCCCCAA CINITIVINAG NINCOCCINC CCCCAAACIN AAAANITINC	780
	THENVANCEOG AACCANTOCCC COCCCOTT	807
35	(2) INFORMATION FOR SEQ ID NO:470:	
40	(i) SPQUENCE CHARACTERISTICS: (A) LENGTH: 782 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1336RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:	
	CATCATGITT AACCCAGATA CGAAAACTGA GAAGCTAGAG TGGATAGAAA AGCTGCGAAA	60
50		120
	ACTAATAGAS CTGAACAGGT TTCACCAACC ATGGGTTAAA AAGTTCTTGA ATAGCAGTGA	
	GAATATTCTC TGAAGAAAAG CATGACCACA GGATTACATA GAGTAACTTT TGTGCAAAGT	
55	THATCIGIAT GUACAATITC ACGUTATAAA TUTTAAAAGI ACTCGGCCAA AATCGGCACT	240

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

	iodinacan andockeri contambi contochia chiankaii kidichela	300
	CITACCATTA TIGOCATTOC CAGAIGAAGT ACCCAIGIIC IOGIGAITGC CIGACCCAIT	360
5	GTTACCACTT GCAGCGCCCA GGTTTGGGGG AATCATGCCA GGAAAGGGAA AGGGCGGGAA	420
	ACCCCGAACA TOOGTOOCAT ACCCATGOGA AACOCCAGOC GOCTOCGOCA GAGAACCGTT	480
	CITITITATIC COCCAAATIG AACTICITIG CITINCONN CCCCCCGCCA AAAANCITAA	540
10	COCCETICCCC CNECCCCENN TCCCCCCAANC TITCCCNNTG NNCITOCAGC CCCCAAACCC	600
	COCCUTATIVE, INVICTIGAZCO GOGGELLIMIN COCCUNDOCY CYCCOCCCC COCMILIBIEN	660
	NIMITACCOC CACCONCCCC CCCCCCGGAA ANCCNGINIT AAAAAAINCN AANAANNIMI	720
15	GEOCOCCORG CTCCCCCCCE CTCCCNTATA COCCCCCCNN GTAAAATNNC NAAGNEENCC	780
	CIN CIN	782
	(2) INFORMATION FOR SEQ ID NO:471:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 793 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOROLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1336UP	
3 0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:	
	ATCCCCATTT TAGGGATGAT CCCGATCACC ACAGCTCCGA GGCCCTTGTA GAAAGCCAGC	60
35	AAGCCCTCCC CGCTGTAGAT GTTGGCCCCCC GTGCGCAAAA ACCCAGGGGG CTTGGTGCCC	120
	TOSTTOGCOC GOCTISTAÇAT CTOCATOCOC ACCTTCATOC TGTCCAATGG GTUGCAGCAG	180
	AGCGCCTCAA ACAGGCCCGC GGTCCCGGCCC GCAACTAGGT TCACGGCCGG GTTGGTAGAT	240
40	TICTTAGAGG ACATGIGGIT ATCAGGGTAT GOCTGCTGGGC ACACTGCGCT GCAGGGATCC	300
	GCTACGCTTC TGGGTCGCGC ACCTATATAT ACAACGGGCA CGGACGGCGG GCGGCCGCA	360
	CCTTGTCTCC GACGCAGOOC CAATAGGAGC TCGCGCATAC CCCCGGGGCA ACGCGGTGAG	420
45	TCAACCCGGC CCGAAGCGGC GGCCAATGGA ACCGTCACGT GAAAAGCAAA GACTTAAAGT	480
	ACTATGTAGC TACACACTTA GEOCTOGGCC ATCTOGCGCA GTCTGCGGAT CGTGGAGCGC	540
	ACCICOCOCC COCACCCCIC CAGACCTICIT ACCCACCACC CCCCACACTIC NTCCTTTCCA	600
5 0	CVAACTICCA NITCCCAAAN NCCCGNAGCG CCCCCCTTCTI TGCCCCAAAA	660
	AGAACATOCT TACCAACTTC TTGTTGCCCT NCCACTTCTT NAACCTGTTT CCNNCACGAA	720
	NAANCCTACC CCCCCCONIT TINCCGNNAA TOOMACCIIN INCMINCITI TACCATIINI	780

	(2) INFORMATION FOR SEQ ID NO: 472:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 767 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1337RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:	
	GATCTIAATT TAAAATTITTA ATTAACTATI TATAATTIAG AAATATATAA TCTAGAGATA	60
	TATAATCITA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGIAAAATA	120
20	ANTAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATITG TOOCATCITA	180
	ATTITIATTA TITAATIGAT TATTATCTAT TTAACATAAA ACATUTTAAA ATGITATAAA	240
	ATAAATAAGA AATTACTTAT AGAATATITA TTAAATAGIA TITAATTITAA TITTAATATT	300
25	AAATATACCA TITTTATTAA TAAATACATT ATTAAGITTA TIAATATTAA GIGATATATA	360
	ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TITCATAATA TITATITTTA TIAGICIAGI AATATTICIA TITAATAGIC TCCCTTTAAT	480
30	TOGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT	540
	AATAATTTAT TATCTAAAGG TATATAAATT AATTAAATCC TITTTTATTA TIATTTAAAT	600
	TATTATTAAT AGTAAATTAT ATTATTTATT TIMITCACCA TAATTTTTTT GAINATAATA	660
35	TATCCTTINN TAAATOOCCA ATTIATNAAT AATTANCIIC NANGAATIIT AATGAANAAC	720
	COCCNITANN ATAAAATTAG TTAANNIVIGN NCTCAAAANN CONATCA	767
	(2) INFORMATION FOR SEQ ID NO: 473:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 799 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1337UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:	
	GATCAATTAA TAAATGGTTT AACTAATAAA GITAATAATA AATCTATTAA TTATATAAAA	60
	CTACCTCATT TTATTGAATC AAATAATATT TTCTTAATCA ATACTACTAA ATCATCATCT	120
55	ATTICACITTA TATTAAATTC ACCACCTCTT ATTICATTIC	180

	TOTTANAMA TIOTTANTA TAMATTALA TAMAMANI TANIONIAT MOTTANTIG	240
	GTAAAACATA TGTTTTAOOG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300
5	ATCATTAATA TAATAACTCT TTAATTAGAG TOGTACCACA AGAATOCTGA AAGCATTAGG	360
	OGTGTGTACC TTACCTCTCT AATTAAAGIT ATAAAATTAT CTTAACTAAT AAAAATAATT	420
	AATTAAATAA ATAAATAATT AATTAAATTT AAAAAGATA AAAAAAGAAA TAAATAATAT	480
10	GITATATITA AATAGATCAA AATITCAACA ATTICCATIT CAITTAGIAC TACATCACCA	540
	TGACCAATGT TACATCATTT AGTTTAATAG GGTTTACTAA TAACCTTTAN CCTTTTACCA	600
	AANNANNOGT ANTANINGGA AAAATTATNC CCTTAATAAT AACCITNAIN AANNATINT	6 6 0
15	ATATACCAAA ANNITNIGAN ATTINAAAAA ATATNOOCCG AANONONIA TITTONGIAN	720
	CCCCCNONTA CNOCNGAAAA AANGANTACC CGTGTTOCCC CNTATANICN MINCCONAAA	780
20	ATAAAAATG NGCCCCCAC	799
20	(2) INFORMATION FOR SEQ ID NO:474:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 771 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPCLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1338RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:	
35	CATCAACCOC AACCOCTCAC TCANGTCCAG ACCGTTATAG ACACGGTCGT CGATGGCACT	60
	ACAAGGCCG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGTGATAAC GGTTAAGGAA	120
10	ATAGTGAAGG AGACAGTTIT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG	180
40	AACGCTTTCT GICTTTTIGT CCAAACCTAC CIGAACACCT AAACTTAGTT ATTACAACAT	240
	GAGTTTTATT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT	300
45	OCCTIGATAA AAGATATICA TOOCIATICA GOGACOOCIC TAATACOCAT TCTCTAGAAA	360
70	GITOCITIGGO TITICATITIA AATOCIOGIG CACCIOGICO GIAACAGIGI CIATAGIAIC	420
	ATTCCGTATC ATTTCTCAAT GAAGTAGATT CCATATCAAC ACTTGCTTTG GTGGAAAGCT	480
50	CATTATICTE ASCAGTAATE OCTTCACCIC TATCCTGTTC CAACATACTT TTTTTAGCTG	540
	CCCGGATTAA CCTCCCTGAA TICCCTTACG ATGCAGTGGA GACCCATGCC GATTTATCAA	600
	ATTTATCTGT CCTTTAAANA ATTTTAAACC TTTGACNCCC CTATTATTAT TTTTTTAGCNT	660
55	ATCGTAATGC TGCCNGANCC CCCNAANGAN ATGGGGFITIT CCNIATTANC CTTTGGTTCC	720
	CCAANITAAA ACCONOCCG GNCCCCCCCC CCCCCCACON GGTGGGANAA T	771

	(2) INFORMATION FOR SEQ ID NO:475:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 796 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1338UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:	
	GATCAGGITT TCCCGTACGT GAGAACGTAT CTAAGGCACA AAGGGCTTTG GGCGACTGTG	60
	COGRECOTTIC ACTITOCINACA TACACCACAA ACCTICTTACIC GCOCCAACTIC GTOCANCACIC	120
20	ACCAGCOGAG GAGOGATTCT GCGCGAAGOG ACGGTGAATT CGAGCCAGCT GGTAGCAGGA	180
	GIGCOGGATC GICTATITIAG TIGCGACGGG CGICGGAACA GGATGCACGT AAACGITIGCG	240
	GTAACACGOG ACCCTGACGC GACGOCTGCT ACGCCGATAG CACGGGAGGG CAAACGACGG	300
25	CAGCOGCTGT COCCAGAGAT GTCTTCACCA CTGCGCGGTA GCAAGCTGCA GCGGCGGAAG	360
	CAGACACTIG AGGCCGGTCC GGGTCGCGCC AGTGGGACAC ACACGGTGGA CGAGCTGGCC	420
	COCCACCTOG ACCOCCOCTG CGASCAGGOG TCGGAGGOGA AGCCGCCGTA CTCGTATGCG	480
30	GIGCIGATOG COGTICOGAT CCTACAGTOG CAGGAGGGCA GCTGACGCTG TTCGCNAAAA	540
	TACOGNIGNA TITOCINCONI CICCCCTTAN TAACCOGTGT TITITAACCCG GOGITOGAAA	600
	ANANCTICCG GACNACNINI INCTIAAACA ANDGINITGI TITAAGGGGN GGNNCCCCC	660
35	TCAAAGGANG GGCCTTTTGG AAAATTAAGG GGGCCNTTNA NGGGGGCCTC NCTTNNCCAA	720
	AAAGGGGGAA TNATTITING GGCCCANATT INNCAAAAAT ININCANIAG GGGCNCINNG	780
	MAANITINI TOXTI	79€
40	(2) INFORMATION FOR SEQ ID NO:476:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 764 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1339RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:	
	CHANGE ALL SALLENGE TANGENER CHANGE THE CHANGE THE SALLENGE THE SALLEN	61

	COOGITICGIG GGCTCGAGCA GCGCAAIGIC CACACCCTOC TGCTGAAAGT AGCCCTIGGA	120
_	CTOCOCTAGA AAAATCOCAA TGTOGTATOG COCAGOCTOC CAATTCAATA GGAATGAAAC	180
5	THICCTAGAC ATCHTOCOTG CAGNOTOCOC ACCTACACCC CATTCCATCC ACCCTCATICA	240
	OCCOCTITAT ATACCOCTOS OCCAAAGATG ATTGAATACG GITCGCAGAC GOCTACTOGA	300
	ATACCCGTCG CGCCACAGC CCGCCACTGG ATGCCATGCG CCAATGCGGA AGCCTCCTAT	360
10	GTGACATGEA CEAACAGAGC AGCFTCCTTA TGCACTTATC GAGCCAAAAC CAACATCTGC	420
	GGAATCACAC TIGACOGAAT CCCCCCCAT GCCCCACCTCC TGGAAACACA AATCCAGCAA	480
	CTAATAGGGC TCAGTGGTAT AACGGCCCCAT CGCTCTCTCA ACGCCAAGTC CCTCTCTGGG	540
15	GAAAACATGT GATCACGTGC TACATATTCA ACCCCCGTCT TACCTCATAG CTGCGCATGT	600
	CCASCCCIGA ACTOTICOGA CCITCOGICT TOCNGAAANC CIGATICCCT TCCITTAATT	660
	COCCCTCTCC NCCAACCATG INTCOCCCAT TIACTICCGT TGCTTTTTTA TTTCGTGCAT	720
20	TGITTTINEA AAAGNOCTG TEAANTAAAT NOONICATIN TOGA	764
	(2) INFORMATION FOR SEQ ID NO:477:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 778 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1339UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:	
	CATCAGCOCA TITUTICCATA GIUCCITICA TIUGAAAAAT COGATCATTA CCATGCTGAC	60
	TATACCTCTA CTCACCAACG CCTTTGCAAA CAAAGACTGG GGCCTTAACC TAATGTCCTC	120
40	TOCOCCAATG TATAACTOGA TATTTOOCTT GATTGATOCA GACCACOCAA CTTGTCCTCC	180
	TAAGCAACAG TCATCACTGG CCGTAGCAAT AGCTACCCTA ATATACAACT ACTCAGTGTT	240
	OSTAGTAAAA CACAACAACC ATGACATOCT AGCAATTGIT GCAGAGGITC TAAACAACAA	300
45	ATACOGCTCC TCTTCCTTTA TCCTGCGGAA CGAGGAGGCC GCATACAGAC TCCTTGTTGC	360
	TTACGGAAAC TTAAGTACTG TGGAAGGCAC CTTCGCACAG TTTGCTCCTT CTATCTCATG	420
	GATAAGGAAG CTGAAGAGCC AGTATGGCCA CATATCGAAA TTCCAGGATA TTTTAAATGA	480
50	TATTTAAAGA AAGGTGTACG TATATATCCT ATTCTTTCGA TCGCTGTCCC GAGGCCTTCC	540
	COGAAAAATG GTGAAAACTT COCTCTFTGA CACACACCCT TTGCCCTTCA ACAGGATAGT	600
	TIGAAGGGAC AIGHICTIGIT GACAANNOTTI GAACCAGGGT ACTOGIIGNAA AATTINAANA	660
55	TOTTITICTOC NOOCAAANON ANTICTNOOG AANTTAACOG GAAAAAAANO COCCIONNOC	720

	CITINITIAN TAACCOCCC CACCUITNIG ACCIIGATIT TIACAAAACC TITIINIT	77 8
	(2) INFORMATION FOR SEQ ID NO:478:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 766 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1340RP	
15	•	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:	
	GATCCCCTGA TATCCACAGE CACTITTGIA TATTACCAGI ATTCTTGACG AGATAATGCA	60
20	GICAACICCI ATATAGAAAC COGATACAGI OGIAAAAACG CAAATGTAGG CAATTATATA	120
	TTACTOTTOT CGACACCACT AACTICICGA TAGCOGCATA TOTTGTAAAT TTGCATACAC	180
	CTITICCCAA CTITICAGIGG TCTCGITGGC GIACTITIACA TGCATCLIGG CCCATTCCTG	240
25	CAAGACATOT GTGATACAAA ATTGAGTCTC CTGGAAAATT ACAAATTCCT CTAAAATGCA	300
	CTTICTAATT AGCCAGGACC TGITTAGFIG CTCAGCAATT GTCCGTTTGT CCCGTTGAAT	360
	TGTCTGTCTG AGTTTATCAT ATTCTGCACC TTTAACGTCC GGATTACTCT CCATAGATTG	420
30	AAGITIGICC ATAITTATIT CCACICICCT CIGCAAATGI GCTAIGITAT TCCCCGCCAT	480
-	AATTITATAC CTATCAAAGA CCCCTTCAGT GCTATAATAA TATCTATGAA GGTCTTAAAC	540
	TICACCGATA GETGITICCIC CACTICCICA COCICCITTO TIAGAGGIAT COCCCACGOT	600
35	ATTGAGATGT TITTIGATAIN NTGGAAATAT GANATTIAAA TATCNIGAAT AGTGCCTCTT	660
	CCTATTOGGT ANAANTGITIN CAGAATTATC AANCAATTCC TCCATCACNC NGCCAAGCAC	720
	CONCOGRECT TONAMACCT GONOMINGOC COGENEGGET NUMANA	766
40	(2) INFORMATION FOR SEQ ID NO:479:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 790 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1340UP	
50		
	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:479:	
	GATCTOCTOT ACCTGAATOG ACTTTOTCTC CTGAAGTAGA AATGTAATOG CCCCTTCCGG	60
55	AATACATAAC AAACATAGOG GAGACAAAAA CAAAAGOGTT ATACAGOCAT CTGCCGTTAC	120

		180
	ATATTATOTIC GCTAAGAAGG GCCAAATCGT TGCCATCGCT TAAGAATATC GCTGAGGTGG	240
5	CCAAGCCCAT CACCAAGGCC CCCCCCCTCC CCCTGCTTGC GTTTGAGGGC CCTGGGCTGT	300
	CCACATGTCG CTGGTATCCC ACCACGGTGC GCACAGTGCA CAATACCCCC AGTAAGGCGC	360
	AGACGACCCT CCTCTCCACA CCGAAGAAGG AGAGTCCGTT TICCCCAATG AACCTGAAGG	420
10	CCTTOCOGAA CGAGTOCCOC TCCCGAGOCT CAGOGTCTCC GGGCGGAAGT CGGATTTGAT	480
	CGAGCGCATT GTCGACTICG AGCTGAAGGG ACCGCTGGGC AGGCGGGGGA CACGGGGGCC	540
	GITCCACAGC CCGGGCACGA GCAGCGCCAG CGTATGCCCC CCGTGGACAA QGTCACCATG	600
15	CCCGACATOG COUTTGACAG AACGAACCCC GTGCCACACC CTGAGAAAAA CTACATACTC	660
	CGGANICCIVI CIVITGIINCCI CCAAGGGGGT TTCCCTCCCC GTTACCIVATT CCIVAAAAGAT	720
	TTTTGCCNCG GAACCCANGA AGAAACCACC CGAACTCCCA GAAGGGGGTNT TTNNNANCCG	780
20	AACCGAANCT	790
	(2) INFORMATION FOR SEQ ID NO:480:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 765 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) Original Source: (A) Organism: Pagl341rP	
	(W) OURWING: EMPTRATIVE	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:	
35		60
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:	60 120
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480: GATCACATOC GATGOGAAAC TOSTATATTG TITTCCCACA AIGATGAAGG TGAGTGIGGG	120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480: GATCACATCC GATGCGAAAC TOSTATATTG TITTCCCACA AIGATGAAGG TGAGTGTGGG GCAGCAATTG TCCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT	
	(xi) SEQUENCE DESCRIPTION: SEQ ID ND:480: GATCACATCC GATGCGAAAC TOSTATATTG TITTCCCACA ATGATGAAGG TGAGTGTGGG GCAGCAATTG TCCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT TGCAATGTGA TTCATGATGC AAATGGAAAC CCCATCCAAG TTTCACAGTC GCAAAAGAAC	120 180
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480: CATCACATCC CATGOCAAAC TOSTATATTG TITTCCCACA ATGATGAAGG TGAGTGGGG GCAGCAATTG TOCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT TGCAATGTGA TTCATGATGC AAATGGAAAC COCATCCAAG TTTCACAGTC GCAAAAGAAC AGTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTG	120 180 240 300
40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:480: CATCACATCC CATCOCCAAAC TOSTATATTG TITTCCCACA ATGATGAAGG TGAGTGTGGG GCAGCAATTG TCCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT TGCAATGTGA TTCATGATGC AAATGCAAAC CCCCATCCAAG TTTCACAGTC GCAAAAGAAC AGTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTG CTGCCGGATGC AACGAAAGTG TCCGCCCATG CTTTACTCCA GGCCCTTTTT ACCTCTAACG	120 180 240
40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:480: CATCACATCO CATGOCGAAC TOSTATATTG TITTOCCACA ATGATGAAGG TGAGTGTGGG GCAGCAATTG TOCGGTTGAC GACTOCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT TGCAATGTGA TICATGATGC AAATGGAAAC COCCATCCAAG TITCACAGTC GCAAAAGAAC AGTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTG CTGCGGATGC AACGAAAGTG TGCGCCCATG CTTTACTCCA GGCCCTTTTT ACCTCTAACG AAAGTGAAGT AACTOCTGGA TGTATTACCT TTCAGCAAGT CAGAAACCTG ACCAGGTTCG	120 180 240 300 360
40	(xi) SEQUENCE DESCRIPTION: SEQ ID ND:480: GATCACATCC GATGCGAAAC TOSTATATTG TITTCCCACA AIGATGAAGG TGAGTGTGGG GCAGCAATTG TCCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT TGCAATGTGA TTCATGATGC AAATGGAAAC CCCATCCAAG TTTCACAGTC GCAAAAGAAC AGTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTG CTGCGGATGC AACGAAAGTG TCCGCCCATG CTTTACTCCA GGCCCTTTTT ACCTCTAACG AAAGTGAAGT AACTCCTGGA TGTATTACCT TTCAGCAAGT CAGAAACCTG ACCAGGTTCG ACTAGTTTTT TATTGAAGTC CGTGCTGTCT CAGTATTTGA ACCAGTTAGT CCCACGAATG	120 180 240 300 360 420 480
40 45	(xi) SEQUENCE DESCRIPTION: SEQ ID ND:480: GATCACATCC GATGOGAAAC TOSTATATTG TITTCCCACA ATGATGAAGG TGAGTGGGG GCAGCAATTG TCCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT TGCAATGTGA TTCATGATGC AAATGGAAAC CCCATCCAAG TTTCACAGTC GCAAAAGAAC AGTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTG CTGCGGATGC AACGAAAGTG TCCGCCCATG CTTTACTCCA GGCCCTTTTT ACCTCTAACG AAAGTGAAGT AACTCCTGGA TGTATTACCT TTCAGCAAGT CAGAAACCTG ACCAGGTTCG ACTAGTTTTT TATTGAAGTC CGTGCTGTCT CAGTATTTGA AGCAGTTTAGT CCCACGAATG AGAAACTTAA AGAATAATAG AATGGGGGAAG ACTCAAAAATT TACGGCTACC ATTAAGACTCA	120 180 240 300 360 420 480 540
40 45	(xi) SEQUENCE DESCRIPTION: SEQ ID ND:480: CATCACATCC GATGCGAAAC TOSTATATTG TITTCCCACA ATGATGAAGG TGAGTGIGGG GCAGCAATTG TCCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT TGCAATGIGA TTCATGATGC AAATGGAAAC CCCATCCAAG TTTCACAGTC GCAAAAGAAC ACTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTG CTGCGGATGC AACGAAAGTG TCCGCCCATG CTTTACTCCA GGCCCTTTTT ACCTCTAACG AAAGTGAAGT AACTCCTGGA TGTATTACCT TTCAGCAAGT CAGAAACCTG ACCAGGTTCG ACTAGTTTTT TATTGAAGTC CGTGCTGTCT CAGTATTTGA ACCAGTTAGT CCCACGAATG AGAAACTTAA AGAATAATAG AATGGGGAAG ACTCAAAATT TACGGCTACC ATAAGACTCA CAGACTTACT CGACTCGAAC GTTTTCGTCC GCACTTTGTC CTGCGAGTCA TATACAGACC	120 180 240 300 360 420

	AAAANCAGNG AACCATACNA TOOGITTAAT AATGAACIVIT CACNI	765
	(2) INFORMATION FOR SEQ ID NO:481:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 810 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pag1341UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:	
	GATCAGAGTA GATTTAGTAA AGAGGTAACC ACCACTGTTC CAAGAAGTCC AGGCCCTTGG	60
20	CHICACCAGC ATTOGRAGIT GCTGIGGCTG GAAATTTGCA CTTAAACGGT CTGAGCTCAT	120
	CTOGTTCOCC ANAGACCTAT GAAGTTTCAN ANCACCANCT TTOCTGCCCCA TTCTATATTG	180
	AAATGIATGA CAGATGOCAG GIOCCTTACC GIACACTGIT TIATTGGIAA CTGGGTCIAC	240
25	ACCITICACE TICACCITIG CCACATGGAT CAACATAGAA ATTAAAAGAG AGCCAACCIT	300
	AGCCTTGATA TIGTGCGCCC AAAGAACTTT AGACTCCTCA ATTIGTGTAT TICTAAACGT	360
	GGITTITIGCC CTTTGGACCA GCTTCTTGAA TTCGTTACTA TTCGCCCTAA CTTCCTTAAA	420
30	AATOGATTIC TCACTCTICA ATAGTOCTIC OGATCIGTAT TCCATCTCGA CAGCCTTACC	480
	TATAGOCAGA ACCOCTCCTG GITGITCTCA TACCTTCACT GACOCCTCCA GITAGAATTC	540
25	CAAGOCTITA CONATTOCCO AAATTGITTA TGAANACACA TTTCNOCTNG ANINACCOCA	600
35	AATTGAAATT ANGOGENCTT TTCCANNOON TGAAANAAAA TGINGAACGG NGTTTCAGTT	660
	AAGCCCAINT ATCACINGON ANCATTONIN AAAAANGCTT CCCCCCTCCC TTTTTAAAAC	720
40	GOGATETINE CAAAAAACON COCCUINAAT GAACCATTIT NOGAAANCOG GAACCCONG	780
	CCCTCNCCGN CTANATTCCN GCAANNCAIN	810
	(2) INFORMATION FOR SEQ ID NO: 482:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 759 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5 0	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1342RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:	

	GATCCTGATT TIGATTICOC CATTGCTGAT GITAATGCAC TCAGTGCTGA TGTCCTATAT	60
	ATCCAGCATG AATTATCCTG GTGGATATGC GCTATCTGCA TTCAACAAAT ATGTGCTGGA	120
\$	CAATAATATC TOGAATGOGA COGTOCACCT AGATGTCTTC ACTIGTATGA CCGGTGCAAC	180
	GCTGTTTGGA CAGCTGCCGG ACTCCTACGG GATCATATAT GACAAGACTG AAGGTGATGA	240
10	ATTATIGGAC GCATGGICAT CGITCGATTA TGICATTACA ACTGATCCCA ACAGCICACT	300
10	GOCTOCTGTT ACAGGCTACA AATGGGAGGC CATCCAAACT ACTGAGGCCT TTGACCGCTT	360
	CGACCITAAA ACTATACCOG AAATAATCAA CTCAGAAGIT OCTAAGCGAT TOCCIATCTT	420
15	AAAAGATGCA ATACTCTCTG CAGACCTGCA ACCTGTGAAG GCTGCGTTCA CAGATGTGAT	480
73	CAGGTGCAGG GATTCAGTGT ATACATATAA AAGAGTTGAG AATTAATAGA ACCAGGCCTC	540
	COCTTACOGA CAGTITICCAT ATAAATATIT ATITATTAAA CITAAAAGIT CTOCGAGTIG	600
20	AGGAGGAATT TGACTGCTGG AGATTCCGAC ATACTGAAAA CATAAAGTGC ACATTTACAG	660
20	GATTOGGCAG THACTIGART CCCCONTOCIN NACCPRAAAT GCCTGATCNA ACTINAAACA	720
	TCCTATTGAA CCCCCTTTGG TCWTCCAANC AAANINTAA	759
25	(2) INFORMATION FOR SEQ ID NO:483:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 802 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1342UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:	
	GATCGGGCAG GCCGCGGAGC AGCAGTCGCG CGCCTTCAAG GAGGCCGCAG ACTTCGGGGC	60
40	CATCATCCTG ACCAAGATGS ACGGGCACGC CAAGGGCGGC GGTGCCATCT CCGCGGTGGC	120
	CGCCACGAAA ACACCCGTIGA TCTTCATCGG CACAGGCGAG CACGTACACG ACTTCGAGAA	180
	GTTCTCGCCC AAGTCGTTCG TGTCGAAGCT GCTCGGCATC GGCGACATCG AGTCGCTGCT	240
45	GEAGCAGTIC CAGACCGICT CCAACAAGGA GGACACCAAG GCCACCATGG AGAACATCCA	300
	GUAGGGCCGC TITCACCCTGC TGGACTITCA GAAGCAGATG CAGACCATCA TGAAGATGGG	360
	COCCCTIGTICC AACCTCOCCA GCATGATICCC CUGCATGAGC GGCATGATGA GCCGCCATCTC	420
50	CGAGGACGAG ACCAGCCGCA AGAIGAAGAA GAIGGICTAC GIGCICGACT CCAIGICCCG	480
	CEARGARCTC GAGTCGGACG GCGCTCTTCA TCGARGARCC CGCCCGCATG CTGCCGGTCG	540
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	600
5 <i>5</i>	CCANATGATT CCCCCCCNIT CCCCCANGCC CCCNANAACA TICCCCCCCCCCCCNIG	660

	COORDINATE COORDINATE COORDINATE CHOCOCONANA NGATINTNACC NGCOCNANCN	720
	TONVITINACT CAACCONCCC NIGANNOCCON CATAATIGGCT NINCCGNNGG GGNCCNGGGC	780
5	CCCCATGCCC CCATTAGGCN AT	802
	(2) INFORMATION FOR SEQ ID NO:484:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 844 base pairs	
10	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(11) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1343RP	
2 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:	
	GATCAACCAA TGTGTTAAGG AAATTTTTAA CGTTTTCCCG GGATTTCCCC ATCTTTCCCT	60
	CTARTICGIA GGAAACATAG TCTGTAGCAC CCATGATATT AGCAAGITTU CGCCGAAGCT	120
25	GAACCAAACT CITAAGCCTC TICACTTGTT TTTCGCAACA ACTAAACATT GCGGTCCATA	180
	CCTOCCTCCG AATACCCTCT GAAGGACAAG CATTCAATAG TGTATACGCA GCATACCCAC	240
	TAGTIGGIAT CITATAGTTA TTACCCATGG TGTCCTTGGT GAGCTGACGA AGAACAAGAT	300
30	GOCTAGTOCC ACTOGRATICC ARATCTITICS ACCGRATCTT TRIGINGCTG GRAGATRATIC	360
	ATTOTOTOT GITCATGAAG TOTTOGOCAA TAATOCKGAT GITTTGOGAT AACTGTATAA	420
	ACTOCTITCT GACTICOGGC GACGCATATG COCCIGCTIT TICAAAATCC TCIAGCAATA	480
35	TATOCCCTAC COGTATCTCC TOCCTCCICA GITTACTCCT TATATTCTCG TCCCATACCA	540
	CTTGTTTTAA TCTTTTGCAA AGCACAACAT CTGTATTCAA GATATCATAA TCTCAAACAT	600
	CIGITCATCA CATTOCCTGA GCTGCCGCAA CAAATTGITC ATCCCGATGT TGCAACCCGT	660
40	TARACTOCING ACARTINGART COCCOGREAT ARRATCOTER TITICATICIAT CHARTCATINI	720
	NONCCCAACC TOTTGTGACA ACCOTONCAG TOCTTACAAC COTACCOGIT ATGATTTTNG	780
	NAATTOCIAC OCIOCNOCAT TIAGITGITC NANATACCIT TAGACCOCC GENEGACITA	840
45	TCAN	844
	(2) INFORMATION FOR SEQ ID NO:485:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 676 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
5 5	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1343UP	

	(XI) SIZUMED MOSKIFITAN, SEQ ID NO. 403.	
5	GATOGATTAA AGGAAGCATO TOOTTOOCGT CATATOATAT AACATTIGTAC COGGGGCTGA	60
3	GOGGACCAG TAGOGAATIT GATAGCAGTG TTCTCCACGT CCCCGCTCCA CTGTGAGCTC	120
	CTTAAAGTAT ACCOSCITICA TACACCAGIG CCCACAATGA TOCGIACTIG ACTIGIAATC	180
10	GAGAGCATTIG GGCTTATACT GTGATTACGA TGAATGTAGC CAAGAGAGAA AAGGTTCATT	240
	CACGATATAC AGTACTCACA TICATGGCAT GCCATCCCCA AATICCAATA CAGCCATTAG	300
	CACCAATGTA GOGCTACTAA TOOGGOGAGO TTAATTGGCG TCAGTTCAGA GTGAATCTCG	360
15	ACCTIAAAAG TCAGATIGAT TAAGIAAGAA AATGACGATC AACAGGGTGC TCAAAATAGT	420
	TGATTACCAG ATTCGGGGGT GTGGTCTAGT GGTATGATTC TCGCTTTGGG TAAGCGAAGT	480
	TOCOGUITCAC TOCOGOTTIAA CTACTAAACA TOTGAGAGOC COTGOGUTCA ATTCCCAGOT	540
20	CGCCCCAAAT TITITGCTCT COCCTCCCGC GGCAAAGGTG AATATCAITT TACAAGTAGT	600
	TAACTOCTCC CACGITIACGT CCTTCTGCAG ACAAGITIGCA GCGGTTTACA ATGCTCAGGC	660
	TATTTTGCGG CTTCAA	676
<i>25</i>	(2) INFORMATION FOR SEQ ID NO:486:	
30 35	(i) SPOUDICE CHARACTERISTICS: (A) LENGTH: 827 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAG1344RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:	
40	GATCCTTGCG TACTAAGAGT TAGACITTAA TTAATAATAT TATTTGTAGA AGATAGAAAC	60
	CATACTGACT CACGTCGTAT TTAACCCAAC TCACGTAACC TTTTAATTGA CGAACAGTCA	120
	AACCUTACIT AGCIGITACA ACCAAGAGGA TAGGITGAGI CGACATOGAG GIGGCAAACA	180
45	TAACTTACAA TAGCTACTCT ATCGTTATAT TACCCTGTTC AATTTTGTTA TCATAATAAC	240
	ATTTAATTAT TATTTCAATA ATTCTCATTA TIGTTCAGAC TATTTCATTA TGTATTATTT	300
	ATTAATTAAT ACATATTGGG CITTCGTGGA TATAATTATT GTTAATCCTA CTCATATATC	360
50	TAGICGITGA ACGITICITAT AACITTATAA AAAGGATTGI TATAAGCITC GCTGCAGATT	420
	GICCTPTATT ATTATAAAAT AATATTAGGA GITCTPTGCA ATTAACCCAA TTTACTCAAT	480
	ATATTIAAAT ATTGATAATT AAAITTCACA ATTTAATCOG ACTATTAATT AATCCCTAGC	540
55	GEAACTITTA TICGITTATC AAATACCATT ACAATAIGIT ATAITIGITC ATTAIGCCAA	600

ACTTACGITÀ TIGINCIACI IGIAGIATTA CNATTATAGC ACAGITACCC CATCATATTI	660
ATTTAATANA TACCCCAANT AGNITTITTT ANCATAAAAA GGANCTAATT TCCCTTTTTT	720
CNCCAANICC INCICTCICA ATATINITAA AAATTITAAA CANAANIAAG AAACCCCINN	780
TNAACCNCAN CTITTITICAN GOCTTICNAN CCINITNAAT ANCCCCN	827
(2) INFORMATION FOR SEQ ID NO:487:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 872 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genamic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1344UP	
(with growth and property of the property of t	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:	
CATCCITATA AAATOOOCAA TACACGTOIT ATAATATAAT ATACAAAATT ATAAATAAAT	60
ATTEMPA ATATAAATT AATAATTAAA GEATEATAAT AATEAATAAA ATTATTEMP	120
AATAAGIATG GATTITTAAC TGAAATTTGI TAAAATGAAA TAAGAATTGC TAGIAATCTA	180
TTAATAAGAA AGTAATOGTG AATACTCTAA CTGTTTCGCA CTAATCACTC ATCACGCGTT	240
GAAACATATA ATTAAATAAA GAATATTAAT TAATTTATTA ATTATTAATT ATTATTAATA	300
TEATTTAATA AATATAATAA ATATTITAAT TEAAATTATG AATTAATGCG AAGITGAAAT	360
ACAGTTACTG TAGGGGAACC TOCAGTGGGC TIATAAATAT CTTTAATATT CCATTTTTAT	420
ACAAATAAAT ATATTTTTTA ATATATTTTA TAATAACTAT AATTAAATAG TTAAAATTTA	480
AATTATAATT TAATAATTTA ATAACTTATT AATTAGAGAG TTAGGGTACA TOOCCCCTAA	540
TOCTATOCAT TATOGTTOGT ACCACTCTAA TTAATAAACT ATAATAAATA AATACTAATA	600
TTTTATATCA ATTAATTAT AATTATTTT TATTAATATT TTAATATTAT	660
ATATAAATAA AGTATTATAA TTTAATAATT AAATAAGAAA TGAAGANAAC GACTCTCANA	720
ATTAAATTOC ATTNATAGIT TACCATTAAA CAACATTCCC TTATTCATAT TATTINATCN	780
ANIAATIAAT ATCITATTAT TNATTAGAAG GANACOVING CNCCCCTAAT OCTUNGCATC	840
TIGIOGIACO NONATIAAA AAGITIACAT NA	872
(2) INFORMATION FOR SEQ ID NO:488:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 835 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1345RP

5		
_	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:	
	GATCCCAACG TCTGATTATG TGTGTGAATG CTGTTCTCCT GCTCCTCCTG AGTCTCCTTA	60
10	CCCTTCCCCT TGTACACTTT CCCGTATGTT CCTCCTCCAA TATACCCCAT GATTTCCTAC	120
	TTCTCCAGCA CTGACACCCT ACCGGOGTCT TTCCGCTGCC GATATGGCCC TATCGAGAAC	180
	ACATTGTTAT TOOCCATTAG CATOGGGGAT TTGCACGTGC TGGCGCTGCC TTTGGTATCG	240
15	AGAAGCTGCT GTTGCTGTTG CTGCGACCAC AGGCTCCGGG TGGATGCCTG GTTGGATACG	300
	TIGAAATACT TATTCTGITG TGTTTGATGC TGATTATTCA TACTATCGGA GGACTGTAAA	360
	OGTATOCOCA TAAAATAGAG AGCTOGAGCT ACCACCTGAC GACTTGTGTT ATTTGTAGTG	420
20	TEAAATOGAT ATOGOCTATG TICTAAGCTC GTITTTAAGT GTAAAACATT GCAAATOCAT	480
	ATGCACACAG CTCATCOGGT TCTACCGACA ACCCTCTTGC GACCGGAGCG GTGGAGCTGG	540
	OSTOCATACT TOCOGASCOC CTATGTAGTA TATACASCOT GOCACGGCTG CGCCTGCCCG	600
25	GETIGCAGGGE CTICAGCAGGA MIGCOCCTTIC CNCCACTGCT TTATCCTCCT GAAAGCCGTA	660
	CAACCNOOGS INVAAATACGG GGCACOCCAAA GCNGCCCGAN GCCCCCCGAT AANAACNICA	720
	CCASCOVIAG NGAGGCCCCG AAANAACANT GCCCTTTTTC AGCGGGCCGT GGCACAAACC	780
30	CCAAGENEGN TCCCCOVITGE GNVITTIAAT NECCNIXOSOG ANDCCCCCNIT NCTCT	835
	(2) INFORMATION FOR SEQ ID NO:489:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 863 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1345UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489;	
70	GATCCCCCCT CACCCCAACC CACTCTACTG GCCCACGGAG ACCCCCAACAG CATTCCCCCA	60
	GOGAGAGCTG GAATAICGCG ATGACCACAT TTCGAAGGCA GCTTACGTTT ACTTTCCGCT	120
50	AACGGAGGGC GCGAGCGCCA CGCTACGCGA GCGCCTGGGC ACGTCCCTCC CAGAACACCC	180
	CATCCTCTCT CTCATCTOCA CCACTACACC CTOCACTCTC CTGTCAAACA CASCCATCTC	240
	TITICCACGAT GACCACGCGI ACCIGCTICT GCAATGGAAG GGTATGCTGG TGGIAGOCGA	300

360

CACAACTGAA CTACCTGACT TTAAATGGAG TGGTGACAGG CCGGTGGTGG TCACCTCATT

55

	CCCCCCTIFIC GACCICCCC GCCICIATIA TACCAATICA CITCHICCG ACCCCITAG	420
	TAGOCCOCTO CTOCATOGAG ACCATOTICAC COCCGACACA OSTACTOGTIC TOGTACATAC	480
5	TOCOUCAGOG CACOGOCCAGG AAGACTACCT AGIAGGTCAG GCGCACGOCA TTGAAGTCTA	540
	CTCCCCAGTC GACCATGAGG GGAGGTATAT TCTGGATGAT ATTCCTCCAC ACCTCCGTGA	600
	TATOCTAAGA GAAGAGAGCG GTAAGCCGCT GAAGGTTACA GACCACAAAG ANTOCNGGNT	660
0	CTTCATCAGT TTGCTANAAA AACCCAAGAT GCTCCTGCAT TCCCTGAATA CCACNCTCNT	720
	NICCCINCAA TOGAGICNAA NAACNIGIIT TCNAGANCIA CCCNNCCGIN GITGCNAACT	780
	GATGGACTGA ACTTCCCCCCN GGAAACCTGA ACACTTTATT TTTCCCTNCC AGGGGAAAAA	840
5	NCGNICAACG ITCICNAAAN CGA	863
	(2) INFORMATION FOR SEQ ID NO:490:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 836 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1347RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:	
	GATCATCATC CCAGCGCCCA TGCCGCCGGC GGCACACCTT CACACCCACC CGTAACTGAC	60
	ANTACTOGAS CACCTTOGTS COCTGGCCCCG CTGGCCGCTG CCTGGCCCAT TATGCAACCA	120
35	COCACACGIT TTATTCCACT TAAAAATTAC TTAAGCTGAC GTTACGCCTG TTGAAAAATT	180
	TICOCTICAC OCAATTITIC TOOGICACAT ATAAAACOOG CIAAGITOCA CAGICAAAAG	240
	GREAGITHT TIGIGITTAG ACTICITITA TGACCICATA GAAGGAATTT GOGAAATCTG	300
10	ACTITICIACO ACCUICICIO CAGITIGGAAG TETITIACATA CTACTOCTAA ACGIGOCCIA	360
	AGITAAGATT TICTTTICHT TAGITTTAAA CICAGIACCI TATTCCATAA AGCGACACTA	420
	CGATGTCTTC TAGATTCTCC CTCGTCTCGA ACCTAACGAG ATCCTTGAGC TCTGTGGGGC	480
15	GGATGCAACA GATGCGGTTC GCATCGTCGA AGTCGATGAC TGTGCGGGAT GCGTTGAACA	540
	GTGCCATCGC CGAACACATG CACCCGTCAT CACCATGTGT TCATCATCGC ACACAACTTG	600
	OCCCAGTAC AACCGTGCCG TTACAAGTCA CCCAAGGCTT GTTTGACCGT TCCCGNAACG	660
50	COGTINGING ANACCCATCA CCGAAANGIT TITIOCCGTCT TOCGTGGGIN CNCCTGAAGG	720
	CNIGACCCTA TGTCATTCAN TNGPTCACTC TCCAGCAGCA NGACANTTCT GAATCCGGGC	780
	CAAATACANN TIOGTGTGTG CNACCNTCAN TGTTTOCAGC NAAGNOOGNC NOONNC	836
55	(2) INFORMATION FOR SEQ ID NO:491:	

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 869 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(11) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1347UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:	
	GATOCTACAG AACTCAACTC TTATATOCAG GACTCAGTCA COGCGTCTGC AATOCGCAGC	6 0
15	AGCCACGCGT GCTCCAGGCT GGGTGGCCAT TGGATGGGTG GGCACGACCC GAGTGGGCAT	120
	GIATTOCTCA TAACGITAAT GIGTATGITT ATOCTOCOCC ACCTOCACGT ATTTOCCCCC	180
	COCOCAATOG GGAAGCTTTC TOCTGATTGT CAACAOCTOC AGGOCGCTCC TOGTAAAATT	240
20	GTGGCACGCA TTTTGCAAGC AAGTCCGATT AGAGACCTAA TTAACTCTGA AGCCCCCCAA	300
	CATATITIAA CACOCCTPIT COTICAACTO CCACTAGAGA GICTIOCGAT TCTOGTGAGC	360
oe.	COCCUTETIT TICCCUTTCG GUICATICUG CUCCAAAAACC CCAUTCUATT CCUTGUCCGU	420
25	CTIATICIGA CATGGACCIG GICACIOCIG GIAACTATAC TCICTITOCA TIOGTITIGOG	480
	GAGCATTIGA CCGGITTIGCT CTTCGCATAC CTTCTAGTTT TGGCGTTATA CTGGTACATA	540
3 0	TAATGATCTA AGTAAAATCT OCAATATTAC ACACGAACGT TAAACTCGCC AGCTOGATAT	600
	ASSCAAAGAT TOCAGATECT STOCTITCCS CCTAATATEC SGAAAGATGA SCASSCCAAA	660
	CCCAATGCAG AGTAGGTTCG TCATATAGTA ACCATCGCGC AGAATGACAA CTTCCGCCCG	720
35	CTTTOGAAGC ACTOCOCTICO GGAAGGAACA TOONATGGGC GAATTTTGGC CACCTTANAA	780
	TINAANAAC TAICATOOCO ATAATACATO OSANACAATT ACCCCCANAA TAICAAGIAT	840
	CNCAAATITT CNITANITCN CCAATACCN	869
40	(2) INFORMATION FOR SEQ ID NO:492:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 772 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (génomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1348RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:	
	GATCCTTCCG CAGGITCACC TACGGAAACC TIGITACGAC TITTAGITCC TCTAAATGAC	60
55	CAACITICAC CACATITICC OCTCIGAGGI OCACTIGCCC CCTCCTCTAA GCACATCCTG	120

ACCCCTCACT AACCCATTCA ATCCCTACTA COCACCCCC CTCTGTACAA ACCCCACCCA	
ASSOCIOACI AMBOLITICA AIGOSTACIA GUALGUGGO GIGIGIALAA ABBOLIGAGA	180
CGTAATCAAC (CCAACCTGAT CACTTOCOCT TACTAGGAAT TCCTCGTTGA AGAGCAATAA	240
TTOCANTOCT CTATCCCCAG CACGACGGAG TTTCACAAGA TTACCCAGAC CTCTCGCCCA	300
AGGITATACT COCTOSCTCC GTCAGTGTAG GCCGCGTGCG GCCCAGAACG TCTAACGCCA	360
TCACAGACCT GITATTOOCT CAAACTTCCA TCGGCTTGAA ACCGATAGTC CCTCTAAGAA	420
GIGCGCAACC AGCAAATGCT AGCAGCACTA TITAGTAGGT TAAGGTCTCG TTCGTTATCG	480
CAATTAACCA GACAAATCAC TCCACCAACT AAGAACGGCC ATGCACCACC ACCCACAAAA	540
TCAAGAAAGA GCTCTCAATC TGTCAATCCT TATTGTGTTC TGGACCTGTG AGTTTCCCCC	600
GTGTTGAGTC CAATTAAGCC GCAGCTCCAC TCCTGTGGTG COCTTCCGTC ATTCCTTTAT	660
TTTCACCCTT GCGAACATAC TCCCCCCGAA CCCCAAAAAT TGATTCTCCT AGGTGCCCAT	720
TGTINCATAA AAACACACOC ATCCCTATTC GCATATTTAT GTTAAATACA AG	772
(2) INFORMATION FOR SEQ ID NO:493:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1349RP	
(II) Green and Indiana and Ind	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493: GATOGITATA TATCAGUCTO TUGCTATAGA TUACTATAGA GCCCACCACT AATGIACAAG	60
·	60 12 0
GATOGITATA TATCAGTCTC TTGCTATAGA TTACTATAGA GCCCACCACT AATGIACAAG	_
GATOGITATA TATCAGICTC TIGCTATAGA TIACTATAGA GCCCACCACT AATGIACAAG TTATAACTAC TOGTAACACG TTATATAACA GGTAGGAAAC GGGGGCGGCG GGGATTTTTG	120
GATOGITATA TATCAGICTO TIGOTATAGA TIACTATAGA GOCCACCACT AATGIACAAG TIATAACIAC TOGTAACACG TIATATAACA GGIAGGAAAC GGGGCCGCCG GGCAITITTIG CCTATGGCTT GGCCAGGIAG CAACTGCTAT AAAGGCGGAC GTTICTCCCG GAGCTTTTTC	120 180
GATOGITATA TATCAGICTO TIGOTATAGA TIACTATAGA GOCCACCACT AATGIACAAG TIATAACIAC TOGIAACACG TIATATAACA GGIAGGAAAC GGGGCCGCCG GCGATTITTG CCTATGGCTT GGCCAGGIAG CAACTGCTAT AAAGGCGGAC GTTTCTCCCG GAGCTTTTTC ATCTTGCGCA GTTTCACTTG CTAGTTAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT	120 180 240
GATOGITATA TATCAGICTC TIGCTATAGA TIACTATAGA GCCCACCACT AATGIACAAG TIATAACTAC TOGTAACACG TIATATAACA GGTAGGAAAC GGGGCCGCCG GCGATTITTG CCTATGGCTT GGCCAGGTAG CAACTGCTAT AAAGGCGGAC GTTTCTCCCG GAGCTTTTTC ATCTTGCGCA GTTTCACTTG CTAGTTAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT CGTTTTAATG GCTGGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT	120 180 240 300
GATOGITATA TATCAGICTC TITOCTATAGA TIACTATAGA GCCCACCACT AATGIACAAG TITATAACTAC TOGTAACACG TIATATAACA GGTAGGAAAC GGGGCCGCCG GCGATTITTG CCTATGGCTT GCCCAGGTAG CAACTGCTAT AAAGGCCGAC GTTTCTCCCG GAGCTTITTTC ATCTTGCGCA GTTTCACTTG CTAGTTAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT CGTTTTAATG GCTGGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT AGCTCCTTAC GCGGACATCC TCTCTGCGAG ACGGTTCCTT GCCCGACAAGT GGAGGCACGA	120 180 240 300 360
GATOGITATA TATCAGICTC TITECTATAGA TITACTATAGA GCCCACCACT AATGIACAAG TITATAACTAC TEGTAACACG TITATATAACA GGTAGGAAAC GGGGGCGGCG GGGATTITTIG CCTATGGCTT GGCCAGGTAG CAACTGCTAT AAAGGCGGAC GTTTCTCCCCG GAGCTTTTTC ATCTTGCGCA GTTTCACTTG CTAGTTAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT CGTTTTAATG GCTGGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT AGCTCCTTAC GGGGACATCC TCTCTGCGAG ACGGTTCCTT GCCGACAAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGGCGGGG CAGTCTAGTT GAGTTTGCGC GCGACGCATA	120 180 240 300 360 420
GATOGITATA TATCAGICTC TIGCTATAGA TIACTATAGA GCCCACCACT AATGIACAAG TITATAACTAC TGGTAACACG TITATATAACA GGTAGGAAAC GGGGGCGGCG GGGATITITIG CCTATGGCTT GGCCAGGTAG CAACTGCTAT AAAGGCGGAC GITTCTCCCG GAGCTTITTIC ATCTTGCGCA GTTTCACTTG CTAGITAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT CGTTTTAATG GCTGGTGTAC CTGATAACGT CAAGGGCGTG GITGAGCTGG ACCCCTGGTT AGCTCCTTAC GGGGACATCC TCTCTGCGAG ACGGTTCCTT GCCGACAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGCCGCG CAGTCTAGTT GAGTTTGCCC GCGACGCATA CAAGAGCTAC GCGGTGCACG COGACGCGCA GAGCAAAAACC ATAACGTACA GCGAGTGCCC	120 180 240 300 360 420 480
GATOGITATA TATCAGICTC TROCTATAGA TRACTATAGA OCCCACCACT AATGIACAAG TRATAACTAC TOGIAACACG TRATATAACA GGRAGAAAC GGGGGGGGGGGGGGGGGGGGTTTTTG CCTATGGCTT GGCCAGGIVG CAACTGCTAT AAAGGGGGAC GTTTCTCCCC GAGCTTTTTC ATCTTGCGCA GTTTCACTTG CTAGTTAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT CGTTTTAATG GCTGGTGTAC CTGATAACGT CAAGGGGGTG GTTGAGCTGG ACCCCTGGTT AGCTCCTTAC GGGGACATCC TCTCTGCGAG ACGGTTCCTT GCGGACAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGGCGGGG CAGTCTAGTT GAGTTTGCGC GCGACGCATA CAAGAGCTAC GGGCTGCACG CGGACGCGCA GAGCAAAAACC ATAACGTACA GGGAGTGGGC GCCCAATGCA ACCCGGGCGT TTCTAGTCGG CGACTTCAAC GGGTGGATGA GACCTCGCAC	120 180 240 300 360 420 480
GATOGITATA TATCAGICTC TITOCTATAGA TITACTATAGA GCCCACCACT AATGIACAAG TITATAACTAC TOGIAACACG TITATATAACA GGTAGGAAAC GGGGCCCGCG GGCATTITTIG CCTATGGCTT GGCCAGGIVG CAACTGCTAT AAAGGCGGAC GTTTCTCCCG GAGCTTTTTC ATCTTGCGCA GTTTCACTTG CTAGTTAGTT TAGGGCTAGG TCCACAAACA TATTCCACAT CGTTTTAATG GCTGGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT AGCTCCTTAC GGGGACATCC TCTCTGCGAG ACGGTTCCTT GCCGACAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGGCGGGG CAGTCTAGTT GAGTTTGCCC GCGACGCATA CAAGAGCTAC GGGTGCACG CGGACGCGCA GAGCAAAAACC ATAACGTACA GGGAGTCGCC GCCCAATGCA ACCCGGGCGT TTCTAGTCGG CGACTTCAAC GGGTGGATGA GACCTCGCAC GAGCTCCAGA ACAAGGACGA GTTCGGGTGT TCACGGTGGT TTCCGACCTG GGCCGACGCC	120 180 240 300 360 420 480 540

	ATTACCHAMA NAMEMENCIAC TEOCHCECCHE COONCECCHE IGE	823
5	(2) INFORMATION FOR SEQ ID NO:494:	
10	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 879 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(V1) ORIGINAL SOURCE: (A) ORGANISM: PAG1349UP	
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:494:	
20	GATCOCGAAA ACTAACOCAC CAAACOCGAC OGAAGCCAGA OCTCTCTTGT AAAGTGOCAA	60
20	GATAGTGTAT GTCTGGCCGG ATGGCTCAGA GGATTTCTTG CGAGCATAGT GGCAGCGATT	120
	GACATATIGGA GITATCATTG CAAAAGCAGT GGCAATAGCA AGACOGGITT TGITCCAACC	180
25	OCCUPACION TOTALICATA TROSCOACAA GOGATTOTIC GAGRAGAAGG CCATCITCAA	240
	CACAACGCTC GCAACAAGGC CTAGAGACCA AGTAATGGCA AACTGCGCGA CACGCGCGTT	300
	GICCITCACA ATGCICTICA AGGICACTOC AAAGTTCATC GTOCTGAGAC CCGTGGCAAC	360
30	CGCAACCGIC ATCAACCICC ACTCCGGITT CICAACTAIG TACGCTCCGA TACCGATTAC	420
	ATTAGCAAGT AAAGGGCCGT ACTGTTGAAT CAACGTTGGG AAAAATGGAA CATAAAGCAG	480
	AACTGGGCTC AATACCGCCG CTATCACCCG CCTCATAGCC GGAGATACCC ATGTACCAGA	540
35	GCGGGAAAAA CCATATCATA CACAATAGGG CAGTCAAGTT CGTCCAGAAC ATAAACGAGT	600
	CAAAGGTACT GACAACAATG TAAAACAGAC TTGCCTGATT GGTGATGGGC TCGTCCGGCA	660
	GETAAACCAG TTCTCGICCT CCTCCGICAT AATCACCTCC TCCCAGCATT TCCTCCATTG	720
40	COCCOCCCC GACTCCCTTG CCCCCCTAGA NACCNNOGIG CTTGTCTTTG ANTOCACAAC	780
	CCCCNCGAAG GCCIGIGCCC IGGGIIGCCN AACITINCCI NAGICCICCC AGITIGCNIT	840
	ACTIACCCIC CNAAAAATIC CAAATATCON GGACNCCON	879
45	(2) INFORMATION FOR SEQ ID NO:495:	
50	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 829 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
55	(A) ORGANISM: PAG1350RP	

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:495:	
GATCTCTTGC AATTCCTGCT COGTCTCTCT GTGATCTCTA TTGATCACCT TTTGGAGTTT	60
OCTOCCTICA CAAACCGICG CAAACTIGIT CATAACTTIC TIATACCGIG CCACTITICCC	120
ASCOAGOACA TOGTOGOTGA TOGTGTGGAG CGCAATTGGA TOCOCATCGG CGGCCATGIT	180
ATCCTTGACC GCGATATTGC GTGTTGATGA AGTCTGAACG GCCTCGTIGGC CTGGACGTIAA	240
OSCGARARAG TRARATTATA TAGRACADOC ATGRGATTOG CTOGRAGTTIC AGGGRACCAG	300
OCCICGIOCG AAGCACCTIA GAGACCCATA GGAACCCACA TOCOCAGGAA CIAGAGAIGA	360
GACCCACCCA AGGTGAACTC GCCCACGGCA CAGGGGCAGT CTTAGCAACG TGGTIAAACAT	420
TAAAAATAAT ACATACGITA CAAGCAGOOG GCATAGCAAC TGCCTGGAGT CATGITTTAG	480
AGAAAAATAG AAAAATTATT ATAATATTCC TTGTGTATGA AATAAAACTG CTTTGCAACA	540
OGOGGCAGAG ATTCAGACCT GOCTGAAGOC GTAAAAAGGAC GAAAAAACCGA ACGAATAGAA	600
TTAAGATAGA AAAGCAGCAC TCGGCCAAGG CGAAGCGGGG CGCGCAAGGC GCCGGGGCTT	660
TOCCTIONONO TOAGOTIGOAA ATOCTOCTICA GTUGATOCTIG CTOCCCCTGT COCCUGTICTOA	720
OCTOCTOCAC TOCTOCTONI ATCOTTITGA TGAAAGNAGG CTGACGCGCG TGTTCACTCC	780
ATCHTONONO CONCOCTOG ATAAATTOCT CAGONOTACC TOTTOGNING	829
(2) INFORMATION FOR SEQ ID NO:496:	
(i) SDQUENCE CHARACTERISTICS: (A) LENGIH: 875 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1350UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:	
GATCCGCATT AAGCGCGACG ACGAAATCAA TACCAAGAAG CTCGACGAGG AGAAGGAGCG	60
GCGCCTCAAC GCCATCATCA ACGGCGCACC TAGTCATATA ACCGTGCATA TAGCGCAATT	120
AAAGGTTTAG CGTCATCGAT AGTTACATAA AGTTAGAATG CATGCTCCGC CACGCGCGC	180
TITCGACTOGG CGAGCCAGCG CGAAAGCCCC TCCTGCCCCC CCCGTACCAA CAACCCCCCC	240
AAGAAGTOGA GITCCTCCCC CCACCOGTCG TAGAGGTCCT COCTGAGTAC GITGTACTTG	300
ATCCCCTCCC CCTTCCACAT COCATTCATC ACCCACTGTG TCTCCGTGCAA CCAATCCCTC	360
COCCOCCTCC TICTICCGACTT CATCATCGAC AATTICCCCGA ACCOCCTCGAA CCCCCGCATA	420
ASCICCAASCA ACCAGASCCC COCASCIGTAC ACTICCOTTSC TGTOCGTCGG CTGGCCCSCCG	480
COCATICAACC CCGGCGCGCA GTACTICAACC GTGGTCGTCA GCGGCTCGGG CGCGGGGTTGG	540

	CALACTECES COCACOTGAA GICCOCCAG AATGCTCCTG CCCGCCACG AGCACGTTCG	500
	COSTICTICAT GTCCCOSTIOC ACCACOCAGC TCTCGCGAAG GAACTGGAGC GCCCCAACAA	660
5	OSTICACOTOC GTACUDICAC CACTODOCCT TOTICACODOC COCOCOCOTT CONOCOCTTC	720
	CANTIGOGOT TCAACCOCTC TACACAACGC COGGACCINCC TOGCCACCGC GAANCOGGGG	780
	GTATCCCNAC GTTINCCGCC GCNCCCCCCN GCAANGGACC ACTINCGGTC NCGANCCNCC	840
10	CCCCCCCNCGT GOCCAAGNOOG AATTNITTAC CNICT	875
	(2) INFORMATION FOR SEQ ID NO:497:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI351RP	
25	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:497:	
	GATCATAATG ATTIGICITA ATTCTTTTCT TAATTATICA TTAAATAATT AATTAATATT	60
	TIATTAATAA AAAATATTTA GAGTTATGIT CGTTTATGAT AAATTCTAAA ACTTTGCAGC	120
30	ACGAACTGAA GACAACTATG TAACOCCTGT AATTAATTAT AAATTATTAT AAATTAAATAT	180
	TCAAAAAATG GTAAGATTTA TOGAGGATTA TCGAATTAAA TAACATGTTC CACTGCTTAA	240
ac.	GICTGIAACC GICTATUGUT TUGATUTTIA TUATUCCIAA CGIAGUCAIC ACCCCCAATA	300
35	CITIAATITI CATITAATIT ATICTITAAT TAATAAAAA TAAATAGGIA TICATIGITI	360
	ACTOCTAAAA CTACTOGOGT ATOGAATCOG ATTTOCTACT TTAGOCTTOG TYOCTCAATG	420
40	TCAATTAATA TATAATTIAA ATTITCACIT TATAAGICIT ATTCATATAA TIATIATTITC	480
40	ATCITIACIT GAATAATICT TAAATTATIT TIATTAATIC TAATTATTAT TITAAATAAT	540
	CATCIACGAA COCITTAAGC CATTACGAAT AACGCTAACC CCTTTGTCTT ACCGCAGCTG	600
45	CIGOCACAAT TITOGITOGA NNGANITAAT TATATATCIC TITTAAAAAT ANAATCTCCC	660
	TCATATTAAT AATITTATAT TCANANTAAT TATCMVIATT TAATAATTAT TCAATTTATT	720
	GTIACCCANA NIAANAANAN ATTATIATIT ACATCCCCNA GTACNGANCA CITCACATIG	780
5 0	CCAAATCCCN COOGITCCNA NAAATGATAT ATTCNANCAC OGATNICTIC TT	832
	(2) INFORMATION FOR SEQ ID NO:498:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 863 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1351UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:	
10	CATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATCAAAT	60
	ATTATATTAA TICTCCATTG GAGCAATTTG AGATTAGAGA TITTATTAGGT TTAACATCAC	120
	CAATAATAGA TITTAGITIT ATTAATATTA CTAATTTTGG TTTATATCTT ATAATTCTTT	180
15	TATTAGTAAT TITACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTTCTA	240
	ATTGATATIT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA	300
	TTOGTOGTAA AGTATGAGGT TATTATTTTC CATTAGTTTA TACATTTTTT ATTCTTATTT	360
20	TTACTATAAA TITAATTAGT ATAATTOCTT ATTCATTTGC TATAACTTCA CATGTAGTAT	420
	TIGIAGIATO AATAAGIATA ATTATTIGAT TAGGICTAAC TATIATIGGT TITIATACIC	480
	ATOGITTAAA ATTOTTTOGT TTATTTTTAC CACTAGGTAC ACCATTAATT TTAGTACCAT	540
25	TATTAGTATC AATTGAATTA TTATCATATT TTGCTAGACT TATTTCATTA GGTTTAAGAT	600
	TATCAGCTAA TATTATAGCT GGICATTIAT TAATGITATT TAGGIGGITT AATATTTAAT	660
	TIAATAGCTA TAAATATTIT AACATTITAT TAGITTCTTA COCATGAATG CNAATTIAGT	720
30	ATOSTITETT ANAATTOOCC ACCCTANTAT CCACCTAANT TGAGGITTITT TAAATCCCCC	780
	ATTITAAAA TCCATTTATT TACATNNATT AANAATAANA TATITAATAA TATCCANNAT	840
	NAA AATTINAATA TITTANAANT	863
35	(2) INFORMATION FOR SEQ ID NO:499:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 831 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1352RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:	
	GATCCIOCAT COTTICGIOG GCCIOCAGET IGATITIGIT GCICICAATI TIATCCITTA	60
50	TCAAATTCAC AACCTGGCAA TCCACCTCAT GCTTTATCTT CAACGAATGC CTCATCGTAT	120
	TETETAACCT GAGGACCATC TOCACCTTOC GTTTAACAAG CTOGACGGTA TOCTGTGTCA	180
	ACAGGITTAT GOCTGGGTCG TCGACCCCCA ATTGGGCATC CCAGGCAGTT ACGTCATCTA	24
55	TGTTGTTCTT CGTGTTCGGA GAGAAGCGAT ATGTAACCGA CTGCATGTTA AGAAGCCGT	30

	ABBUMBLE CIGCICCOC AUBICUST CONSTANTIC GUIGIGIIG AIGITGAIGG	360
	COTOCTCACA CAAATCOCTC AACAGOGAAA GCTGCTTGAA GGGGAAGGGC ACGTGGTGGA	420
5	ACASCGACCE TECETCCTTC CCCCAGCGGC TCGCGGGGGG GAACGGGTTG TGCTGGTGGT	480
	COGACAAGTT COOCCACCTC AGGGACOGAT OGAGCATCAC QGGCGCCTGC TTCGCAGGGC	540
	CCACCTCCCC ACCCTCCCCC TGCCCCCAACC CCACACCTTC TACTCCCCCC CCCCCCCC	600
10	CTGGCCGAGC GCCCCNGTCA GTCTTCTACA CCNCTTGACT CCCCCCACTC CTCCGTNGAT	660
	GACTIONICOGO OCTOTNICATO COGTIGOTICOC ACACINCACAT CTICOGAATGN TITTICCACCAC	720
15	CACCONONIAC AACTITOCAC ACCOGGAAAC TONVINGNVI TINGGACCOT GECTITIACNO	780
15	TOCAATOOON TOTOCTOCAT TITITGNAAAA CTOCCCCCAA COCACCCCTC N	831
	(2) INFORMATION FOR SEQ ID NO:500:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 832 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genomic)	
-	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1353RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:	
	GATCTAACTA TTAATGTGIT CCTTGAAATT GTOCTGAAAT ATAACGACCT CTTAAATGAT	60
	GICTATCITG ATGACGATGT CGTCAAGTTG AGCCAATGGG TACTTCAAAC GIGTAATGAA	120
35	TAAAAATATA CAAGOOCAAA GOOCAATAAC CITTACOCTA TATATCTIGI AATATATTAA	180
	GITAATICAA CCATITACGT GCCATATICT GCGCTGGCAT GGTATCCGTG ATTITATAAT	240
	ATATATTICT COCAGOGGAA GCAGAAACAC TCAAGATCOG CGATTGCCCGA TAAAAGAATT	300
40	GCTCCCTGAT TGATTGTTGT TCGAAGGAGA TGCAGATGGA TTGTCCAGAA AAACCGGTTT	360
	TANGACTOGI TCATCAAACT TGTTAAACCA TTGCCCATCG GCTTGCAGTA TATTGCCCAA	420
	GGITTICGCGG ATATTICTTIC TGICTAATGA TAATCGTCCC ACAGGCTGGT CAGCGCCTGA	480
45	TOCACAGOGC GAAGAGOGTC GGTCTATCAT AGGAGGAAAG CTTTCTTGAT CCCGGGAGGC	540
	GGTCGGGCTG TCGGCTAAAA ATGGAGGTGC GTCTAATGAA GACATTAGCT GGACAGGTCT	600
50	AGGGGCTTCC ATATCAAATT CATCATCGGT ATCCTCCTGT TCTTCTACGC ACCCTGTCCT	660
50	TATGITTAGA ICTCCAGCAT ACCGCAGTAT ACCTCCCAAT ATGATACGGT GAGAACCCCA	720
	CTACCACCCA GTGCCCNAAA AGAACTTGAC CCCCTGTNAC CCTNCATGCA TCCACNACCC	780
55	CACCCCCCCA ATCNCNCTGT ATGGTATGAC CCTCAGANAN CCNCCTCAGA TC	832
,,,	(2) INFORMATION FOR SED ID NO:501:	

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 877 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1353UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:	
15	GATCOCCCCA CTCTGTCCTTC CATGTCCTCC ACAACTTGAC CACTGTATAC CAGTTTGACA	60
	TCAGAGGGGG AAATCATCAG TGTGTGGCCG TACACAGAGC AAATAAACTC CTTTACTTCC	120
	TOCACOGTOG TOTOCACTOT CACTITICATA GICTICATOG CCAACACOGA GICCGAAAACG	180
20	AACTOGATAG TIACACCATC CCCGTCCTGG CCGTGGTTGG TACGGAACAT AATTAAGCAA	240
	TGCCACAATG GGGTGGGCGC AAAGTCAAAG CCCAATACCT CCTGTAGGCT CAACCCCGCG	300
	TETTETISCCC CETCTTCGCC GCCCAGGTAC ACAGGGGTAC GATCGCCCTG CAACTTGGAA	360
25	TOCAMOCATO TOOTTOOGCA CATOOTTICTT GITOGAACAC AGGITICTTOC AGCITOCTOCG	420
	CICGIACICG ITCACTATAT CACATGOCAT OGICCOCAGO GOCAGOACAG ACGICTICAG	480
	AGGCACACGT TGCCTTATCA CCGCCACCAC TTTATCCATG GAAAGCGTGT TGACCTGGAA	540
30	CTTGAGGTTC ACATACGCAA ACTCACTGTC GCCATGGTAA GCCAGGTCTA CAGTGCCGCC	600
	TOCCACCTICC TOCCCACATO CAGOTOCAGA TOCACCAACO COCCOCCACA GOCTOCAATO	660
	TCCTCGCACA ACATGGTCAG ATTCGAGCGG ACGCTGTTGG TATTCAGACA GTATTCCTCA	720
35	GSCGSCCAAG CGCCATGITC TCCCCTGATG CATGATAACC AATGCCNTAC TGCNATACCT	780
	NGCNACTICAT AANFTOOGGE ANGCCOGCCC NITICACGAAG AAGATOCANG CTCCCNITICA	840
	AATAGNAANN CHGANTGAAC TOOCGNATHC CNAATCT	877
40	(2) INFORMATION FOR SEQ ID NO:502:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 871 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1354UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:	
5 5	CATOGAACAC GOOTGIGOCA GOGAGOTTIAG GGTOGTGTOC ATOCAATTICA CATOGAAGCA	60

	AAAACCGACC ATGCTTGTTG AACCGAAAGG CGCATGTAGC ATGGCCCTTT CCCAACGGTT	120
	GAGATOCTOG TTGCGCCCTC TTACCCTTGT CGTAAATTCT CGCAAAGTCA GCCTGGTCCG	180
5	TOGTICAGOAG COOCTICAAGG GCATGOCCCA GCTGCGACAG AATGATICTICG COGTICTGCAG	240
	AAGAGTICTIGA OCTICAAOCTG AAAATTOOOG GOOCCTOCGA CCCGCCCTTGC AGCAGCATTG	300
	ACCACCICAT CITICACCAC TITCCICACCT 0000CICTIT 0000A0CAGC CITCCCACACA	360
10	OGTIGOCIGACO ATTICAGAGOO COGGAAGITIGG ATTAGCAGATA ATGCAGGTIGO GACAGCACAC	4 20
	CACACATOSC ACTOSTIGAC GATACATACO GIOCTIGOCO TICCTIGOGO COCTOCASCA	480
	GTCGCAGGTC CCGCGAGGGC GGCACGAAGT CTGCGATGGC CTCAAAATGGA AGTCCTGCAC	540
15	CTTGATCACC COCTCGATGA AGGOCTOGAA GITGTACACC CCCGACCGCC GGTCCCGGAG	600
	CESCACCACE GACAGERGE TOGAACAGGE AGCETTECAG CECGTTGCGC AGCEGGGGC	660
20	GCACCICIGI TOCACIOCTO NINCCACCOC AFFOCTGAAC GCCCONIGAT TACAAATTGT	720
20	TONOCTOCCO GCCCCCCTTG CCCCCCTTGC CCCTCCCCNCC CGCGCCACCC CCGCCNCNNT	780
	OCATGANNET TONCTGATTN NOCAAACCCC TTCANNITGT CCCGITTTNT CANGGNCANT	840
25	NCCCNNICNI TGINCONVIT NAATOCCCNC N	871
20	(2) INFORMATION FOR SEQ ID NO:503:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1166 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1355RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:	
40	GATCATOGOC AAAAAATTOG GAATAGGAAA CTGTTTOCAG TACTCATCAA GGTCAGTAAA	60
	AATGITTIGCC AGCAGIGAAG ATTGCATCCT TATCTTGCCCA TTTGCCGATA GGACATTTGT	120
	TICGATATAC CIGIGGICAG ACCAAAACAG ICITGOCAGI IGGGIAAGIT CTOCTAAAAA	180
45	CAAATAAACT TOTOTTOTOG AAGTOTTACO GTACGOGATT CTATTCAAAA TOCTOTOCAA	240
	GTCCTGGCCA TCACGCAACA TATTATTTAA CGACTCAATG AAGATATTAC CAACTTCGGT	300
	TEAAATGCAC TGAACTGCGT CCAATCTCTG TTGTATCTGA TCAATATTTA TTAAAGGCTT	3 6 0
50	TOCANTOCAG TICTICAAGT TOCTTAACCC GTAGTITIGIT CTAGTATGAT CTAATACCCA	420
	TAACAGGGAG CCTTTACTGC TCCTATCTGT ACTGTTCTCA AAAATATCTA AGCTTTCAAT	480
<i></i>	ACCECTAAGA ACGAAGAATIC ATGTGCGTCT TCGACCAGAA TGGTTTAAAG TTTTCCTTGA	540
55	AGAAGAGTAA ACNINICATTT TIGAAGPTIG TIAGGTAGCC ATGCACCACC ATGAGCGCTG	600

	TTTGCAGAGG AACGITGCCC TTAAAGGCTG GGTGCGGCTC ACTGAAGATI TCTTCATACA	660
	ACCCGACGAG CTCGATCCTA TTTAGAGTGA TATCGGAATC TGAAGTATGA AACACCTTTT	720
5	CGATTICTGA GCCAAGGCCA TCTCCGACCA CAACTTCACT CGGGTTTGTG TATTTTATTC	780
	OCCICIOCAA ACCOTOCCIC ACAAAACCOT COTOTITICAA CICATOCAAC ATAACTICAC	840
	COCTOTTORG ATTRACACTA ACCAGGARGT ATCOCGTGTA TGARGGITGT COCTTOCACA	900
10	CAAGACCCCA CACAGAAGCG CTATCACCCA GGACCCGACG ATCTTTGGTT CGAACGTCTC	960
	ATTIGATIOCCA TAGGITACCCC TOGTIGAATIAT ATTIGGGITACT TCCCTCGAGA AAACAGAGCT	1020
	TGAGGROCCA CTGTTCTTTT TCACTGCGGA TGTCTCTGTC TGCTCCACGA CCCCCACTTT	1080
15	CACATTICTICS TOCATICAAGC OCTOCAACTIC CACTTOCACA COCCTICTICTIC OCAATOCTICC	1140
	AGTACOCAAA CITCITGIOC TIGIGA	1166
	(2) INFORMATION FOR SEQ ID NO:504:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 887 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1355UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:	
	GATCATGCTA TCAAGTGCAG AGAACACGGA TAGAGCCTAC TCTGCAGGTT CGGCCTCGCT	60
95	CACOCCOCC CACAACICCA ACCACCCC AAATACCCC TICCCCACA ACACCCCACA	120
	GOCCIGOCAG CCCATOCTGI CGCCGCAGAG CATCCTCCCA CTGCTAATAT TGCTGAGCGG	180
	GEOGRITICO COAATOCOGA TIGOGOTGAT CATOAGTOCA AACAACOTGO AGAACOTGOT	240
10	GATICGACTIAC AGCCAGTICOG GCAAGCACDC CACGTICOCAA TIACACGCCCA TICCCCGAGAA	300
	CCTGGTGAGC TACCACTTCC GGACGTCCAT GTCCGAACAG CCTAAGTGGC GGCTGCATTC	360
	CAAGAATGAG TOOGAOCTAG AATTTGAGAT CCCCAACGAC ATATCGAGCT COGTGTACAT	420
15	ATACTACAAG CTGACGAACT TCTACCAGAA CCACCGCAAG TACGTGCAGT CCTTCGACCT	480
	CGACCACCTT AAGGGCAAGG CTGTTGCACC AGACAAGCTG TCCGACACGT GCCACCCGCT	540
	CTOGACTAAG GACGGCAAGG CTGTCTATCC CTGCGGCCTG ATCGCCAACT CAATGTTCAA	600
50	CEACACCTIC ACCCCCCCTCC TCCCCCCCTCT CCAACCCCCCT CCCCCCACTA CAACTCACCC	660
	AACAAGGAAC ATCGCCTGGC ACACAGGCCG CAACAGGTNN CAAGAAGAAC AAGCTACAAC	720
	COGOCAGANA INGIGOOGOC COCOGOCTIG GCACGAACGI TICCCOCNAA IGGNIANNAC	780
	AANCCAACCT COCTGACTINN CTACTTGGGA GAATTTCCCC TINTTGGANTG INCCCTGCAG	840

	NCTGCONCCT INTRAANCTIN ONTINCAAAAA AAAAGCAACN CCCTCCC	887
	(2) INFORMATION FOR SEQ ID NO:505:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1356RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:	
	CATCTACATA TOCATCAAAA CATGTOOCTT CATGOOCATC AGTAGTTATG TTTGOOCTGA	60
	GAGGOGAGCC ATTICCACCT TCTCTGCACA ACTCCATATC ATTICCATCA TCAACCTCAT	120
20	TATOSCTATO ACCATOCITA GIOGAGIAIG CAAACCAGGG TUACACAGCA AGCCCAGAGC	180
	TATCACTICA AGACATATOT GIOCICATOC GGIOGOCCOC ATCATAGIOC GAIGACTICG	240
	TESASCATIT AAASTCATTC TECCEACCAT TCTGTCCCTC TACTCACCTT CCACATTCGT	300
25	TITICACTITIC GTACAGAATG GACTCATCIT GGAACITGAG ATCTATOGGT TIGTGATCAT	360
	ACCOGACTOT TITTITCAACC TICHTICTCG TCATTGCCAC GCAGTITIATC AAGCTAGAGC	420
	CCAAGGAATG CTGCTTATCA AAGTTCTTCT TAGCCATGGG CATTTCGTAT CTATCATCTA	480
30	TOOCTIOGIT OGAACCATAC TICACCIOGI AGCCATACIT IGIATUATAA TAAGAGITGC	540
	GATAATOCTT OGTACCAGAA CTACCOSCAC TGCTAGACTC CAATATGGCT TGGATGAGGA	600
25	CTGCGCACGC GAAGTTTACT GCCATCCATA TCAATTTGGG CVTGGCTGCC ACATTCGAAA	660
35	ANANTAAGAA GAAGTACEAC TAATOCTOCA CTNOCTACOC OGTOCNTAGC AGOGAACCOG	720
	CTOCTOTOTA NONCATOCAC COCCOTOCTT GCTTAGCTCC TACNOCONIG TOCTTOCATA	780
40	ACCCACCOCG TGTCACCOCA TOCOCTGANC ATTINTGAGAG ANN	823
40	(2) INFORMATION FOR SEQ ID NO:506:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 873 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1356UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:	
55	GATCTGAACC ATATTACCAA AACCAAACAA AGAATTCGGG CCCAAGCGAC CCGTCCGCCC	60

120

GTAAAGCCCT ATAACCAGCT TACGCGTCTG TGGGCGCCAT AGAAAITTGC ATTTTCAACG

	GAACCAACAC GTCAATOCCA AACTACACTT ATCATGCCTT AAAAGGGATT ATCTTTTCTA	180
5	ACCACCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	240
	GOCCOTTICGA CTOCAATATC CTACTITCTIC AGCCGAAGAT AGCCGCACGAA AATCTICCGCC	300
	OGAGCAAGCT CAGAATTATA TIGTAGGACCA AACATTIGTCA OCAACOCCTIG COCOGAGTTC	360
o	TOTTATOCAG TAGOGOGATT TOCTOOGAAT GOOGTTOCTT TITTATOGTIT CTTTTTTGAG	420
	OSOCATOTOC AGAAOCGATG ACCTOCAAAG CATOTTGTTG CATOGATOAC OGAGOCCACA	480
	GOOCAGGTAG AGTAAAGCCT AGTCACCATG GTGGTAGTTG ATAATAGCCG CGGAGGCGCA	540
15	TTCCCATACT ACCCCCCTAA CCTCCCCAAAC AACCTACCCA CCCCCCCC	600
	GACTACGACT ACAAGTACCT GTTCACGCCG CAGATATTCA ACCCCAGAG AAGCTTCAGC	660
	CATTITCTCG ATCIVATOCAA AATCCCCCGGT GGTGCTTGGG TGCCNTTGG GGNINCACNC	720
20	COCNNECAAN NCTGECCEVT TINVITINCINCO NCCAATINNIG AATACCECCNE CINCECAANIT	780
	TGAAACANAA NCCIVACATINC TIVATIGGOCT TINCONGRIGT NGAACGGOOC TICNINNAAG	840
	GUSVAATANN COCTIGNGAA TOCTTAANAA AAT	873
25	(2) INFORMATION FOR SEQ ID NO:507:	
3 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 840 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI357RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507: GATOCCACCG AGGACATOGA AGAGGGACTA CTGTACCOCA TOGACAAGCT TOGCTGCCGA	60
40	TIGAIGADOG AAGADOGAGA TGAAATGACA GATGOOGGA COOTGOOGAG OOTGATGTGG	120
	AAGGAAATGT TITICIGCCGT COGTATGGTG TCCAGGCTCA TGGTAGTACC TGCATGAITC	180
	TERCTITICOS TEATOSOCIT CARGERGADO STRACCACT TATAATAGTO SERGOCOSTT	240
45	OCTOBOCCAA GUAGCTOOCA TOCAGTGTTG TUUGACAAAT ACGAGTACOG GTTGETGTTC	300
	TTATTOGTOG TGTTGTCAGA AATGTTTOCA AAGGAATAGA AACCATTTTC CATGGTGGTC	360
	CASSOCACIT GOCAGITCIG TOCOGGIGIC TOCOGGACAT GACATITCAT TICTIGITCT	420
50	OCOCCOCTT CCOCAGGAAA ATGCCGCCCC TGTGCCGCCA TGTCCTCTTC CTGCTTGTGT	480
	COSTRUTISTIC COARCICOCO TAGGGGGCTTG COOTGAAGAG TITICAAAGCT TTTGAACTTC	540
	AAGGAGGGG ACGCCGGGCC CACGAAACGA TATCGCTTTA CTCCTCCTCA GCTTCCCGAT	600
55		

	AGGCATUTON ATGCCATTIT ATTAATATAT TTCCCCCGTC CGAACCCCAA ATGTATGTCT	660
5	CCCGGTTGGC AAGGGATTCC GACTTATATA TTATTTGATG TCCACCACAG GTTTCCNAAA	720
3	TATTATACAT CNATTOCCNA ACCTCCCCNT TAINCATCAT COGACCNCNC CNCATTTGTA	780
	CNCACTAACN TOCACATINIC CONATININIT AACCCATCAA CNCACCITING CIGCCCATCT	840
10	(2) INFORMATION FOR SEQ ID NO:508:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 888 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1357UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:	
25	CATCCTCCCC TTCCCATCCA ATTGTGTTCC TTCCGTTGAC CCCATATCAC CTCAAAACCG	60
	GCTCCGAAGC CACCAGCACC TTGTCGCTAT GTGACTTAGC CGGCTCAGAG AGAGCAGTGA	120
	CACAGATAGT ACGCCGGAAG GAGGGTGCGT TCATCAACAA GTCATTGCTA GCGCTTGGAA	180
30	COGNICATIAGO CAAACTIVAGO ATGITTOGGAA GOCAGGOCCAA TOGGCTOCAG COGNICTOCOG	240
	CAGCOGGCCA CATACOGTAC OGTGACTICAA AGTTGACCOG CATOCTTICAG CCAGCATTGA	300
	CAGGAGACAG TATCATTACG ACCATCTOCA CCATCGATTC GAAAGCCGAG TCCTCAACCG	360
35	AAACCACCAA TACCGTCCGC TTCCCCTCC CCCCAAGAA TATCCCCTC AACCGTCCCA	420
	AGAATGAAAT GGACTOGCAC GOOGAGAAAG ACACCATCAT CCAGAACTTG CGCAAGCAGC	480
	TTGAGGAGCA GCAGGAGACC ATTGTGATGC TCGGGGGGAG TGCTGCAGGG CCTAGGGGCA	540
40	ACCIOCAC CAGOCOCCIE CACABOCOCIE GOGIOGGOGG CACOCAGOTI IGAGOCAGOG	600
	CACGCCACAA CATTGGAAAA AAGGNTTGCT AAAGGTNGAA AACAGCATGC TCCCAAGAAGA	660
	ANCTOCCAGO CATICOGAAA AAGONICTOG AANNAGGAAA TGATGIOCTO CGAAGAACA	720
45	CANTITICNCA NATICITNAA ATCTCCCCCT TGGAAATCCC CCCGTCCCCC CAAAACCAGG	780
	NINCAGGGT TGATITCCNC NGCCCCATTA CCGNVITACI TICAAAANIA AAINCACNCC	840
F.0.	CCCAGGNCON NGAAAATNON TTCCCCCCCCN TWTGGNGTTC ACCGCCNA	888
50	(2) INFORMATION FOR SEQ ID NO:509:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 833 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1359RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:	
10	GATCCATGIT TATTCACCCC GCTCACTCGC GTAAACGATG CTTTACGITG CTCACATCGC	60
	OSCCACCATT AACAGOGIAT CACATTITIAC GITICOGIGC AGCAAAAAGT OGGICGGAAC	120
	ATRATOCTOC AATROCACGA TROGTICCOCC CAACCOCCTA ACACGTOCCA TCCTGCTCCC	180
15	CTCCCCACCG CCCCCTCCCC CTCTCCTCCA TGAAACTCCC CTCCACCGTA TGACCCCACC	240
,~	GOCATTOGCC CTGCCATTAC TGCACGCCCC ACCGACAGGT TTCCCCATGTC AGCATCCACG	300
	GCAAACCCCC AGAAATCGAT AAGTAGCAGG ACACGCGTCA GAAACACCAG TGTGGTATCA	360
20	TOSCOCACIA GGASCITACIC AACCITCOCTT TITCCISCAACC ATGCCCCGCC GCAGGITCCA	420
20	ACCOCCACCA GCCTCACCAA GCCCCCCATTG CTAATGTCCC TTCCCCCCCAA ACCCCGTCAC	480
	AGCTAAAAGA GAGGCCCCA CGAAGGCATA TAGCTGGCAG GAAACGATAC GATTCAGCGC	540
0.5	ACTOSCAGOS TAAGGAACAG GAGCATCACA TOGAACAGTO GOOTGIGGIN TOCATOOCTG	600
25	AAGSTNGACA CTAACCIGAA AAGCGGGGT TGGCACTAAN TACAAACNIT ACCACAGTAG	660
	ATGCCNAATA CTCCTCACAA ACGAACTCCG ATTNCTNACC CGTGCTCNGG ANANAAATCT	720
	NCCAAGAACN TINAACNCAA TIGGCCACTA CCCCTCTIGA TCCCTCTINN ATCNCACGGT	780
30	TTGGGANCGG GNENGCAAAG COCTGATGEN ATCCCTGACN AANTTGGACT NIVI	833
	(2) INFORMATION FOR SEQ ID NO:510:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 871 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL359UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:	
	GATCOGRIGIA GRACACOGRIT TCCGGGCCCCG CTTCTGGCCAG AGCAGCTCCC ATCACCGCGG	60
	TACCCCACAA CTGCCCCCCC GCGTCCCCAAC ACTAGTCCCT GCTGCTGATG CCCGCCTTCT	120
50	AGICGITGCC TAITTTATTC CTGCCGCGCA TGITGCCGCT GICACGGCGI AICTCGATGT	180
	SCICCEACCAG CACCOCTATIC TICCOCAGAC COTTCCTGTG CATCTGGTGG CACCACCGCA	240
	ACCECCECAC GAGCIECERIE ATECECTECA CECCCTECCC TETCATTCES TYTCTECACT	300
5 5	ACCOGNOSTA CAATOCGICA TATACATOGG CATCOCCGAT GCCGCCACCT TTGTTGGTICC	360

	AGAAGAACTG CAGCGCACTG CTGCCGTCAT CGCGCACAAT CACGGGCCCA GTGGGCCCAA	420
	CTACGAGTAT CTGAAGCTGC TOCACAGGGC GCTGCACTCA ATAGCCGAAA GGTTTGGCGC	480
5	CCGCTTGTGC GAGCTGGAGG ACCATTATCT GGACGAGCTG CTCGAAGCGG TCGACCGTCT	540
	ACCOCCCAG COCTICTICCOG COGTIAGGTICC CTICATICTTCT (CCTIAAACCCA CGCCCAAAACA	600
	ANGACAGCAC CCGCCGCTCC GGGTAGCGGC CGGCCGTCGT GACCAGTTGC TAGCGTTTAC	660
10	TTOCATACCC STATCTOCTT TAACCGITTG GAAGGITTAN CATCATTAGT TANITTGTCC	720
	OCTITICATION COCTOCINITIC OCAAGOOGON COTATTITIAA NITIACONOOC GWITTAACONO	780
	NCCTGAACAA AAATGAATTC NITTINGANAN TCCCCNATTT TNAGGATATC CCCNGTTTGA	840
15	ATTOGANAAA CIGATTTOOC MITTITININI A	871
	(2) INFORMATION FOR SEQ ID NO:511:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 850 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1360RP	
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511: GATOCTTCTC CTCCGCATTC ACAGAATATA TOCTCGCGGT CATATOCTTC GCGGTCGAAA	60
30		60 120
<i>30</i>	GATCCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA	
	GATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCCATGTGAT GTCGGCCAAA TGCCCCGCGT	120
	GATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCCATGTGAT GTCGGCCAAA TGCCCCGCGT GCACCCGGTA GCGCACAAAA GGCGCAAAACT GCCGCTCAGC ACTGACCCCT GGAGTCCGCC	120 180
	GATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCGATGTGAT GTCGGCCGAAA TGCCCCGCGT GGACCCGGTA GCGCACAAAA GGCGCAAAACT GCGGCTCAGC ACTGACCCCT GGAGTCCGCC AAATCTGAAG AAACCTCCCCA CATGCCACAG CAAAGAGCTT ACCGTCTGTC GAAAAACTTCA	120 180 240
35	CATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCCATGTGAT GTCGGCCAAA TGCCCCGCGT GCACCCCGGTA GCCCACAAAA GGCCCAAAACT GCCGCTCAGC ACTGACCCCT GGAGTCCGCC AAATCTGAAG AAACCTCCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GAAAACTTCA CGTCGTTTAC TTTGTCCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA	120 180 240 300
35	GATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCCATGTGAT GTCGGCCAAA TGCCCCGCGT GGACCCGGTA GCGCACAAAA GGCGCAAAACT GCCGCTCAGC ACTGACCCGT GGAGTCCGCC AAATCTGAAG AAACCTCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GAAAACTTCA CGTCGTTTAC TTTGTCCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA CAAGGATTGC CCGACCGTCC ACGTCAACCG AAAGAAGCAG TGTACCCTGG GCATTGACGT	120 180 240 300 360
35	GATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCCC GACCATGTGA GCCATGTGAT GTCGGCCAAA TGCCCCGCGT GGACCCCGGTA GCCCACAAAA GGCGCAAACT GCCGCTCAGC ACTGACCCCT GGAGTCCGCC AAATCTGAAG AAACCTCCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GAAAACTTCA CGTCGTTTAC TTTGTCCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA CAAGGATTGC CCGACCCGTCC ACGTCAACCG AAAGAAGCAG TGTACCCTGG GCATTGACGT CGATCCTCCG CTATATTCCT TCTATGCTCA TATTCAAAGC TAAACGACTT GTTACCAATC	120 180 240 300 360 420
35	CATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCGATGTGAT GTCGGCCGAAA TGCCCCGCGT GGACCCCGGTA GCGCACAAAA GGCGCAAAACT GCCGCTCAGC ACTGACCCCT GGAGTCCGGC AAATCTGAAG AAACCTCCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GAAAACCTTCA CGTCGTTTAC TTTGTCCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA CAAGGATTGC CCGACCCGTCC ACGTCAACCG AAAGAAGCAG TGTACCCTGG GCATTGACGT CGATCCTCCG CTATATTCCT TCTATGCTCA TATTCAAAGG TAAACGACTT GTTACCAATC AGGTCAAACA CCGATACCCT GTTGCCAACG GGCGACAATA GCAGCGTTCC ATCCTCCGAA	120 180 240 300 360 420 480
35	CATOCTTCTC CTCCCCATTC ACAGAATATA TCCTCGCGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCCATGTGAT GTCGCCCAAA TGCCCCGCGT GGACCCCGGTA GCCCACAAAA GGCCCAAAACT GCCGCTCAGC ACTGACCCCT GGAGTCCGCC AAATCTGAAG AAACCTCCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GTAAAACTTCA CGTCGTTTAC TTTGTCCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA CAAGGATTGC CCCACCGTCC ACGTCAACCG AAAGAAGCAG TGTACCCTGG GCATTGACGT CGATCCTCCG CTATATTCCT TCTATGCTCA TATTCAAAGC TAAACGACTT GTTACCAATC AGGTCAAACA CCGATACCCT GTTGCCAACG GCCGACGAATA GCAGCGTTCC ATCCTCCGAA AACACCACAT TTCCCTGTCT GTATACAGGT CCTAGCAGAT TGGAAAACTT GAAATCAGAC	120 180 240 300 360 420 480 540
35	CATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCGATGTGAT GTCGGCGAAA TGCCCCGCGT GGACCCCGGTA GCGCACAAAA GGCGCAAACT GCCGCTCAGC ACTGACCCCT GGAGTCCGGC AAATCTGAAG AAACCTCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GTTATATTCA CGTCGTTTAC TTTGTCCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA CAAGGATTGC CCGACCGTCC ACGTCAACCG AAAGAAGCAG TGTACCCTGG GCATTGACGT CGATCCTCCG CTATATTCCT TCTATGCTCA TATTCAAAGG TAAACGACTT GTTACCAATC AGGTCAAACA CCGATACCCT GTTGCCAACG GCCGACAATA GCAGCGTTCC ATCCTCCGAA AACACCACAT TTCCCTGTCT GTATACAGTG CCTAGCAGAT TGGAAAACTT GAAATCAGAC TTCATCGTAG TCCAATGCCT TGCCTTGCTT GATCTTTCAG TGGTGTACCT CATCTCATCT	120 180 240 300 360 420 480 540
35 40 45	CATOCTTCTC CTCCGCATTC ACAGAATATA TCCTCGCGGT CATATCCTTC GCGGTCGAAA TAATGAACCG TGAGTCCCGC GACCATGTGA GCGATGTGAT GTCGGCCAAA TGCCCCGCGT GGACCCGGTA GCGCACAAAA GGCGCAAAACT GCCGCTCAGC ACTGACCCCT GGAGTCCGCC AAATCTGAAG AAACCTCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GAAAACCTTCA CGTCGTTTAC TTTGTCCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA CAAGGATTGC CCGACCGTCC ACGTCAACCG AAAGAAGCAG TGTACCCTGG GCATTGACGT CGATCCTCCG CTATATTCCT TCTATGCTCA TATTCAAAGG TAAACGACTT GTTACCAATC AGGTCAAACA CCGATACCCT GTTGCCAACG GCCGACAATA GCAGCGTTCC ACCTCCGAA AACACCACAT TTCCCTGTCT GTATTACAGTG CCTAGCAGAT TGGAAAAACTT GAAATCAGAC TTCATCGTAG TCCAATGCCT TGCCTTGCTT GATCTTTCAG TGGTGTACCT CATCTCATCT	120 180 240 300 360 420 480 540 600 660
35 40 45	GATOCTICTO CTOCGCATTO ACAGAATATA TOCTOGOGT CATATOCTTO GOGGICGAAA TAATGAACCG TGAGTCCOCC GACCATGIGA GOCATGIGAT GICGGOCAAA TGCCCCGCGT GGACCCGGTA GOCCACAAAA GOCGCAAACT GCCGCTCACC ACTGACCCCT GGAGTCCGCC AAATCTGAAG AAACCTCCCA CATGCCAGAG CAAACAGCTT ACCGTCIGTC GAAAACTTCA CGTCGTTTAC TTIGICCTTA AAGTTGAAAT GATGTATCAC ATTCCTCGTC TTTATATTCA CAAGGATTGC CCCACCGTCC ACGTCAACCG AAAGAAGCAG TGTACCCTGG GCATTGACGT CGATCCTCCG CTATATTCCT TCTATGCTCA TATTCAAACG TAAACCACTT GITACCAATC AGGTCAAACA CCGATACCCT GTTGCCAACG GCCGACAATA GCACCGTTCC ATCCTCCGAA AACACCACAT TTCCCTGTCT GTATACAGTG CCTAGCAGAT TGGAAAACTT GAAATCAGAC TTCATCGTAG TCCAATGCCT TGCCTTGCTT GATCTTTCAG TGGTGTACCT CATCTCATCT	120 180 240 300 360 420 480 540 600 660 720

	(2) INFORMATION FOR SEQ ID NO:512:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1360UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:	
	GATCEATOCA AACCACEACA ACTACTINGA NEAGTOCTIG AAAATTAAAA GIGTATIGAG	6
	TGAATITGAA AATGACGTAC COGATAAGAC AGATATCAGA GGAGITCTCA ATCCGGTTGC	12
20	ANTIGITIGGT TOCOGREAAC ATGRETTCTC TGAAAAAACC GGRETATTGG GACATCTCCC	18
	GOCTGCAAAG GAGCAAGTAT TCGCAACATT CTTTGCACGT ACCCTTTCGT ATATTGGTGC	24
	AAAGITACAC TATGGCCATC CIGATTTIGT TAATGCTATA TITIGTCACTA CCAGAGGIGG	30
25	TGTATUGAAA GCTCAAAAGG GCTTACACTT AAGCGAACAC CTTTTTGTTG GGATGAGTTC	36
	CATATTACGT GGGGGTAGGA TTAAGCATTG CGAGTACACT CAATGCGGGA AAGGCGGTGA	42
	TITAGGATIT GGGTCCATIT TGAACTICGC TACTAAGATT AGTGCGGGTA TGGGGGAGCA	48
30	AATACTOTOA ACCGAATACT TITACTTGIG TICAAATCTC CCACTOGACC GITTCTAGIT	54
	TCTACTATGC ACATCOGGGA TACTACTTGA ATATGTTTCC AATATCCCTT CTAACCCCTT	60
	AATTANENAA TITANICCCG NAITAAIGGC GETCCTGGTC AANCCNACCA AAAAININNA	66
35	NATICINITÀ ACCOCCADAN CIGCADANTI TATIGITOCC ATINAACOCN TAACCADGI	72
	NCCCONICNE GNITHANCNA TOCNINICCE NCCGGINCCE TICCCAGITT TONAAGAAAA	78
	ATTTAAAAAC CNACNOOGG TTNOOCGGAA AATGAAACIN NIANAAGNGC CCCCTTTCAA	84
40	ATTITITT C	85
	(2) INFORMATION FOR SEQ ID NO:513:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 831 base pairs (B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1362RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

	GATCATAAGC TATTGGGTAC CCGFTGTAGC CTAGCCTTAA AATAATGGAC ATTTTGGAAT	60
_	TRAGITATIG COTOGAAATA AGGTATATAT ATTOCTICCA AGITTAATGT COCTITITAAC	120
5	TCACTAAAAT ATOCATGIAA ATTGTCTCAA TTGGACTTTC ATGTTCTATC TATACACTAA	180
	CTCCGATGCG ACTCATTGTG CITCAGTATT CAAAACATGT TITATATATG TAATATGCCG	240
	ACCTAGAACG CAACTAAATA TGAGAGSCAA CTTAGTCGCT GTCGCTGTCG CTGTTTGAAT	300
10	COCTOGAATC TTTTTCATAC ATGATCTOGT COCCATTATC TTCTTTTAGA ACOCTAAGIT	360
	CCAAGICCIT AIGAGATICC TIGITCICTT GAGAGACCTC GICATCAAAG AIGATCITGG	420
	TETTEGARAC GACAGGCAGG TITTCTGCTT GCGACCTGTG ATAGCCTTCA CTTAGCAGTG	480
15	ACCCCTCGAG GGACACCATT CTGCCCGCAG TGTAGACATT TTTAACAGTA AATTTGAGTT	540
	TTCCGTCCAG CTGCTTACCG TTGCCGTCAC CCAGTGGCCT AGAGACCGGC CCTTGCGCAT	600
	COCTIGIOGAG AATOGITTOG CTOCTCOCGT TOGTACTCTC TTOGITATICA ATAAAGTOCA	660
20	ACCATCCCCA ATGITATTIC CTAATGAACC GTTTGAACTT CGTCATCCAN CAACCAINIT	720
	GITGAGGIGA CNNITGAAAT CONCOCNOGA CNATOCONAT TTINGNGACA NOONCAATIT	780
00	CCCNCCCCN NITAANCCAG GNIATCIGNI CCANIGANIA CATCIONCIT T	831
25	(2) INFORMATION FOR SEQ ID NO:514:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 854 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1362UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:	
40	GATCATACCT GCAGGCTGCC AAGCAGACAT GCTGACATCA TACAGCCAAG AGAGCAGCTA	60
	COCTGTCACC GAGCTGGAAC AGAGOCTAAA CGAGTTTCOC ACTAAATGTA GAAAAAATOC	120
	AAGCCACITT CAGGCACTAC TTTCACTGGT AACTGAGATA GACCATCCCG ACAGCAGCCC	180
45	OCTAAGTCAC OGTACAGTAG TOTTGACATA CATOGAATAT OGCTAAGGAA GGAGGTGTAA	240
	TAGGACACAA AATCATGAGA AGAGTATTOG CITIGTOCACG ATOCCGTOGG CACAAGATCA	300
	AATGOGTGCA CAACAACGAG CCACCCTGCT CTTACTGCCA GCACAAAGGC ATAGOGGAGA	360
50	ANTOCCIGIT ATCATTICCG CCCANGANGA GOCGCANGAN GCCCGANCTA TACTTAGANG	420
	GOSTTOGCAT GOCGCTGGGC GOGTATCCGG TGCAGCAGTT GGAAACTGCA GATCTGCACG	480
	AGCATAAAGC CAGAGCGGAC GOCTICTGATG AAAGOCAAGC TOCTIGTGCAT GOOCAGGACT	540
55	ATACCATOSC GASCAASCTG COCAGATGTA CGAGCTGOCC AGCAGATGTA CTACOSCTGC	600

	CCARROLLY TOURSTAN TOTANSTAN TOCCARROLL CCCARROLLS TACATACTOC	660
	COCCAATTOC CACCOGGATT CTAAACOGAA ANAATOCAAC NCATGGAACC NOOCNTACTT	720
5	TMTTGGACTIG TCCCCAGTIGC CCNATGCATN GIGCACTTIGC ATMGAGANNI TGTCATCCTT	780
	CCCCACTGCG NTGTTTANAT GANACCNCCC AAGAATACCC CCTGACCGTC TTTGGTTCTT	840
	TTTGCCCCCC NCCT	854
10	(2) INFORMATION FOR SEQ ID NO:515:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 853 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1363RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:	
2 5	GATCATTATC AGCATTAATC TICAACTOOG CATTGCCTCT TAAACCAATA ACAAAACCOG	60
20	CAGATITICC TOCAATICCS TAACGATCCT TITAACCCCTT GAGCGATACT TOAAAAACCC	120
	CTTCACTAGG CCAGCGAATA TTAATCTTGG CATGGAACAT ATTCCTAATT TTATCCCAGA	180
30	ASCCTATTIT CTICCATGCA TCAACIGCAG GITTCGAAAA ATIGTCTAAA CAATTCATGG	240
	OCTOTOGRAT AGCAGCTICA TRACAGOCAC COCATGTCAC CATCOTGATG TCTTTCCAGT	300
	GINTATCCAT TGTTACCTGA CTGTAAATTT TAATAGGCGT TAAAGACCGG CGCAAGCGCA	360
35	ACGAATAATA TAGGTCTATC TCAGAAGAAG TAACGCAAGG AACAAGGGGC ACAAATATCG	420
	TICGIAGCIC CTIGGITGAT ICAAICATAT CCICCAGIAA TAAAGAGGIC ACCATACAAA	480
	TGIATAGCCG GAAAACAACC TTGTTGGGAA GOCATAGCTT COGCATATGG ACTAACGGTA	540
40	GINGGGITAA CCITINAAANA GCCCCCTTAA TICACCCANC TIGOCTICCA ATIVIAAAAGG	600
	GAAGCCNCCA MITATICTOG GITAMITTITG GAACCCCMIT INCCCNCAAN TITAATNAAT	660
	TONONNITTI ACCOTTOCCA CATNANGGOT TAAANTINICA TGITTITACCC CCCCONGCCAA	720
45	GANNICONCC ATTITICGAAA TGITANANIC CANACCCCCT TINCATNI'IN NAGGANCTIC	780
	AACTGICCNI TINCCCCAAA AANITAATCC CCCNAAAAAT TCTTTCCTCC TGGGGNITTT	840
	CCCCCCTTAC CNT	853
50	(2) INFORMATION FOR SEQ ID NO:516:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 858 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: INA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1363UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:	
10	GATOGAGGAT ATTITOCGIAC COTGGATGIC GCTCGATGIC AAGTACATGG GTGATCGGTT	60
	OCCUPITICA GIGICOCTIC AAAATATCAA OCACAATAAG GICTGICTOC TGAAGTCTOG	120
	TOCOCTOGAG GITCTCOOCT GITTCACAAA AGACAGTCCC TITTOGACTAA CATGIGITGA	180
15	ACTGAGTGTC AAGTTTUTTU AACTGACAGT GCCTGTGAGT AACCTACTAG CACTATTTAC	240
	CITOGGCAAA GAAGAAGATG AGGACGTCCA AGGCTTTGCT CGTAATATTT TOGATGGCAT	300
	GACOGAAGAT CCACAACTGA ATGCACACAA TTGTGTGCAG ATGATGAGAT CAAGAGTTAC	360
20	CACGITOCAT ACCTACTITT COCATCTAAC TAAGGITGAT TITTITIGITG ATAAGGITAA	420
	CCIGGCAGAT ATACCACCCA GCTTATIGCC TGAGITGICA TCIGCCTGIG AGCCITTGAA	480
	ATACGAAGIT GOGCTTICIA GITTTACTIT TCAAGICACC CGITTTAGCA CCCGAACAGC	540
25	CASSIATAST ATCCTTTICA AAASICIGAT AGACOGTAGE STCCGTATCA CATISTCATC	600
	GTTGCAGTGC GCTCTCAGTT AATGCCCCTA AAATGCCCCT GAAAAGGCTC CTGAATACAT	660
	CCGGITTIG AAGTTCCCAN TTATATCCAT ATGGTCANAC TATACTTTIC CTGAAAATTT	720
30	CACTOGRICCA COCTORPTICT CANACAAAGT CAATOGROGG CAGITTICTICC CCTACCNIAA	780
	NATIGAAAIG AAACCCCCAN CITGAACCCC GIINGCAAIA CIGIANGACI AITINIICCN	840
	CANAACCCCN CCACGNAN	858
35	(2) INFORMATION FOR SEQ ID NO:517:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 842 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1364RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:	
	GATCACATOC ACGICACGIT COGTIGOGCTG GGCACACCTA COGACAAGGA CTGGCCTGAG	60
50	GICTOGICCI TCAGCOCGIA CAACAAGATC CAGGIATACC CGCCTCCGIC GCCCAGCCAG	120
	CTGCGCAGCC GCTTCATCGC TGCAACTGAG AATGCCCTCG ACCTGATGTG CGGTATGCTG	180
	ACCATOCACC COCACAAACG GTOOGACACG ACTOOTTOCC TOCTCAGTCA GTATTTTGTA	240
55	GAGCITICCOG ACCCGACACC TCCTACOGAA CTTCCAAAAC TAAATAAGTA ATGACTATGA	300

	TARCHASH COTATALTOS CARCITITOS GITTOTOCTE TOABSCEATO ALAFTOCTE	360
5	TTATOGTATO GCAGACGITG COTGAAAAAG ATTCAACGTO TCOGTAACAG ATTTGCCCAG	420
5	ACTACTIGIT GAAAGAACAA AGACCAGAGC OCTOGGATOC TCACCCCAAT GAGGAACCCA	480
	CTCCGCCTTA TTGSCGCTGG CTGCAGGTTC CTTAGCACCA ACAATAGGCC GCCACTGCAC	540
	AAGATETTTE CETECAAGAA GETGGTGAAC AGGATGETGT TECCGACETTG ATAGCCCACT	600
10	GACCITCOGG AAATTACTIG CCTTGTATAC GAGCAGTIGT ACACCCAATT AGACAGTTAT	660
	TACGOGCAAT TIGITATACC CONCONCTIC ANGGONOCGA CNITHTATCC TGAAAAQNIG	720
4.5	CINGAAAAAA TCCCCCCCNAA NGAAAANNCC ATCCCCCATCT ANITONCTNG AAACAACTCC	780
15	TITACTOCTE CCCAAINGAN ACCAAAATON COOCCGTACC TIGACCCINI CACCCGCINC	840
	CT	842
20	(2) INFORMATION FOR SEQ ID NO:518:	
20 25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 869 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1364UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:	
	GATCTAGTGC TTCACAAGCT AGAAGCTCCA ACCATGAAAG AGGGATCGAT CCTGAGAACA	60
35	CITITICIGI GGAGGCITAT CAATOCTCIT TCTATCCGCA GCTTCTTCCA COCAGATGAA	120
	TACTOSCAST COCTOGASCC TOCCCATGIT AAGSCGITTG GATATOGTGG GCTGACTTGG	180
	GAGTGGCAGC ATGGGCTGCG CAGCTATGCA TTCCCGATGC TCTTTGAAAT GTCGTACTAT	240
40	GIGGOGIGGA TACTOGGIGI GOCCACCOGG ATGGOGCIGC AGGGGITGGC ACATGGCACG	300
	GOGGLGIGIC GOGGGGGGGG GCGGGGGGGC IGGCCCCAL CAVGGCCCIC	360
	TOGGAGCTICC COGAGGCAGC GCAGGAACTIC GTICGAGTACT ACCCCGTATT GTIACCCCCG	420
45	CGAGTGGTGA TGGCGGGGTT ACCAGCGTGC GGGCAGTTCT ACAGCGTGCT GCTGGTGCCC	480
	AAGCTGTATC TOCGAGTCOC GGATAAGGGG GACGACCCAG AAGGGCGACG CGGGGCCGGT	540
	CAGOOGETIG GOGCIGAATG CTGACCATGA CAAACTICIT CAACTGITIC TICGOGAACG	600
50	CAACGITICAT CACTOCTINCA AAATAACCOC CACNOCGNIC COCHCTAACC NATITIOCATT	660
	GRANCCOCCE COCANCITTE GITCHONIGE GCTTCCACCIN CAACTITINGC GCTGGCTGCN	720
	THISOCIOCC CIOCACOSOC NATACHTHIT ATCHIOSOCT COCTOCCTOT TOTTGIOCCA	780
5 5	ACCTIGITICCC CACCAAAGGT CCACTICNVIT ANCCTIGICCC TRAGGITICCCC CCNGCCCCCC	840

	GOGITITION ATACCANINA NACIOCIOCT	86 9
	(2) INFORMATION FOR SEQ ID NO:519:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 839 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1365RP	
15		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:519:	
	GATCTGCGGC CGGCGGAAGA CGCAGAGGAA AGCGAATCGA GCGCGGGAGA GCGCTIACTCG	60
20	ACGGACAAAA GCAGTTACGC GTCCTCCGTG CAGGGGGTGC TCAGAGGGAG GACAGGGTCG	120
	GCAGCCAGOG CAGATIACAGC AATIGAGCAGT TCAACGGCAG CCAGCGATIAG CGCGGCCGC	180
	OCTANGATOG ATOCAGOCGA COCAGATGAC OCGAGOGGCA OCTTOGAGCT GOGOCTTGCA	240
25	COCCIOCOCA COCAGGACOC GOCIGIGGAC ASCOCAGACA (COCCEAGOGG COCCIOCOCG	300
	CCCTCCCCCC CCCCCCCCCC CACCCCCCCC CCCANCCCCC CCACCCCACCC CTCCCCACCCACC	360
	CCGCCCCCC COCTGCACCT GCCCAAGCAC CGCGCCACC CGGGCCACCC GGCCGGCGGC	420
30	GAGCCOGTOC GOCCOCCOCC CACCAACCCC TTCCGCGTGA TTTCGGTCGG CGGCTCCAGC	480
	ACCITICAACC GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	540
35	AAGGCCGCAC CCGTGTCCGC GAACGAGCAG AGCATGCTCA AGTTGCCGCG CTIAGCNCANC	600
00	TACCCIGACC AIGAATICNI CNACIGIICA AAGANATIAA TIICCIGANA ACNIGAANAA	660
	ANCOGRICCCT GENCTEGAAG AANCOCOGIN ANTAACNACC CCCTNGACAG CTCNGATTIC	720
40	CICCNOCITA TIMIAAAAAA TIICAAAINC GGGIGGINCT TCCCCCNCIN COCAACWITT	780
	TAAAANETTC OCACGGOVIN NIGNNOOCHN NATTIGGCCC CCCGITOCHT THOOCHGGI	839
	(2) INFORMATION FOR SEQ ID NO:520:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1365UP	
55	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:520:	

TOGGACCOC TOGACCAGTT GUIDELUGA CUTTARUCG CHACCOCAT GUIDECCARGANG TOGGATURE ACTIVATES ACTORDOSCOS CHOCOCACT CUCUTTOCAA CHOCATICAAG COCCURRENT TOTACCACCAC CHOCOCACTCA THOCAACCAC CHOCATICAAG ACCOCCURRENT ACTIVILIZAA THOCACCAC CHOCAGAGAC CHOCATICAA COCCOCCCCC ACTICALIZAA THOCACCAC CHOCAGACAC ACTORDOSCOS 420 COCCACACCAC CATURULAA THOCACCAC CHOCAGACAC ACTORDOSCOS 420 COCCACACCAC ACTURACAC COCCACACAC COTCACAGAC CHACACCACTC COCCACACCAC TOCACACAC COCCACACAC COTCACAGAC CHACACCACAC COCCACACCACAC COTTACACAC COCCACATTA CHACACCACAC CATURACACAC CHACACCACAC COCTTOCACAC CATURACACAC COCCACATTA CHACACCACAC CATURACACAC CHACACCACAC COCTTOCACAC CATURACACAC COCCACATTA CACACCACACAC CATURACACAC CATURACACAC CACACCACACAC CATURACACAC COCCACATTA CACACCACACAC CACACCACAC		CATCACGTGA CGTTCATGCA GCGTGCAGCA CTGCACGACA GCGAAGCGGT GGTGCGCGGG	60
TOGGATORIO ACTITATOCA GETOGOGOGO CTOGOGOCOT COOSTITOCAA CIGCATGANG COGGGISTOG GETOGOSTUAT TOTOGOGOGO TOCOGOGICA TOCOCAGGIGA ATOCOGOGOGO AGOCOGOGOGO ACTOCOGOGO ACTOCOGOGO ACTOCOGOGO ACTOCOGOGO ACTOCOGOGO COOCOGOGO ACTOCOGOGO ACTOCOG		ACOCCOCCOCC COOCCCTCCA CCTGTATGTG COCCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCC	120
COCCUTION FOR SEQ ID NO:521: (1) DIPORRATION FOR SEQ ID NO:521: (A) LENGTH: BAS dispersion (A) ORGANICAS GALACANAGE (A) ORGANICAS (A) ORGANICATI A CITOCOMPA CITACOMPA (A) ORGANICAS (A) ORGANICATI A CITOCOMPA (A) ORGANICAS (A) ORGANICATI A CITOCOMPA (A) ORGANICAS (A)		COCCACCOCCO TOGACCACTT GCTCCCCCCCAC CCCTTACCCC CCACCCCACT GCCCCCCCCCC	180
ACCOCCICE ACACTICUCAN TIGOCACCAC GOOGGIGGG GOOCTICAN COCCOGOCOC AGTOCCICE ACACTICUT CTOCTTACAC GOOGAGAA ATGCTTACT GOOGGCGG AGTOCCICE ACACTICAT CTOCTTACAC GOOGAGAA ATGCTTACT GOOGGCGGG COGGAGGGG TOGGGGAGGG GOOGTICAT TACTGCGACA CTGTCCGIG TITICACATGT 480 GACACCCACA CCTTCANGT ACTGCGGGGG GOOGGGGTT ACTGCCACAC CTACCGGATG GACACCCACA CCTTCANGT ACTGCGGGGG GOOGGGTTA GGTCCCCACA GCTACAGGAC GOOTTCCCCC GCACTITITA TIATATANICA NGCANGCTTT CCCNCCACAC GCTACAGGAC CONTTCCCCC GCACATCCT CCCCCCCAAA CCACTACAAA GAAATACCA ACCATTCCTT TNITTCCCGG GCNGGGAAT TITCCCCGCA TIMINAGCCC CCCCCGGINN TINCTCCACC CANTTCCCCT GCCCAATCCT CCCCCCCAAA CCACCACCAA CCGTCTCGAN TINCTCCACC (1) SEQUENCE GGARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: Incleic acid (C) STRANDELNESS: single (D) TOFOLOGY: lineau (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) CRGANISM: PAGI366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGG TCAACCAATG CCTCCGACAT TCCCGGCATA CCGGACTCAC TCCCAAAACC GAACAACCAC GACACCTCCC CCGCCGTGCT TCCCATGGGT CCCGTCCTAC CCCTTCCACC GACACACCAC GACACCTCCC CCGCCGTGCT TCCCATGGGT CCCGTCCTAC CCCTTCCACC GCCAATTUAC TTCATCCACG ACCTGCACA TCCCACAAG CCTCCCACA GTTTGTTGCC GATCCATTCC TCCACTACG ACCTGCCACG CTCCACAAACCT TTCCAAATCT CATAAAAATG CACATGGCAT CCACCAAGAC GTCCCACAA GCCTCCCAA GTTTGTTGCC CATAAAAATG CACATGGCAT CCACCAAGAC GTCCCACAA GCCTCCCAA GTTTGTTGCC CTTCTTGTCG TACCCACTC ACACACCAC GACCATGAAA TCCGTCCATAA ACCTCCAAAACC CCTTCTTGTCG TACCCACTC ACACACCAC GACCATGAAA TCCGTCCAAA ACCTCAAAAACC CTTCTTGTCG TACCCACTC ACACACCACA GACCATGAAA TCCGTCCAAA ACCTCAAAAACC CTTCTTGTCG TACCCACTCA ACACACCAC GACCATGAAA TCCGTCCAAA ACCTCAAAAACC CTTCTTGTCG TACCCACTC ACACACTCAA GACCATGAAA TCCGTCAAAAACC CTTCTTGTCG TACCCACTCAACACTCAAACACCAA GACCATGAAA TCCGTCAAAAACC CTTCTTGTCG TACCCACTCAACACACACAACACAAACCAAAACCAA ACCCAAAACCAA ACCCTCAAAAACCAACACAAAACCAAACCA		TOGGATGTOT ACTITIATOCA GCTGGGGGGG CTCGGGGGCCT CCCGTTCCAA CTGCATGAAG	240
ACCCCCIC ACTICLICAN TIGOCACIAC GOOGRAGINA ATCCCTTACA COCCCCCCC AGTOCOCTIC ACACCTGICT CTCCTTACAC COCGACINGA ATCCCTTACT COCGCCCCC CCGGACCCC ACACCTGICT CTCCTTACAC COCGACINGA ATCCCTTACT COCGCCCCCC CCGGACCCC ACTICANGET ACTICCCCCC GACCTCTTA ACCCCCCCC ACCCCCT TO ACCCCCCCC GACACCCCACA CCTTCANGET ACTICCCCCCA TOMINACCTTA CCCCCCCCCACACACACACACACACACACACAC		COSCITATOR OFFICEREAT TOTOCCCCCC TOCCCCTICA THOCCACCOG GUATAAHOGG	300
COSSACCOC TOSSCRACE COCCUTICA TACTOCCACA CCTGTCCGIC TITCACATGT TOGGTGAAGA TCGTTCAGAC GOCGATICAC GAGGIGGTTI ACTOCCAGAC CTACCGGATG CACACCGAC CCTTCAAGGT ACTGCGGGG GGCGGGGAC GGTCCCGGCA GCTACAGGAC GCGTTCCCCC GCACTTTTA TTATATATICAC AGGTCCCGGCA GCTACAGGAC CTGTTTTINC ATATAAAGGAC COCCCGGATA CACACTACTAC AGCACTTCTT TATTCCCGAG GCNGGGAAT TTTCCCCCGA TATAAAGCAC CCGCCGTAN TGCCGTTACC CANTTCCCCT GCCCAATCCT CCCCGCGAAN CCACCACACA CCGTCTCGAN TINCTCCACC 840 CGNCTTGACC T (2) INFORMATION FOR SEQ ID NO:521: (3) SEQUENCE GARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: TALCLIC CCCCGGACAC (C) STRANCEMENESS: Single (D) TOFOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGG TCAACCAATG CCTCCGACAT TCCCGGACATA GCGGATGAGA TTGCCAAGGC GGAGAACGA GACACCTCCG GGCCGGTGTC TGCCATGGGT GCCGTCCTAG GCCATGACC 120 GAGGCCTTTC GGTCCTTTGA ACCICCTTAA CAGTTCTGCC GACCICTTGA ACCACCCGGG ACCAAAGCCT GCTCCCCGTG CTCCCACAGG GCTCCCACAG GCCTCCTAA ACCACCTGGT GGCAAATTGAC TTCATCATGG ACCICCAGG CACTCCAAAG GCTCGCCCGC AGGTCCTAC GATCGATTGAC TTCATCATGG ACCACGACGA GTCCCACAAG GCCCCCCCAA GTTTGCTACCC CATAAAAATG CAGATGGCAT CCACCGACGA GTCCCACAAG GCCCCCCCAA GTTTGTTGCC CCTTGTTGTTGC TACCCACTG ACCACGACGA GTCCCACAAG GCCCCCCCAA GTTTGTTGCC CCTTGTTGTGC TACCCACTG ACCACGACGA GTCCCACAAG CCCTCCCAA GTTTGTTGCC CTTGTTGTGC TACCCACTG ACCACGACGA GTCCCACAAG CCCCCCCCAA GTTTGTTGCC CTTGTTGTGC TACCCACTG ACCACACTCCA ACCACACAAA TCCGGACTACAA TCCGGACTACAA ACCGACTACAAACCCT TTGCCACATGCACCT TCCACACGACTACAA TCCGGCACACAAAACCCT TTGCCACACACACACACACACACACACACACACACACACA	U	ACGCCGCGCC ACTIGUCCAA TIGGCCACGAC GOOGGGIGCG CGCGCTGCAA CGGCGGCGC	360
TOGGIGAGA TOGTICAGO GOGGATCACG GAGGIGSTIT ACTOGAGAC CTACOGGAIG GACACCACA CUTTCAAGGI ACTGCGGGG GGGGGGTT ACTCGGCAC GCTACAGGAC GOGTICCCCC GCACTITITA THATAINING NGGNECTIT CCCNSCAACH GCTAACTIG CIGITITINC ATATAACGAC COGGCGGINC CGACTINCAAA GAVANINCAC AACCNITCTI 720 TINITICCGAG GCNGGGGAAT THICCCCGGA THINNINGCCC CCCCCGGINN TICCGGITACC 660 CANCTICCCT GCCCAATCCT CCCCCCGAAN CCNCCNCAA CCGICTGGN TICCGGITACC 670 CANCTICCCT GCCCAATCCT CCCCCCGAAN CCNCCNCAA CCGICTGGN TICCGGITACC 671 (2) INFORMATION FOR SEQ ID NO:521: (1) SEQUENCE GARACTERISTICS: (A) LENSTH: 823 base pairs (B) TYPE: Inacleic acid (C) SIRANDENNESS: Single (D) TOGGLGGY: Linear (ii) MOLECULE TYPE: INA (GENCMIC) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGG TCAACCAATG CCTCCGACAT TCCCGGCATA CCGGATGACA TTGCCAAACC GGACAACGG GCACCTCCG CCCCGGTGTC TCCCATGGGT CCGGTCCTAG GCCNTGCACC 120 GAGCCATTC GGTCCTTTGA ACCICCTTAA CAGTTCTGCC GACCTCTTGA ACCGGCCTGA ACCAAACCCT GCTCCCGTG CTCCTAACGG CATCATGGGG GCTCCTTGA ACCGGCCTGA GGCAATTGCC TTCCACTGG CTCCTCAACGG CATCACAGGG GCCCCCCCAA GTTGTTGCC GATGUGICA GATATGGTAC TCCACGAAGG TCCACCAAACCT TTGCCAAATAT CCATAAAAATG CAGATGGCAT CCACCGACGA GTCCCCCCAA GTTTGTTGCG CCTTGTTGTGC TACCCCCTT ACCCGACGA GTCCCCCCAA GTTTGTTGCG CCTTGTTGTGC TACCCCCTT ACCCGACGA GTCCCCCCAA GTTTGTTGCG CCTTGTTGTGC TACCCCCCTT ACCCGACGA GTCCCCCCAA GTTTGTTGCG CCTTGTTGTGC TACCCCCTT ACCCGACGA GTCCCCCCAA GTTTGTTGCG CTTGTTGTGC TACCCCCTT ACCCGACGA GTCCCCCCAA GTCCCCCCAA GTTTGTTGCG CTTGTTGTGC TACCCCTT ACCCGACGA GTCCCCCCAA GCCCCCCCAA GTTTGTTCCCCCCCCCC		AGIGCOCIGC ACACCIGICT CTOCTTACAC GOOGAGGAGA ATGCGTTACT GGAGGCCGGG	420
CACAGGACA GETTGAAGST ACTIGGGGGG GEGGGGTGA GETGCGGGA GETACAGGAC GUGTTGCCCC GUACTITITA TIATATINGC NEGONECTIT COCHSCANON GETAAACTITG CIGITITING ATATAAGGAC COGGCGGTNC GEACTINGAAA GENATINGCNC AACCINITETT TANTICGGAG GENGGGAAT TITUCCCCGA TININDSCCC COCCCGGTNN TIGGGTTACC CANTICCCCT GECCAATCUT CECCGGCAAN CENCENCAA CEGTGGGAN TITUTCCCCC 840 CONCTINCE T (1) SEQUENCE GEARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: INLEGIC acid (C) STRANDENIESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) CRANDISM: PAGI366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAAGGG TCAACCAATG CETCGGGGAT TECCGGGATGACA TITUCCAAAGC 60 GGAGAAGCAG GACACTCCG COCCGGTGT TECCATGGGT COCGTCCTAG COCATGCACC 120 GAGTCCTITC GETGCTTTGA ACCHCCTTAA CAGTTCTGCC GACCTCTTGA ACCACCCGGG 180 ACCAAAGCCT GETGCCTTGA ACCHCCTTAA CAGTTCTGCC GACCTCTTGA ACCACCCGGG 180 GGAGAAGCCT GETGCCTTGA ACCHCCTTAA CAGTTCTGCC GACCTCTTGA ACCACCCGGG 180 GGAGAAGCCT GETGCCTTGA ACCHCCTTAA CAGTTCTGCC GACCTCTTGA ACCACCCGGG 180 GGAGAAGCCT GETGCCTGTGA ACCHCCTTAA CAGTTCTGCC GACCTCTTGA ACCACCCGGG 180 GGAGAGCCTC CTTCCAAGGG CTTCCAAAGG CCTCCCCCAA GTTTGTTGCG 100 GATGUGTCTA GATATGGTAC TCCACAAGGC GTGGAACTCA ACCGGAACCT TTGCCAAATTCA 100 CATAAAAATG CAGATGCATC CCACCGACGA GTCGCACCAAG GCCTCCCCCAA GTTTGTTTGCG 100 CATAAAAATG CAGATGCATC CCACCGACGA GTCGCACCAAG GCCTCCCCAA GTTTGTTTGCG 100 CATAAAAATG CAGATGCATC CCACCGACGA GTCGCACCAAG GCCTCCCCAA GTTTGTTTGCG 100 CATTGTTGTCG TACTCCACTG ACAACATCGA GGCCTCCCCAA GTTTGTTTGCG 100 CATTGTTGTCG TACTCCACTG ACAACACCGA GTCGCACCAAG GCCCTCCCCAA GTTTGTTTGCG 100 CATTGTTGTCG TACTCCACTG ACAACATCGA GGCCTCCCCAA GTTTGTTTGCG 100 CATTGTTGTCG TACTCCACTG ACAACATCGA GTCGCACAGAA GCCTCCCCAA GTTTGTTTGCG 100 CATTGTTGTCG TACTCCACTG ACAACATCGA GGCCACCAGAA GCCTCCCCAA GTTTGTTTGCG 100 CATTGTTGTCG TACTCCACTG ACAACATCGA GGCCACCAGAA GCCTCCCCAA GTTTGTTTGCG 100 CTTGTTGTCG TACTCCACTG ACAACATCGA GGCCACCAGAA GCCCTCCCCAA GTTTGTTTGCG 100 CTTGTTGTCG TACTCCACTG ACAACATCGA GGCCACCACACCA	-	COSCABODOG TOSSOCASOG COCCESTOCTE TACTOCCACA CCTETCCETE TITICACATET	480
COGTICCCCC GEACTITITA THATATINGE NGGENECTIT COCNECACN GETARACTIC CIGITITINE ATATAGGAC COGGOGINE CGACTINCANA GRAFINGEN ARCONTECTT 720 TRITICCGAG GENGGGAAT THICCCGGA TRINNGGCC COCCCGINN TECCGITACC 660 CANTICCCCT GECCAATCUT CCCCGGCAAN CENCENCAA CCGICTGGAN THETICCACC 840 CONCCTENCE T (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: INLEGIC acid (C) STRANGENIESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGG TEAACCAATG CUTCGGAGAT TECCGGCATA GEGGATGAGA THECCAAAGC GGAGAACCAG GACACCTCCG COCCGGGTCT TECCATGGGT GEGGATGAGA THECCAAAGC GAGTCCTITC GETCCTITGA ACGICCTTAA CAGTICTIGCC GACCTCTTGA ACCACCCGGG ACCAAACCCT CTICCCGGTG CICTCAAAGC CATGATGGGG GETGCGTCTA ACCACCCGGG GGCAATTGAC TICATCATGG ACCGTGCAAG TEATCCAAAG GETGCCCCGG CAGACCAGGT GGCAATTGAC TICATCATGG ACCGTGCAAG TEATCCAAAG GETGCCCCGG CAGACCAGGT GATGGGTTAA CAGTATGGTAC TECCAGAATGC CETGGAACTCA ACCGAAACCT TIGCAAATTAT GCATAAAAATG CAGTATGGTAC TECCAGAATGC CETGGAACTCA ACCGAAACCT TIGCAAATTAT GCATAAAAATG CAGTATGGCAT CAACCGAGG GIGCCACAAG GCCTCCCCAA GTTTGTTGGC CATAAAAATG CAGTATGGCAT CAACCGAGG GIGCCACAAG GCCTCCCCAA GTTTGTTGGC CATTAAAAATG CAGTATGGCAT CAACCGAGGA GCCCTCCCCAA GTTTGTTGGC CTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGAATTA ACCGGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGAATTA ACCTGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGAATTA ACCTGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGATTAA ACCTGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAA TCCGTGATTAA ACCTGATAGA CCTTGTTGTGC TACTCCACTG ACAACATCGA GACCAACAAAA TCCGTGATTAA ACCTGATAGAA CCTTGTTGTGCC TACTCCACTG ACAACATCGA GACCAACAAAAATCAAACCT TTGCAACAACAACAACAACAAAAAAAAAA	•	TOGGTGAAGA TOGTTCAGAC GOGGATCACG GAGGTGGTTT ACTOGCAGAC CTACOGGATG	540
CIGITATINE ATATAAGSNE COGGOGING CGACINCAAA GWAATNOCHE AACCNITETT 720 TINTITOCGAG GENGGGAAT TITICCCCGGA TWINNEGCCE COCCCCGINN TIGEGGITACE 780 CANTITCCCT GECCAATCUT CCCCGGGAAN CENCENCEAA CEGICTOGAN TINCICCACE 840 CENCETRICE T 823 base pairs (A) LENGTH: 823 base pairs (B) TYPE: Incleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGG TCAACCAATG CUTCCGAGAT TGCCGGCATGAGA TTGCCAAAGC 60 GGAGAACCAG GACACCTCCG CGGCGGTGTC TGCCATGGGT CCCGTCCTAG GCCATGCACC 120 GGAGAACCAG GACACCTCCG CGGCGGTGTC TGCCATGGGT CCCGTCCTAG ACCACCCGGG 180 ACCAAAGCCT GCTCCCGGTG CICTCAACGG CATCATGGGG GCTGCGTCTA ACACGACTGAG 240 GGCGATTGAC TICATCATGG ACCGTGCAAG TCATCCAAAG GCTGGCGCGG CAGACCAGGT 300 GGAGAACCAG TCATCCAAGG CTCCCAAGG GCTGGCCCGG CAGACCAGGT 300 GGAGAACCAG TCATCCAAGG ACTGCAAGG GCTGGCCCGG CAGACCAGGT 300 GGAGAACCAG TCATCCAAGG CTGCAAGGA TCATCCAAAG GCTGGCCCGG CAGACCAGGT 300 GGAGAACCAG GATATGGTAC TCCAGAATGC CGTGGAACTCA ACCGAACCCT TTGCAAATATT 360 CATAAAAATG CAGATGGCAT CCACAGAGG GTCGCACCAG GTTTGCTAAATAT 360 CATAAAAATG CAGATGGCAT CCACAGAGGA GTCGCACCAGA GTTTGTTGGGG CTTGTTGTGG TACTCCACTG ACCAGACTGA GCCCTCCCAA GTTTGTTGGG CCTTGTTGTGG TACTCCACTG ACCAGACTGA GCCCTCCCAA GTTTGTTGGG CCTTGTTGTGGG TACTCCACTG ACCAGACTGAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGG TACTCCACTG ACCAGACTGAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGG TACTCCACTG ACCAGACTGAAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGGG TACTCCACTGG ACCAGACTGAAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGGG TACTCCACTGG ACCAGACTGAAA TCCGTGATTA ACCTGATAGA CCTTGTTGTGGG TACTCCACTGG ACCAGACTGAAA TCCGTGATTAA ACCTGATAGA		GACAGOGACA GCTTCAAGGT ACTIGOGGGGG GGGGGGGTTCA GGTCCCGGCCA GCTTACAGGAC	600
CIGITITINE ATATAGGRE COGGOGGINE CONCINCANA QUARINGENE AACCNITETT TRITICCEAG GENGGGRAT TITICCCCGCA TRINNESCE COCCCCGINN TOCCGITACE AMOUNTED CONCIDENCE T (2) INFORMATION FOR SEQ ID NO:521: (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: Intelic acid (C) STRANDENDESS: single (D) TOFOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCANCOG TOAACCANTG COTOCGAGAT TECCGGGATTA COGGATGAGA TITOCCANACC COMMANCAG GRACACTOCG COGCGGAT TECCGGCATA COGGATGAGA TITOCCANACC COMMANCAG GRACACTOCG COGCGGAT TECCGGCATA COGGATGAGA TOCCANACC GAGTCCTITE GETECTITGA ACGIGCTITAA CAGITCTGCC GAGCTCTTGA ACCACCCGGG ACCANACCCT GETCCCGGGG CICTCANACG CATCATGGGG COGGCCGGT ACCACCCGGT ACCANACCCT TITOCTCCGG ACCTGGCAGA TOCCANACCT TITOCCANATAT GGCAATTIGAC TITCATCATGG ACCGTGCAGA TOCCANAGA COTTGCCACC TITGCANATAT GGCAATTIGAC TITCATCATGG ACCGTGCAGG TICCCANAGA COTTGCCACC TITGCANATAT GCATAGAAATG CAGATGGCAT CCACAGAGG GTCCCACAGG GCCTCCCAA GITTGTTGCC CATAGAAATG CAGATGGCAT CCACAGAGG GTCCCACAAG GCCTCCCCAA GITTGTTGCC CATAGAAATG CAGATGGCAT CCACAGAGG GTCCCACAAG GCCTCCCCAA GTTTGTTGCC CATTAGAAAATG CAGATGGCAT CCACAGAGGA GTCCCACAAG GCCTCCCCAA GTTTGTTGCC CATTAGAAAATG CAGATGGCAT CCACAGAGGA GTCCCACAAG GCCTCCCCAA GTTTGTTGCC CATTAGAAAATG CAGATGGCAT CCACAGAGGA GTCCCACAAG GCCCTCCCAA GTTTGTTGCC CATTAGAAAATG CAGATGGCAT CCACAGAGGA GTCCCACAAG GCCCTCCCAA GTTTGTTGCCC CTTGTTGTTGCT TACCACTCCAAGA GACCATGAAA TCCGTGATTGA ACCCGATAGAA CCTTGTTGTTGCT TACCACTCCAAGAACACT GACCACAGAGA GCCCTCCCCAA GTTTGTTGCCC CTTGTTGTTGCT TACCACTCCAAGAACACT TTGCAAATACAACACT TTGCAATACAAACACT TTGCAATACAACACT TTGCAATACAACACACAACACT TTGCAATA	0	OCCUPANCIA OCCUPANCIA CONSCIPIO DE CONSCIPIO C	660
CANTICCCCT GCCCAATCCT CCCCGCGAAN CONCONCAA CCGTCTCGNN TINCTCCACC CONCCTENCE T (2) INFORMATION FOR SEQ ID NO:521: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: nucleic acid (C) STRANDERIESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGG TCAACCAATG CCTCCGAGAT TCCCGGCATGAGA TTCCCAAAGC GGACAACCAG GACACTCCG CGCCGGTGTC TCCCATGGGT CCCGTCCTGA ACCGCCGGGG GAGTCCTTTC GGTCCTTTGA ACCGCGTGTC TCCCATGGGT CCCGTCCTGA ACCGCCCGGG ACCACTCTG CTCCCCGGG CGCCGGTGTC TCCCATGGGG CCTCCCTGA ACCGCCCGGG ACCACTCTG CTCCCCGGGG CTCCTCCAAGG CCTCGCCGGG CCAACCACGT GCCAATTGAC TTCATCATGG ACCGGCGG TCATCCCAAG CCTCGCCGG CCAACCACGT 300 GATCGGTCTG ACCGGGGGA TCCCCCAAGG CCCCCCCCCC	o .	CIGITITING ATATAAGGNC COGGCGGTING CGACTINGAAA GWAATINGGNG AACGNITCIT	720
CGNCCTCNCC T 851 (2) INFORMATION FOR SEQ ID NO:521: (i) SEQUENCE CHARACTERISTICS: (ii) SEQUENCE CHARACTERISTICS: (iii) MALENGTH: 823 base pairs (iii) MOLECULE SECRIPTION: SEQ ID NO:521: (iii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (iii) ORIGINAL SOURCE: (iii) ORIGINAL SOURCE: (iii) ORIGINAL SOURCE: (iiii) MOLECULE TYPE: INA (genomic) (iii) MOLECULE TYPE: INA		INTITICOGAG GONGOGRAAT TITICOCCOGCA ININNEGCOC COCCCOGINN TECCGITACC	780
(2) INFORMATION FOR SEQ ID NO:521: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 823 base pairs (B) TYPE: Incleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATOCAACGE TCAACCAATG COTOCGACAT TOCCGECATA COCGATGACA TTGCCAACGC 120 GEACAACCAG GACACCTCCG COCCCGTGTC TGCCATGGGT COCGTCCTAG COCATGCACC 120 GAGTCCTITC GETCCTITGA ACGTGCTTAA CAGTTCTGCC GACCTCTIGA ACCACCCGG 180 ACCAAACCCT GCTCCCGTG CTCTCAACGE CATCATGGGG GCTGCGTCTA ACACCACGGT 300 GATCCGTTCACCTTTCATCATGG ACCGTGCAAC TCATCCAAAG GCTGCCCCCG CAGACCAGGT 300 GATCCGTCTA GATATGGTAC TCCACAATGC CGTGAACTCA ACCGAACACCT TTGCCAAATAT 360 CATAAAAATG CAGATGCCAT CCACCGACGA GTCCCCCAAA GCTTTGTCCAAATAT 360 CATAAAAATG CAGATGCCAT CCACCGACGA GTCCCCCCAAA GTTTGTTCCC 420 CTTGTTGTGC TACTCCACTG ACAAGATCGA GACCATCAAA TCCGTCATTA ACCTCATACCA 480	c	CANTICCCCT GCCCAATCCT CCCCGGGAAN CCNCCNCCAA CCGICTOGNN TINCTCCACC	840
(i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 823 base pairs (B) TYPE: FULCleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGG TCAACCAATG CCTCCGACAT TGCCGCATGA CCCGATCACA TTGCCAAACC 60 GEACAACCAG GACACCTCCG CCCCCGTGTC TGCCATGGGT CCCGTCCTAG CCCATGCACC 120 GAGTCCTTTC GGTGCTTTGA ACCIGCTTAA CAGTICIGCC GACCICITGA ACCACCCCGGG 180 ACCAAACCCT GCTCCCGGTG CTCTCAACGG CATCATGGGG GCTGCGGTCTA ACACGACTAA 240 GGCAATTGAC TTCATCATGG ACCGGCCAAG TCATCCAAAG CCTGCCCCGG CAGACCACGT 300 GATCGGTUTA GATATGGTAC TCCAGAATGC CGTGAACTCA ACCGAAACCT TTGCAAATAT 360 CATAAAAATG CAGATGCCAT CCACCGACGA GTCCCCCAAG GTTTGTTGCG 420 CTTGTTGTCG TACTCCACTG ACAACATCGA GACCATCAAA TCCCGTCATTA ACCTCATAGA 480	3	CONCCTGNCC T	851
(A) LENSTH: 823 base pairs (B) TYPE: DUCLeic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI366RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGE TCAACCAATE CCTCCGAGAT TGCCGCCATA GCGCATGAGA TTGCCAAAGC 60 GGACAACCAG GACACCTCCG CGCCGGTGTC TGCCATGGGT GCGCTCCTAG GCCATGCAGC 120 GAGTCCTITC GGTGCTTGA ACCIGCTTAA CAGTTCTGCC GAGCTCTGA ACCAGCCGGG 180 ACCAAAGCCT GCTGCCGGTG CTCTCAACGG CATCATGGAG GCTGCGTCTA ACACGACTAA 240 GGCAATTGAC TTCATCATGG ACCGGTGCAAG TCATCCAAAG GCTGCCGCGG CAGACCAGGT 300 GATCGGTUTA GATATGGTAC TCCAGAATGC CGTGAACTCA ACCGAAAACCT TTGCAAATAT 360 CATAAAAATG CAGATGGCAT CCACCGAGGA GTCCCCCAAA GTTTGTTGCG 420 CTTGTTGTCG TACTCCACTG ACAAGATCGA GACCATGAAA TCCGTGATTA ACCTGATAGA 480		(2) INFORMATION FOR SEQ ID NO:521:	
(VI) ORIGINAL SOURCE: (A) ORGANISM: PAGL366RP (XI) SEQUENCE DESCRIPTION: SEQ ID NO:521: GATCCAACGE TCAACCAATG CCTCCGAGAT TCCCGGCATGAGA TTGCCAAAGC 60 GGAGAACCAG GACACCTCCG CGCCGGTGTC TGCCATGGGT GCCGTCCTAG GCCATGCAGC 120 GAGTCCTTTC GGTCCTTTGA ACGTGCTTAA CAGTTCTGCC GACCTCTTGA ACCAGCCGGG 180 ACCAAAGCCT GCTCCCGGTG CTCTCAAGGG CATCATGGAG GCTGCGGTCTA ACACGACTAA 240 GCCAATTGAC TTCATCATGG ACCGTGCAAG TCATCCAAAG GCTGCCCCGG CAGACCAGGT 300 GATCGGTCTA GATATGGTAC TCCAGAATCC CGTGAACTCA ACCGAAAACCT TTGCAAATAT 360 CATAAAAATG CAGATGCCAT CCACCGAGGA GTCCCCACAAG GCCCTCCCAA GTTTGTTGCG 420 CTTGTTGTCG TACTCCACTG ACAACATCGA GACCATGAAA TCCCGTGATTA ACCTGATAGA 480	o	(A) LENGTH: 823 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 521: GATCCAACGE TCAACCAATE CCTCCGAGAIT TECCGECATA GCCGATGAGA TTGCCAAAGC 60 GGAGAACCAG GACACCTCCG CGCCGGTGTC TGCCATGGGT GCCGTCCTAG GCCATGCAGC 120 GAGTCCTTTC GGTGCTTTGA ACGTGCTTAA CAGTTCTGCC GAGCTCTTGA ACCACCCGGG 180 ACCAAAGCCT GCTGCCGGTG CTCTCAAGGG CATGATGGAG GCTGCGGTCTA ACACGACTAA 240 GGCAATTGAC TTCATCATGG ACCTGCAAG TCATCCAAAG GCTGCCCCGG CAGACCAGT 300 GATCGGTCTA GATATGGTAC TCCAGAATGC CGTGAACTCA ACCGAAACCT TTGCAAATAT 360 CATAAAAATG CAGATGCCAT CCACCGAGGA GTCCCAGAAG GCCCTCCCAA GTTTGTTGGG 420 CTTGTTGTCG TACTCCACTG ACAAGATCGA GAGCATGAAA TCCGTGATTA ACCTGATAGA 480	5	(ii) MOLECULE TYPE: DNA (genomic)	
GATCCAACGE TCAACCAATE CCTCCGAGAT TGCCGGCATGAGA TTGCCAAAGC 60 GGAGAAGCAG GACAGCTCCG GGCCGGTGTC TGCCATGGGT GCCGTCCTAG GGCATGAGC 120 GAGTCCTTTC GGTGCTTTGA ACGTGCTTAA CAGTTCTGCC GACCTCTTGA ACCAGCCGGG 180 ACCAAAGCCT GCTGCCGGTG CTCTCAAGGG CATGATGGAG GCTGGCGTCTA ACACGACTAA 240 GCCAATTGAC TTCATCATGG ACCGTGCAAG TCATCCAAAAG GCTGGCGGCG CAGACCAGGT 300 GATCCGTCTA GATATGGTAC TCCAGAATGC GGTGAACTCA AGCGAAAACCT TTGCAAAATAT 360 CATAAAAAATG CAGATGGCAT CGACCGAGGA GTCGCAGGAG GCCCTCCCAA GTTTGTTGGG 420 CTTGTTGTGG TACTCCACTG ACAAGATCGA GAGCATGAAA TCCGTGATTA AGCTGATAGA 480		·	
GAGACCAGE GACACCTOCG CGCCGGTGTC TECCATGGGT GCCGTCCTAG GCCATGCAGC 120 GAGTCCTTTC GGTGCTTTGA ACGIGCTTAA CAGTTCTGCC GACCTCTTGA ACCAGCCGGG 180 ACCAAAGCCT GCTGCCGGTG CTCTCAAGGG CATGATGGAG GCTGGCGGTCTA ACACGACTAA 240 GCCAATTGAC TTCATCATGG ACCGTGCAAG TCATCCAAAAG GCTGGCGGCG CAGACCAGGT 300 GATCGGTCTA GATATGGTAC TCCAGAATGC CGTGAACTCA AGCGAAAACCT TTGCAAAATAT 360 CATAAAAAATG CAGATGGCAT CGACCGAGGA GTCGCAGAAG GCCCTCCCAA GTTTGTTGGG 420 CTTGTTGTGG TACTCCACTG ACAAGATCGA GAGCATGAAA TCCGTGATTA AGCTGATAGA 480	0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:	
GAGTICCTITIC GETECTITICA ACCIGCITIAA CAGTICTICC GAGCICTITGA ACCAGCOGGG 180 ACCAAAGCCT GCTCCCGGTG CTCTCAAGGG CATCATGGAG GCTGCGGTCTA ACACGACTAA 240 GCCAATTGAC TTCATCATGG ACCGTGCAAG TCATCCAAAG GCTGCCGCGG CAGACCAGGT 300 GATCCGTCTA GATATGGTAC TCCAGAATGC CGTGAACTCA ACCGAAAACCT TTGCAAAATAT 360 CATAAAAAATG CAGATGGCAT CGACCGAGGA GTCCCACAAG GCCCTCCCAA GTTTGTTGGG 420 CTTGTTGTGG TACTCCACTG ACAAGATCGA GAGCATGAAA TCCGTGATTA ACCTGATAGA 480		GATCCAACGG TCAACCAATG CCTCCGAGAT TGCCCGGCATA GCGGATGAGA TTGCCAAAGC	60
ASCARAGOCT GCTGCCGGTG CTCTCAAGGG CATGATGGAG GCTGGGTGTA ACACGACTAA 240 GGCAATTGAC TTCATCATGG ACCGTGCAAG TCATCCAAAAG GCTGGCCCCGG CAGAGCAGGT 300 GATGGGTCIA GATATGGTAC TCCAGAATGC CGTGAACTCA AGCGAAACCT TTGCAAATAT 360 CATAAAAAATG CAGATGGCAT CGACGGAGGA GTCGCAGGAG GCCCTCCCCAA GTTTGTTGGG 420 CTTGTTGTGG TACTCCACTG ACAAGATGGA GAGCATGAAA TCCGTGATTA AGCTGATAGA 480		GGACAAGCAG GACAGCTCCG CGGCGGTGTC TGCCATGGGT GCCGTCCTAG GGCATGCAGC	120
GATOGRICIA GATATOGRAC TOCAGAATOC OGTGAACTCA AGOGAAACCT TIGCAAATAT 360 CATAAAAATG CAGATGGCAT CCACGAGGA GTCGCAGAAG GCCCTCCCAA GTTTGTTGCG 420 CTTGTTGTCG TACTCCACTG ACAAGATCGA GAGCATGAAA TCCGTGATTA AGCTGATAGA 480	5	CAGTOCTITIC GGTGCTITGA ACGTGCTTAA CAGTTCTGCC CAGCTCTTGA ACCAGCCGG	180
GATOGGICIA GATATOGTAC TOCAGAATOC OGTGAACTCA AGOGAAACCT TIGCAAATAT 360 CATAAAAATG CAGATOGCAT CGACOGAGGA GTCGCAGAAG GCCCTCCCAA GTTTGTTGCG 420 CTTGTTGTGG TACTCGACTG ACAAGATOGA GAGCATGAAA TOCGTGATTA AGCTGATAGA 480		ASCARAGOCT GOTGOCOGGIG CTICTICARGOG CATGATIGGAG GOTGOGTICTIA ACACGACTAR	240
CATAAAAATG CAGATGGCAT CGACGGAGGA GTCGCAGAAG GCCCTCCCAA GTTTGTTGGG 420 CTTGTTGTGG TACTCGACTG ACAAGATGGA GAGCATGAAA TCCGTGATTA AGCTGATAGA 480		GGCAATTGAC TTCATCATGG AGCGTGCAAG TCATCCAAAG GCTGGCGCGC CAGAGCAGGT	300
CUTGUIGG TACTICGACTG ACAAGATOGA GAGCATGAAA TOOGTGATTA AGCTGATAGA 480	60	GATOOGTCTA GATATGGTAC TOCAGAATGC OGTGAACTCA AGCGAAACCT TTOCAAATAT	360
5		CATAAAAATG CAGATGOCAT CGACCGAGGA GTCCCCAGAAG GCCCTCCCAA GTTTGTTGCG	420
GTTCOGTIGAA AAGAGCCCTG ATGTATTIGAA TCCTGTCCTA GAAGTTCCTGC AAGCTTCCGT 540		CITIGITIGICG TACTICGACTIC ACAAGATICGA GAGCATIGAAA TCCCGTGATTA AGCTGATAGA	480
	55	GTTCCGTGAA AAGACCCCTG ATGTATTGAA TCCTGTCCTA GAAGTCCTCC AAGCTTCCGT	540

	GAAGGICAAC AGATIGATAC CCTCCGAAAG AATTITINGAC TIACACCCAC AICCIGGAAA	600
s	CTTCATMITT GCTGCGAGIT ACAAACTGGC ATTICCCAAT CIGCCATTTG TICCCTTAAC	660
3	GCNCCCCAAA GGITTGCACA CONUNVICCI' NCAGGYTICA AINOCTACTC CINVINNCONA	720
	CCNANGAATC CHNITOGOOC TINITTAANN CAAATCNONC CANAINIACC CCCAOGITTT	780
10	TTTTOCAAAN COCTTTIANA CCTTTOCOOC CCTCCCTTIN NAT	823
	(2) INFORMATION FOR SEQ ID NO:522:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 854 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1366UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:	
25	GATCTIATCA GCATAAATGA TITIGCTCCCG GAAAGTCCAT AAATTGCTCA TATATGCCCT	60
	CTGOCGAGA TAATATATOG GACTTTCCCC ATTTTCACCA TTTCTACCCG GCATCATTAG	120
	CTTCGTAGGC TTCTTAGGGT TAGTAAACGA TTGCAAAACA GGCCACAACC CCCCAAGGAC	180
30	CCTGAAAAGA GAAGACTTGC CGCAGCCATT NOGACCTATA ATCAATAGAT GGTTACCATG	240
	CITCAACTCG AAGITAAGIT CGGGGATAAG GACCTGATTA GCAGGTGTCA CTAGTGGAAC	300
35	ATGAACGAAT TGAATCTTAG AATCGICGIA TICITATAATG ACCTITITICC CATCAGTCTT	360
25	CGAACTACTT CCAGCGTCTA GCCTGTCATT GAAATTTGTT AACCGTAGGG CCTCTCCCTT	420
	TACCTCCTCC ATACTACCCC CCAGTTCCAC ATACCCCCCA ATACATCCCC ACCCAGTTAC	480
40	CAGTAAACGT CTGTTGGTGA TAAAATCAGC GGTGACATCC TCAGCCATAT TAGAACGAAA	540
	GAAGACGGGG ATAGAGCATA ATATCAAGCC CAGCAGGGCC CCAGACGTAC TTCACCACAA	600
	AGCTAGTACA ATTOGTACAG TOCTCTTAAA TTTATCTCCC CCCCCTNAGA ATAAGTTACT	660
45	GGTTANAAAN AAAAACCCAA TCCCATATTC GGTNTTTGAC CNTGAATAAA CNNINCCNCN	720
	TIGCTICACC NCACTIGAAT TIATGACCGA ATTACCNOCA TITTCCCCTG ACATACCGTT	780
	CANTIGOING THIGACCICC CACTINATIAT GATTINAAATC AACCCATOON GICCITCINGC	840
50	TTTCCCTGCN CATC	854
	(2) INFORMATION FOR SEQ ID NO:523:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 824 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPCLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1367RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:	
10	CONTIGUEDOS COLLIGIOSOS CALALISACOS CALACOCOSOS COCNIGUESOS.	60
70	CAGGCCCACC GOGCCTCCGC CCTGTTGCCC TAGGGGATTG TTCATTGCCT GTGTTGCCTC	120
	CTGACTGTCC ACTCGACCTC TTGTATCCCC ACCTTTCTCC CAAGTGCGCC CCAAACTCTG	180
15	TITICCIGIC IGICCAGAGI TICCGICTCI GOCIGCGCIA CIGCCIACCI GCCGITIGGI	240
13	ATGGAGGAGA AGTGTGTGTG TATCTGATTT GTTTATCTGC TTTCCTTCTC CTATAAGCTT	300
	TITIGIAATGA AAAAAATTAT GAAAACOOGA AATCTOTOGA ATTTOGAAAT GCTOCTOGGG	360
20	CHOOSITISTY CAACTICCAS COCCECCSIC TESTICIACY SCIENTISTET TESTETASCY	420
20	TROSCIATET TETCHOCHOG GETTCOCTTC TETTTTCHOC AACOCAAGOG COCOCHOCGE	480
	CONTRACTIC COACCITICANT COACAACTICO COCCOCCC CAACCCACCC COCTACTITAC	540
05	CGGGCAACTC TGCCGCCGAT CCCCTGCGGA GGCTTACGGC AGCGCTTATT TAATTGTTAC	600
25	GUAAGUCACG TOGAGCUAGC ACGUGCUTOG CAGCUCAGCC OCACGUCAGG TAGOGUGUGA	660
	CTAATCGCGG CGACCTGGTG GGTTAAANCA CGGGTTACNC CGTTAAGTTG GAAACGCNCC	720
	AATAAATTAC NTACCONTTA AACACACGGG ANAAAAANAN NCCCGGCICA NAAGNANCTT	780
30	TIGOCCITICA AGCCCCGTTCC CCCAAGCCCCG GNOCNCCCCA GAAN	824
	(2) INFORMATION FOR SEQ ID NO:524:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 850 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1367UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:	
	GATCHTATOG GIOGITICTICT AGGCCTIGAAA GCCCGGATATIC GACAGTCGAA ATOGCCAGCA	60
	GAATTTATTA TAAAACGIGC ACGIGAGCGT COGTTACCCCG GTTGTATATT GACGCCCACCC	120
50	TATGREACTG GITCCCCTTC TACAGGAGCT TCTAACGCGG ATGACTTTCT GCTCCGGFTC	180
	CTACOGGEAT GTGTTCAGTT AGGCAAAATT CCTGATATTG AAGGAACTGT TAATATOGTA	240
	CCAGFTGATT ATGTGGCACG GTTAGCAACA GCGOCTTCCT TCTCGTCATC AGGCAATACA	300
55	CATATGATGG TIGTAAATGT CAATGCGAAA CCAAGAATAT CATTCAGGGA CTATCTACTA	360

	GCACTGAAGG AATACGGGTA CCAGGTAACA TCAGTTCCTT ATGACGAGTG GAGTAAGGCG	420
	CTTGAATOGT CGAGTGATGA AGAAAATCCT TTGTATCCCC TATTGTACCT TGTCCTAGAT	480
5	GACTIGOCUA AAAACIGOGO AGTOCTGAAC TOGATACTAC TAATGOGAAA TITIGITTUAG	540
•	AAGAAGATTT TOCCCCCGACG AATATTGAGC CAATTATCAT TACTTCOGTG TCATTAGAGT	600
	TGTGGGTCCC CATATCTCAT TTTTGCATAA TTTAGCTCCC NANAANAACC ACCTAAAGTT	660
10	CCCAGCCCCT GCCNATATIC NCTCTCCCGA CGAACAAATT CCTTAATANC NCATACCNCT	720
	GCNCCGAACA TACANCAACC CNTAAATACC NCAAATTGIN GACAACATGA NIGITTATIT	780
	TITITIATATI ACAACCIATI ATTAACCAAA TININATCAC GATCNICINI GACGCCCICI	840
15	CTGACAAAIT	850
	(2) INFORMATION FOR SEQ ID NO:525:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 825 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1368RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:	
	GATCATCTGA AGTAATATAG AATCTGCATG GGCGCAAACC GTTGCGGTCC AATGTACCGC	60
	COGTIGUAGOG GOCATOGGTA AAGGTGAGCA ACOCAGGGCC ATCCCATGGT TCCATCAAAC	120
35	AGGCGGCCCA GTCAAACCAA GCCTTCAGGT TAGAATCCAT GTCCTTGTGG TAGGCTTCTG	180
	GAACCATCAA GCACATCGCT TCGGGTAATG ACAGAACACC ATTTATCACT AGTAATTCTA	240
	GCACATTGTC CASCGCGGCA GAGTCGGCATC CGCCTTCTTC GATAATCGGA TAAAGCTTCT	300
40	CCAGITOGIC TIOGAAAACG GCGCAIGCCA TGACACCITC CTTCGCACGC ATCCAGITIT	360
	TGTTGCCTCT TAGGGTATTA ATTTCACCGT TGTGTGCAAG CCAGCGCAGA GGCTGGGCAC	420
	GGTCCCAAGA TGGGAATGTA TTGGTTGGAG AAACGAGAGT GTACCAGCGC CAGGTGAGAC	480
45	TIGAAATGAG CATTOGICAA GICGIOGIAA TAATTATACA CCTGGCAGOG TCAATTGACC	540
	TTIGTACACA ATTIGTCCOGT TATTTAGGAG CACACAGTTA ACAGTTCTGA TACCGATGGC	600
	CGITAAACCC NYCTTICTT AAAINTIAAA CIGGCATCCN GAAGICICIC GINAITIANCC	660
50	TGAATCINCN CCCCATACTC CTGCCCCATAT TTCTTTCNCN CAACAACGIT TTTGAAATCC	720
	TTTCCCAAAA CCAAGGAACC NAAAGAAATN CTNTGGACNC CTCCAACCCN AACCCNNATT	780
c.c	TAACAATOOG TACTNOCCAA TITNITCAAG CNNAACCTGT NINCT	825
55	(2) INFORMATION FOR SEQ ID NO:526:	

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 839 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1368UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:	
15	GATCGTGACG ACTITIGIGIT TTACTTCAAC OGTATTGCAA CGATCTTGGT TTCGCCGGCT	60
	TTOGATGACA TTOCTATOGT GOGGGATGAA CTGCCATTGG TGACTGCATC CGGATATCAA	120
	CTGCAGAAGC CTGTTCATGT GAATTTTGAC AAGATTACGG CTGTGAATAT TGTGCGCTCT	180
20	GEOGRACIGIT TOATGGCTIC CCTACGCAAA ACAGTGCCAA ATATATCCAT CGGTAAATIG	240
	CICATTCAGT CTGACTCTCA AACAGGTGAG CCGCAGTTAC ATTGCCAGTT CTTACCAGTG	300
	AACATTOOCG OCTOTTTOGA OCAGGTOCTA TIGATOCATG CACAAATAAT CTCAGOCGCA	360
25	GCAATTATCA TOOCTATTCA AGTOCTAGTT GACCATOGTG TTGAACTATC AAAAATAAAG	420
	GITATTGTCT ACTTAGCCAC TGAAATTGGA ATAAGAAGGA TAATAAATGC CTTTAACAAC	480
	AAAGTATCAT ATATOCOGOC GAAATTATAT CAGACGAAAG TATGACAGAT GOCCAATGTA	540
30	CTGGGCGAGG GTGACATTCA TCGACTCAAG ATACTTTGGC TGTGACTGAT TCAGAGCTTT	600
	TOCTOCCCAN OCAGGAATTA ANAACTTTTG GTOCTATTOC ATGITACAAT ATTAGCATTT	660
	ATCATCCATA CCATAGCTGC TITACNATAG CATNTAATTT TACTATCTTT NAACCCACCC	720
35	AGACTATTIT TOCCCCONTA CITTACNAAN ANITTAANCA ACTGACCCCC CGNTATAATT	780
	CCCCATCCAA CACCCCCCCCC CTCNTAANAA ANACCNACTT CCAACCAGTG CCAACCNCC	839
	(2) INFORMATION FOR SEQ ID NO:527:	
	(i) SPOURNCE CHARACTERISTICS: (A) LENGTH: 851 base pairs (B) TYPE: mucleic acid (C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1369RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:	
	GATCGCCTAC TIGTCTCAGG AACTTGTTAT CATGAGAGAT GATATGTGCA ACAGGTTTAA	60
55	GCGCAATAGC ATTATTTTCC CAACAGTGGA AGAGCAACAG AAACAGGAAT ACATGCTGTT	120

	ACAGCAGGAG CTCCAGGATG ATGAACGTAG TTCGGATCTC TCCATTAGTC AACTGATTAA	180
5	GTCCAGGGAC CAATTGCCTG CCAGTGTCCA GGAGTCCAGG AAGATTAGTCA AAACCATCCT	240
	CGATCAGCAA CACCITTICGC CCITTIACCTC GCAGGIGCGC CCTATAACGT GOGACTATGA	300
	CTACACGITE CACCIGICOC CAATACCCIC CACIATEATC ATTIGCGACC CAACIGCACC	360
10	GAAATATGAT GITACTTACA ACGOCTGCAA GAGTATCAAT CCAGOCTCAT TTCTCCACAA	420
	GCGCAGCGIC AACTATACIG AGTACACICC TICGITACGG AAAGCAACAG AGGAACAAAT	480
	TETCETETAG GACTITAAAC TTACATATAA TETCAAATAT AAAGETITCA GAOGTOGICA	5 4 0
15	TETTICETAT GCATATITET TCAACTITIC COGTAATATC GTATOGCATA CAGTAGACOG	600
	COTCAATNOG AACAACCOON OGTOCTTCTT CAAACTOONC COCANNCAAT COCAAAAAAT	660
	TMTGGAAAAC TTCCACCTAG ATTTTCTGGC CATCGCNGAT GCCCNCCNCT CTTTGATTCC	72 0
20	TINCANCCCCA GANNAATCING CONCTITOCT ONTCATCCAT NOCONTINGS CCAATTCONA	780
20	NOGITIAAANG COOCCCCONC TITTCAACIT INGGATTIIN MINGITTCOG TOGGCNNOOC	840
	COGTINICAGAC C	851
25	(2) INFORMATION FOR SEQ ID NO:528:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 858 base pairs (B) TYPE: nucleic acid (C) STRANLELNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1369UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:	
	CATCAACACG AAGCAGAAGA AGACGCOGTA COCATGTACG TGCCACCTGC TGCCGTOGGA	60
40	GSCGGCCAAG GCCATCGCTC TGCAGCGCCA CACCGCCTG GGCCTGGTAA TATGCGTGCA	120
	CCCCACGGIG GACACACGGG CGCCGCACAT ACAGAGCATT CTGGCCGCAGC AGCAGAGGAA	180
	GTACGOCCC ACGGTGCCAA CCATCCGTGT GOCGGTGATT AATTCGATCG AACATTGCGA	240
45	GITGITTTIC GOCAAAACOC TOGACOGCAA CACACOGGAC TACCIGGIAA ACGIGAGCOC	3 0 0
	TOCAMOGIC GIGITOCCCC ATGICGICCC GACCCICACCICA GOCCAMIATA	360
	TICGCAAAAC CIGAGGIACC TGATAGACIG GIIGGATACC CCTGAGAGGC CATGGCCGIT	420
50	GCCGGACTIC TATCCGGTGA AGGTATACAC TGCAATGGAC GTGGAGCGCT CGCTGCTGAC	480
	CCACCTCAAA TACTICCCCAG AATAATGACT CCCTTGGAGG ATGCGTTTTA CCAACGGCAA	540
	GARACTTACC ATACTTCCIVIT GGACARAGGA ACCGTGGARA TGCGCCGATC TCCCTACTAC	600
55	CCAAATAAGC GTTTTGAAAA ATGACTACAT TNGAATOOON CONACCAAAA TTGAACACTC	660

	CCCGGAANNA NCATACNAAN CCAAAAGIIT GCTAAATATC TCTITCCNIN GTACACTGAC	720
	COCNACINIT OCAGGAAAG GNCTGPTTT AAACTICCAC TCNCACTINA TITTACCCCT	780
5	CCCNGCATCC ACCNAANCAA CACCIMITON AACCATAGAA CAMPITTICCT TITIAAAACAC	840
	TNAGAAGCAT TTNAAAAT	858
	(2) INFORMATION FOR SEQ ID NO:529:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 834 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1370RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:	
	GAICHTGIAC AACTGAGOCT AOGICTIGIT GHGAACGGT AACCHCCACA TICATIATHG	60
25	OCTOCAATAT GOAGAACOOC GAAGITIGETA AACTOGTCAG TOCTGATATG ATTAAAGGAC	120
	GCACAGTCAG CACAATGGAT GCAGCTGCTG CGCAGTCTAG CGGTAGCCGC CAGCGTTTAA	180
	CATIGAATICAC ACACGAGTIGT AGAGGAAAGC CTGCCGTTTTT ACCACGTCTT TGCAAAGCCA	240
30	CHATGCAACA CGAGATGATA GAGITCAGGA ATGCCTCATA TITCAATGGA AATGCCCAAT	300
	TGICTTOGIT AAAGCGIGGG TITGGAICIA TGACAAGAIA GITATIATOG CITCCCAAGG	360
	GGTACCATCC GTTACTGAAT AGTACTITAT CITCTTCATT GTATTGCCGA ACTTCGAGTT	420
35	CHACGANTA TOCATCATOT GITTCAGAGT OCTICCTOTO TGTAGCAGTA TTAATGGTTT	480
	CCTIGIATGA AACTOCIACC TICCCTACIC TIACAGCOCC CITAAATICA TIGAGCAGCC	540
	GROSSCIECT ATTROCAGIG CATROCCCCC ATCCCATRCA TCACTGICIG ACCAGICICC	600
40	TCATCOCTICA CNAATACCAC NACGGITTOCC CNCTCGTTAG CTGCNNCANG ATCACCONAT	660
	ANCOTITINE TOCCCAANIT COCCOGNOON NCANCONCCE AAAANGGIGG NGGIANICAT	720
	GOGINITICO CANTIGNANT TONOCITTIG AAAAACAATO COCTITAAGN INNAAGNONA	780
45	AANDOGFFICE CITICTAANTIG TGTCCCCTTIG GOCCCNCNNC CCCAATNCCG AGAT	834
40	(2) INFORMATION FOR SEQ ID NO:530:	
50	(i) SPQUENCE CHARACTERISTICS: (A) LENGTH: 840 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomi⊂)	
55	(vi) ORIGINAL SOURCE:	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:	
	CATCOCAÇÃO GACCACCCA TICOCACOCT TOCATOCAAG CAGGACACCT TICACAATITI	60
5	TCTCCCCCAC GTGACATCCG ATGACCCCCG CCACACCCTG GTTTCCCCACG ACGATCCCCCC	120
	CACCTACCTG GCCAAGCTTT TATGACGGCT GTCCGTGCTT TTAAATTGTT ACATACTGTA	180
	CATATICOCT TIAGICGIAC CACATITICA TCACCICTIC GGAAACCOCG CIGOSOCIICA	240
10	CCACCCCAG GICTGTCATC ACCCCGTAA TGTGCTCGTG CGACGTGTAG TCCATGGACG	300
	OCCUTABORE CIGOTOTORIO TOGICOCTOC COCACARACIO CACOCOCTORA COCUTOCATOG	360
4.5	CCAACTOCTC GGGGGAAAGC GGGAACATCC TTACAAACTT GTGCGATTCG CTTACCACGT	420
15	ACAATGOCTT GCGTGCGTTC TTGGCGAGGA CCCCTACCGT GTACGTCCCC ACGAGATTTA	480
	TCATGCCGCC GGACTCGGCC ACGCCCTCGG CGCCAACCAG CACTTGTCGA TITTIGTGTAT	540
20	GATGGACCCA CCGCGCTGTC CACGATCATC GTCACCGGAT GCCCTTTGCT TGCAGCAGGT	600
	CATACAGCIG CTIGCCCIGC CCCGAAGGCC CGTGCTCCGT CACGANACAC CGCAAGCAAT	660
	CACTOTOACO TOTTACTOAC ACGAAANNOG COCOCAAACO AGTTOCCAAA AAGTOTOCTO	720
25	TGITAGATCC NCCCATCTIT GINCTTTTIN TNCACGCTTG CCCCAANCAA AACGTCCNIT	780
	CONCINEITION TOCTIONACCO COCTIONICANA INTITTITITICO COCCOCINOCO NATITIONICI	840
	(2) INFORMATION FOR SEQ ID NO:531:	
3 0	· · · · · · · · · · · · · · · · · · ·	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 835 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1371RP	
10		
••	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:	
	GATOGAGAAC AACTAOGACA ACAGOCAGOC AGACOGOGO GAAGOGCTCA AGOCGAGCTA	60
15	TATTITIGAG TACCTROCCT COCTCATGIA CCACCOCCC TCAAACCTGA ACCCCCTCTG	120
	CAACOCCATC ATCITICOCCG GOGTICGAGGA COOCCAGGCC TICCTOCGIT ATGITGGACCT	180
	CAAGGGGGTC AAGTACTCCG CCCCAAGCTT GGCTACTGGC TTTGGCGGCC ATATGGCCAT	240
50	TOCTOTOATG OGTAAACTOG CAGATOCOGA AAAAGACGTO GOOGGGTOG ACCTOTOAAT	300
	TECCOCEAGOS ACTATOCTOS AGIOCATEAA GETETTATTO TACOCOCATE COCCUAGUTO	360
	CCCTCCCTTC TCCCTTCCCA TCATCCACAA TCATCCCGT CTCACCATCG ACCAACTCGA	420
		-2.0

AGTGCAAAAC ATGACCTGGG GGTTCGCCAA GGATATTCGG GGCTATGGCA CCCAGAATGT	480
CIGAGTACCG GCGCGCAAGC GCCGCACCTG TATACTATCT TGTCGCGGCT GCTCGCCAAC	540
COCTOCCTAC TCACATACAT ATCAAGATGC ATAATCAATC TGCTCATGAA CGCACCTCTG	600
TITTGTGGAT ACTICTICTCG COCGTATCCT CAGTACOCTG GAGTGCAAAA ACAGOCACTT	660
TGAAACAACA CGAGTCGCAG CTAAGGNGAN ATCCGANTAA NCAACNCACA CTTCAATTGA	720
CTTATGAAAT OCCCAAGGTT GATTGAACTG ACGTCCTTGG AACNINGOCN CGTGGAAACG	780
CCCTCTTCAN TIGAACCAAA GTCCACAANN AGGIATTINI TINAACCGIT CCGCC	835
(2) INFORMATION FOR SEQ ID NO:532:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 850 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1371UP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:	
GATCCATTGT GOGTTTGGAG GTCACGCCAC GGACGTGGAC ATGTACGTGA TGAGCTTCGA	60
COCCACCTC TICATICGTG COCCACCCAA CAACCTICAG TICCCCACCT CTCCCCCCCA	120
GAGTIGGGG TACCTIGGGT ATTACAGGGG ATACAAATTIC GAGGGCATGG CGCTCCTGGA	180
COCTOCOGLIC COCCEANACIC COCCOCENDEL LICITOCACADC COCCOCEANAC SEGLICATICOS	240
CAACCETICCG CAATACAGGA CTGTGATGAG AACCEGCGTC GGGGAGCACA AGCTGGTGCT	300
COGRECTERS ATCERCEDED TEATTGRETT CCGCGROCCT ACCOCCACA ACCTGRAGEA	360
CTACCTOGAG CTGAAGGTGT GTCAGAAGAA CCCCAACTTC TCAGAGAAAC TTTTCTCTTC	420
TIGOCTOCAA TOCTITICTOG TOCOCATAAA CAGOCITAIT AITOGAITCC GOGATGAGAA	480
ATTOGROCTIC AACAGOGTOG AGGAGTTOGN TAOCTCACAG ATCCCACACO TICTTAAAGGG	540
CACGGAATAT TCCAATGTAT GTGTGGACGC AATACAGTGG TATGGTGCTC TTACGAAGTG	600
OCTATOTICAS CTICCOCCOCOS CCTICAANACA CTITCAACTICT ACAGCTICTICC NGCTICCCOVIC	660
GRECTIACET MIGCNECCCT GOCCNACAAT ACTECOCCNAN MOGGACNATT MICCIGITIG	720
TTCCCCAAIT GGCGCGCCC CNATATAANN CANATTCCNN CNITINTTTCC CTINIGNITT	780
TAAAAACCCN TINTTCCCAC CNATTINCCC AGANNACANA GGNNVICCCC ACCANNCTIN	840
CCCANCCNCA	850
(2) INFORMATION FOR SEQ ID NO:533:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 835 base pairs	

	(C) STRANDEINESS: single (D) TOFOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1372RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:	
	GATCTEAAAA TAAGATAGAA TOGTAATAAA TATCATTCAG GTACAATAGA TOCTOGTGTT	60
15	ACTABAGGAT TACCTOGRAT ATRATTATCA OGRITOCTA ARGUATTAGG TGRARAGRAT	120
	ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA	180
	TRACCATOCA TIGGTAATCT ATCTRAATTR COTGTRATAC CTRAIGGAIT TGATGAACCA	240
20	TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA	300
	TAATGAAATA GAAAGAATCT TATAATAGTA OGATTACTAA CACTAAATGA TOCTCATAAT	360
	CATAGTACAA TATCATTTOC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA	420
25	CCACCTCAAT GICACATTIG TOCATATACT AAACAATAAC CTAAGAAAGC TGCIGCTATA	480
	GITAAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CICTAGGTGA TITTATAAGAA	540
	CCATAATATA AACCTTTACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA	600
30	TTANGATUCA TATATCTAAT TAATCAACCT AGTTGTACTC TCTCATAATA TGTTCTACTG	660
	ATGANAAAGC TAATCCATAT TANATGAATA AGCAINNCTA AAAAATACCN GINAGAATTG	720
	AATACTAACN TAACCTATAA AACCNAATTC NTOCATATAA TGAGAAGGTG AGGGAATCAT	780
35	ACNACTATAA CNATTTAATA TATTGATTCT ATTNCCATTT INFININAAT TITTC	835
	(2) INFORMATION FOR SEQ ID NO:534:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 854 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) CRGANISM: PAG1372UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:	
50	GATCTAGAAT TATTAAGTCA ACTATTAACT AATATCTATA ATAATAATGG TTTATCATTA	60
	AAATCATTAA AGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA	120
	TANTAATAAA TITAATAATA ATTAATAATI TAATATAAAT AAATAAAATA ATTOTATTAA	180
5 5	AAAAAAAATT TAATTAATIT ATATACTITA GATAATAAAT TATTAGATIT AAGTATICIT	240

(B) TYPE: nucleic acid

	AATAATATAT TATTAGGTAA ATAITTAGTA GGTAGTAATA TCCAATTAAA GGGTAGACTA	300
	TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT	360
5	TATATATATC AATGAAGTAA ATTAAAATAAT TTATATAAAT TAAATTATAT ATGACTTAAT	420
	ATTAATAAAC TIAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAAATTAAA	480
	TTAAATACTA TITAATAAAT ATUCIAAAGT AATTICITAT TIATTITATA ACATTITAAA	540
10	ATGITTIATG TIAAATAGAT AATAATCAAT TAAATAATAA AAATTAAGAT GOCACAAATA	600
	ATTOCATTIT CITTATGAAT CAATTAACIT ATGGITICIA TITATITIAC NAITTAICNC	660
	ACTACINATG TITTTTTACC NNIGAATTIN ANAATATATA CICNONANIA NATATTONCA	720
15	AATTATAATA TIAATTAAAT TIAATTAATC TATTATGATC CINNFINIAA ANATATGAGA	780
	ANAATTEAAT ATATATATNG AAATATNITIT ATOCCCCNOG NCACTIGAAN AAAANTATAG	840
20	TTTCNTCCCC ACAT	854
20	(2) INFORMATION FOR SEQ ID NO:535:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 827 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1373RP	
	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:535:	
35	GATCTTAATT TAAAATTTTA ATTAACTATT TATAATTTAG AAATATATAA TCTAGAGATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAAIG GAATTATTIG TOOCATCTTA	180
40	ATTTTATTA TITAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA	240
	ATAAATAAGA AAFTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA	300
	AAATATACCA TTTTTATTAA TAAATAGATI ATTAAGITTA TTAATATTAA GIGATATATA	360
45	ATTTAATTTA TATAAATTAT TEAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TITCATAATA TITATITTITA TTAGICIAGI AATATICIAT TTAATAGICT ACCCITTAAT	480
	TOGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACITAAATCT	540
50	AATAATTTAT TATCTAAAGT ATATAAATTA ATTAATCTT TTAATTATAA TTTAAATCAT	600
	TATAATAAGT AAATATATTA TTATTTTATT AACATAATTT TIGATAATAA TATACCATTA	660
	TTAATGONN TTATAANAAT TATCTINAAG GATTINNIGG AAANGCITNN TTTTAGAAAT	720
5 5	TREETAAANG TERRETAAAN NOOAATOOON AATTATTAAA TTAATTTAAN AANAANNANC	780

	CTITINITNA ATITAGITIN AMITTAACCC NCICCCCINT TIAANAT	827
5	(2) INFORMATION FOR SEQ ID NO:536:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 831 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1374RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:	
	GATCAATGAT AAATCGAAAT AAACTGATAC TATTGTAGCC ATTTTTCTGA ATTAGCACCT	60
20	GGAAACACTT TITTAACCTGT TCCGGAGTGG TCTCTGACTG ATTGGAGTTG AGGGTCTGGC	120
	COSTRACTOR CTCTOCTGTC CTCTTROCTC CCACGITTTC CACTGCCCCC CCCTGCGTCG	180
05	CCACACOCCT CTTCTTCTCA ACTOCCAGTG GCCCCAACAT GTGGTCCACT ACCGTTGGTG	240
25	COCCOCCAAG TIGCTOCAAT AACOCACCCA TCTTAAACCA GTTGAACTGT GCAAAATCTC	300
	CATACOCTTC GAATTOCCTG AGATAGGAGT TOCOCTOCAT GCTCTGGGGA AGAGCAGCAT	360
30	COSCATOCIG ATTIGGIGCIC TCATCTACAG CGICOCTGGT AGCATCTCCA TCATTITTCCA	420
	TECTIGICGIT CIGEGUATUG CTASCATCGT CTGTTTCCGG ATACATAGAG CCAGGUACAC	480
	TCACGTGATT CAACTCAAGG TAGTCTTCCA GCAGAAACGG CTTCGCCCCG TTCACAAACT	540
35	CCTCAGGGCT CAAAAGCTIC CCCGCATTIG TCAGTTTTAG ATTGGGTATA CTCAAGCTIG	600
	CAAGTOOCTG ACOCTCATCA CGOCATOGGA ATCCTGGGCA AAAGAGAATT GACCTCAGTT	660
	CAATCGCCCG CCCTGCTTTA AAAACATATT AACTCTCCCN CCGCNCNCAG GANAGAATNC	720
40	TCCCGTACTT CNANCAVAGNC ANCINIGCCC MICATCICAA ATTGCCAVACC INGINANITG	780
	GANCONITCC CCABCCCCCIC TGCCCCCCTA TIGANGVICG NCCCCGITTCG A	831
	(2) INFORMATION FOR SEQ ID NO:537:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 856 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1374UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:	

	GATCTTAAAG GCGGATATAA AAGCTGTACA AAAGAAGATG AACAAGCTTC CAACGCTTCT	60
	AAACTITICAT ACTITCCGCCA TIGCCTTGGA AGATGAAGGC GAAACAAAAG AAAGTACCGA	120
5	ATTTAGGGCT ATTATTAAAG AGTTTGAAAC ACAAAATAGT TTCCAGAAGA TTTTATATGG	180
	GAATTAATAG ATAAGACTAG CATCTTTCGA AAACTTTATA TAAACCAGGC AGATTAGCTA	240
	CCTICTACAAT GICCTTCAGA AGTICTICGTOG ACGCTAGGAG TOGCCTICTIT ATOGTTGGGA	300
0	AAACCACTIG TITCCAGAACT GITCCCAATAT GCTCTGCCTT GGAAATATAA TAAGCGCGAA	360
	CATCOCCATC GATTIGTGTCG TCGTTTATAT CTACGTGCTC AATAATCTCA GCAATATACA	420
	ACAAGOCAAG TTGTOGAAGG ATTCCTTCTA GOCACTCCTT TTCCGAGGAC CAATCTACCT	480
15	TAGTTCCCAT TCTGTAGAGG AAAAATGGAA GTTTAGAAAG AGGCGGGACA TAATCCTTTA	540
	AAAGTAAGG TACACTCTTA ATGCGAACGT TOGTCAAATC GGICTOGTCT CCACATATTT	600
	CAATCCAGTA ATAGTTCTCT ACCAITCTCT CATGTCCACA CTGTTGAGTT ATTCCAAATA	660
20	TOGANTOGGA COCNITATOC ATCTTAGATA NOSTTOGTAT ATCCCTAACT TOCCCANTCT	720
	CAACCNCANC CINGATAINA TITICCCGAAN TITIGMAAIN MMAICCCAT TGANAAAAIT	780
	CCTTCCTTAG GACCTATCAC CCAAATANIT AACCGCGVIT NANGATCCCT GVITGGTCAC	840
2 5	AACONONGGI CITINNIN	856
	(2) INFORMATION FOR SEQ ID NO:538:	
3 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 828 base pairs (B) TYFE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1375RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:	
	GATCTTAATT TAAAATTITTA ATTAACTATT TATAATTITAG AAATATATAA TCTAGAGATA	60
	TATAATCITA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
45	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATITIG TGOCATCTTA	180
	ATTITIATTA TITAATIGAT TATTATCTAT TTAACATAAA ACATTITAAA ATGITATAAA	240
	ATAAATAAGA AATTACTTAT AGAATATTA TTAAATAGIA TITAATTAA TTTTAATATT	300
50	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GIGATATATA	360
	ATTIAATITA TATAAATTAT TAATTIAATI TAATTIAATI TAATAATTAA	420
	TITCATAATA TITATIITTA TIAGICIAGI AATATTICIA TITAATAGIC TACCCITTAA	480
55	TROGRIATIA CIACCIACIA ARTATITACC TARIARIAI TIATIAAGA TACITAARIC	540

	TAATAATTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTTATTAT TATTTAAATT	600
	ATTATTAATT ASTAAATTAT ATTTATTAT TTTATAACAT AATTTTTTGA TAATAATATA	660
5	TCATTATTAA ATGGTAATTT ATTAATAATT ATCTTTATGA TTTATGACAA CCATATATTA	720
	TAGANATIGI TAATAGITGA CIAATATOON ATOCAACCIN TATINATITA NAGATCATAN	780
	ACCITITATA CAATTATTIT NATATAACAT NIACCINATT ANAATAIN	828
10	(2) INFORMATION FOR SEQ ID NO:539:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 688 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1376RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:	
25	GATCHATTIT GOOGACITOC CHIATCHACA THATTCTATC AACTAGAGGC TGHICACCTT	60
	GGAGACCTGC TGCGGTTATC AGTACGACCT GGCATGAAAA CTATTCCTTC CTGTGGATTT	120
	TCAAGGGCCG TOGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	180
30	ACCCCATCTC COGATAAACC AATTOCCCCG TGATAACCTG TTAAGAAGAA AAGATAACTC	240
	CTCCCAGGCC TCACGCCGAC GTCTCCACAC TCAGTTACGT TGCCGTGAAG AATCCATATC	300
35	CAGGITCCCC AATATTAACC GGATTCCCTT TCGATGGTGG CCTGGAAAAT CAGGCCTTTG	360
33	AAACGGAGCT TCCCCCATCTC TI'AGGATGGA CTAACCCACG TCCAACTGCT GITGACGTGG	420
	AACCITICCC CACTICAGIC TICAAAGITC TCATTIGAAT ATTIGCTACT ACCACCAAGA	480
40	TOTOCACTAG AGGOCCITOG ACCCAGOTITI ACAGOCTAGG CITOGICACT GACTOCAGGO	540
	CTGCCTACTC GTCAGGGCGT CATATTCTGC CCTGACGGTG GAGTATAGGT AACACGCTTG	600
	AGCGCCATCC ATTITICAGGG CTAGITICATT CGGCCGGTGA GTTGTTACAC ACTCCTTAAC	660
45	GGATTOCGAC TTCCATGGCA COGTOCGG	688
	(2) INFORMATION FOR SEQ ID NO:540:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 757 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
5 5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1376UP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:	
GATCCAAGGA ACCTTICCTT CTGGCTAACC TAGGGTACTT GTACTCTAGG CGAACCANGA	60
CTTTTACTIT GAAAAAATIA GAGIGITCAA AGCAGGCGCA AGCTCGAATA TATTAGCATG	120
GAATAATGGA ATAGGACGIT TGGITCIATT TIGITGGITT CTAGGACCAT CGTAATGATT	180
AATAGGGAGG GTCGGGGGCA TCAGTATTCA ATTGTCAGAG GTGAAATTCT TGGATTTATT	240
GAACACTAAC TACTOCGAAA OCATITIOCCA AGGACGITTIT CATTAATCAA GAACGAAAGT	300
TACCOCCATICG AACATGATCA GATACCGTCG TACTCTTAAC CATAAACTAT GCCGACTAGG	360
GATCOGGETGG TGTTTTCTTA TGACCCACTC GGCACCTTAC GAGAAATCAA AGTCTTTGGG	420
TICTOCCCCC ACTATOCTICG CAACCCTGAA ACTTAAACCA ATTGACCGGAA CCCCACCACC	480
ACCACTOCAC COTOCOCCTT AATTTGACTIC AACACOCOCA AACTCACCAC CTCCACACAC	540
AATAAGGATT GACAGATTGA GAGCTCTTTC TTGATTTTGT GGGTGGTGGT GCATGGCCGT	600
TOTTAGTIGG TOGAGIGATT GICTOCITAA TIGOGATAAC GAACGAGACC TTAACTACTA	660
ANTATOCTOC TOCATTTOCT GTTGCCCTTC TTAAAGGACT ATCCGTTTCA ACCCANTGAN	720
TITICACCATA CAGRICTOTICA TOCCCTAACT TCTGGCG	757
(2) INFORMATION FOR SEQ ID NO:541:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 821 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic)	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1378RP (>ci) SEQUENCE DESCRIPTION: SEQ ID NO:541:	
GATCCITATA AAATGGCCAA TAGACGTGTT ATAATATAAT ATACAAAATT ATAAATAAAT	60
TEATTEATA AGAIGATEA TAGIGATEATO AGAITAGEA TEAGAGEATA AGAIGATEA	120
AATAAGIATG GATTITTAAC TGAAATTTGT TAAAATGAAA TAAGAATTGC TAGTAATCTA	180
TTAATAAGAA AGTAATOGIG AATACTOTAA CTGTTTOGCA CTAATCACTO ATCACGOGTT	240
GAAACATATA ATTAAATAAA GAATATTAAT TAATTTATTA ATTATTAATT ATTATTAATA	300
TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAATGCG AAGTTGAAAT	360
ACAGITACIG TAGGGGAACC TGCAGIGGGC TIATAAATAT CITTAATATT CCATTITTAT	420
AATTAAAAT TEATATATIA ATAATEA TATTTTTATA AATTTTTTA ATAAATATA TEATAAAATA TEATAAATAA	480
ATTATAATTT AATAATTTAA TAACTTATTA ATTAGAGAGT TAGGGTACAT CCCCCCTAAT	540
OCTATOCATT ATOGTTOGTA CACTICTAATT AATAAACTAT AATAAATAAA TACTAATATT	600

	TIME CAME AND LABORATE AND LEAVE AND LABORATE AND	660
	AGIATININA TITNATAATA ATAAAAATGA NAAAACGACC CCIAATAATA ATITGCATTI	720
5	ANANITACCC TTACACCICC CNITAAATIT TTACCCINAT ANCONINTIA ATTAACCANG	780
	GVENNCCCON TOCTCCCONN TGTCCCCCCCC ATTNNANTTT A	821
	(2) INFORMATION FOR SEQ ID NO:542:	
10	(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 852 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1378UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542;	
	GATCCTTGCG TACTAAGAGT TAGACTITAA TEAATAATAT TATTTGTAGA AGATAGAAAC	60
25	CATACTGACT CAOGTOGTAT TTAACCCAAC TCACGTAACC TTTTAATTGA CGAACAGTCA	120
	AACCCTACTT ACCIGITACA ACCAAGAGGA TAGGITGAGT CGACATOGAG GIGOCAAACA	180
	TAACTIACAA TAGCIACICI ATCGITATAT TACCCIGITC AATTITIGITA TCATAATAAC	240
30	APPTAATTAT TATTUCAATA APPCICATTA TIGTUCAGAC TATTUCATTA TGTATTATTT	300
	ATTAATTAAT ACATATTGGG CTTTCGIGGA TATAATTATT GTTAATCCTA CTCATATATC	360
	TAGIOGITGA ACGITICTIAT AACITTATAA AAAGGATTGI TATAAGCTIC GCTGCAGATT	420
35	GICCTITATT ATTATAAAAT AATATTAGGA GITCTITIGGA ATTAACCCAA TITTACTCAAT	480
	DODGITOCATATTA ADMITTACA ATTITATOR ACTATTAATT AACCOTACOG	540
	TAACITTIAT TOGITATOAA ATACOATTAC AATATGTATA TITTGTTOAT TATGOCAAAC	600
40	TTACGITATT GTICIACITG TAGGIATTAC AATTATAGCA CAGTTATACC ATTATATTTA	660
	TITATATATA TOCCATATAA GITTITATTA ACATATAAAC TGINCATTAT TIATCINITT	720
45	ATTATAAATT ATRATATATTA ATTTAMAATT ATTAMAATTATATATATATA	780
45	TONITITIAA TAATAAATTA TIAAGGACIN TOOAACCIIT TIGAAAGACC COOCACINOC	840
	ATTAAATGTC NT	852
50	(2) INFORMATION FOR SEQ ID NO:543:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 845 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1379RP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:	
	GATCCAATTC TCTCGGTAGT TTCCTTCCAT ATAGAGACTG ATCAACTAGC CACATTCCCA	60
10	CAACAAAAGA GITTCTATCT AACGTGCCAT CGCGTCTTGT ATCTACCATG TCGTAGATTT	120
	GAGCCAAAGT ATCTTGAGGT AGATTGCTTC GAGACCAGAT ATCTGTAACA ACTAAGTTCA	180
	ACATTAGACC ATCCTCTGGC ACCTCTCTTG TCTCATCGTA GTTACCGTTA TTCCACCATG	240
15	GGAGCAAGTC AAGATAAGTG TCTCTATTGC TGACCCACAT TCCCTCGTAA CGCTTTCTTT	300
	CCCTTTCAGT TAOGTACCCA ACATCAAGGT GCGACTTCCA AGGITTGTCT TCGTTGAAGG	360
	AATTACGGIA TCGAAGATTT TGACGIATCT TCTCGCCCCTT TTTGCCCGCAT CTTCTTCCTG	420
20	GACTICGACT ACGGGAGITG COGTCGCTTC CGTAATCCTC TTCAGAGICT TCGCTGTCAT	480
	COCTTAGTTG ATGGGGCTCT GAGCTGGAAC TGTCATTAAG TATACCCCCC ATAGTGGTTT	540
	TIAGCCOCAC ATOCAATTTA CTCTOCACGA GAGCGITATC GITCTOCGIA TATATATGIG	600
25	ACCITICACCO GIGATICITIC CIGOCOCCIA GOCCAGITTIC COCATICOCCC TIGAAACCIT	660
	CATCCACTIG GANIOCTOCG TIGANANITT GGIATIAAIN CAGGAANATT CCTCCGIAGI	720
	CCAGTICATA GGAATTIGIT CATGTCAATT ACAANCTITC NACGGGAATC TITTIGGGACT	780
30	CNIGICACGI CGANGNATNI GICNICCGIA CANCICCCGA INCNOCAAAN INNOCNOCATT	840
	CINCIN	845
35	(2) INFORMATION FOR SEQ ID NO:544:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 855 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1379UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:	
	GATCCOGAAG TIAACACTOC CTOCCATTCA TAACTICOCA ACACCCIATG TOCCTICICAA	60
50	CATAGICGAT GGAGCACATG AATTGGGGTA TCAATACTGA TTTCATAATG CTTTCTGGAG	120
	CCATTGACCT TGCGTGACAA CCTCAAACAT ATTTGCAGCC AATGGTTGGA CTTTATGTGG	180

GGAGATGCAG TATTOGGATG TATGCACTGT TOGTAGTTCA ATCTTTCGGG GACAAAAACC

TOGTAAGTCA ATTGTCTCTT TGAAGCGCCA CCCGCTCCAT CATCCAGCAG GTTTCCTAAG

240

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	THE DEEP COCCUPIED IN THE TRANSPORTED TOCKTONIC	360
	TOGACCAGCA AGAACTICIT TGIAGOCTOC ACTOGGIGIA CITTOGGACC TITTACAATAA	420
5	TACTOTAAAG TTTCCCTCAG GAATATTCTA ACCOTGTGGA GCACGACATT AGCOCGTGGG	480
	TTTACCCAGA GOGATATTGG TAGAAATGGG TCCAAAAACTA TATCTTTGGA TGCAATTACG	540
	ATPICATAAC TCAATTCTTT TICCCAGICA CGIGATATGA CTATOGGITC GGIAGCPICT	600
10	ACACAGTICG CACATAGIGT CCGCATAAGT TAATCGCAAC ACCACGIGGA CATTGCACTT	660
	ANGGICCIAT GCCCICAATG TCACTCAAGC AGGIATITIAC GTICCCNATG TIACTAGAAT	720
	CTTCTTGCTC GACNCCGGAN TNGANCCCCA AGAAAAAATA TCCCCGCCCNG AAAANAATTT	780
15	CCCTGGNGTG ACGTGTGNAT NACCCNACGA AAACNTOCTC CTTCGAANGT NCCTTATATT	840
	CIVITAAANA ATANA	855
	(2) INFORMATION FOR SEQ ID NO:545:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 847 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1380RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:	
	CATCOCATOS ACCITOSCCAA AGTAAGOCAS OCTCTOGACO CAGATOCAGI CGACAAGGTG	60
35	AGGAAGCGTG GTGTTCTTAC CCTCGAACAC AATTGGCTCC TTCTCGCCCG GCAAGTGGAC	120
	CGCCAAGGIC GGCITCTTAG TIGGGTACTG CACAAATACA AAGTCGITGC GCAGCAGGIT	180
	GGCCAGTTCG TAAAAGGACT CGTTCAGGCC CTTCACGCCA CCGTCAAGCA CCACTGCGGT	240
40	CITOGACTOC GCAAGCAGGI CCTCCAGGIC CTCGGCGGGC TCCTTGCCCT CCAGCACCGT	30 0
	CACGGCCGGC TCGGCCTCGC GCAGCATGTA CGCCACAATT TCCTCGGCCT TGCGTGCGCC	360
	CGTGTATGOC ATOCCCTCCT CTGACGCCCC ACTGTGGAAC ACCTTCAGCG TCGGGTACCC	420
45	GCGCACGTTC TGGCCCGCCC ATAGATCCAG CTCCTGCTGG CAGTCCACCT GCGCCAGCTT	480
	GATGCCCTTC TCGGCCAGCT CCCCAGCCGC CTTCACGTAC TCCGGTGCCA GGTGCTTACA	540
	GIBSCCACAC CAIGSCGCAT AAAACICCGC CAICACAAGC GGGITCICCT CIAAGAACIT	600
50	CCCCAACGIC ICICCGGTCA ACTICACACT GCAGAGTCCT CTGGTGCAGT GGCATCTTGG	660
	GCCTGTGCAA CTGTGCCAGC AACCGGCGAT GCACAACACA AACCGCTTGT CCAAAANCNT	720
	TCTCGCTGCC TCTATCCTAC CCGTGGTTIN GIGNACTCTG TGGCGATCAA ANCCGGNING	780
	CNATTITICI TITATACIGA TOCAGAATIC ACCOUNTONO AAAACNVIIN CONGAAAAGA	840

	NCGNGIN	847
	(2) INFORMATION FOR SEQ ID NO:546:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 860 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1380UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:	
	GATCTOGOCT GITGTGAGTG ACCOCGAGTT COCCGAATTG TACCAGTGCG ACACGAACGT	60
20	GCCGACGGIA TCGTTTGCCA GCGCGACAAC GCGCACGGTG CCCAACCCGA CCGCGTCCAA	120
	CIGCICCIGG TACAICHIGA CCACGICCIT GCCCAICGCA TCCTIGAIGT TGAAGCCCIT	180
	CGTCCAGCGC ATCAAAGTGC CGCTCGATAG CCATGTCTGC GCCACGGCAT ACCACAAACGT	240
2 5	AAACCCGAGC TTCAGTTGGC CGCCCTCGCT CTGCAGCACT TCACAGTGGT AGCCCTTGAC	300
	AAACOCCATT GIGCOCTTCG CGATCAAGCC GAACAACTCG TCTGATGTTA CGTCGTCGTC	360
	AMSCAGCTCC TCGGGGATCT TCGACTTCAA CTGCTCCAGC TTCAACGTGT GATCACCGTT	420
30	GAGACOCACC GAGCACACCC GGAAATTCGT GCCCCCAAGG TCCCCCGCCA AGAACGTGCC	480
	CTCCTCAGTG CCATTGGGCC TGCCCATCAC GTACCACGGG ATCATCGGAA GCCCACGGTA	540
	CTCCCGTCCG TCTCTCCGTT CTTCAGACCT GTTCCATACA TTCGATGAAG TACGCGGTCA	600
35	ACTOGOGGAG TITTGTOCTOC GICACCTOGA AATOCTTACA TATTTOGTOC ACTOCTOCTO	660
	CACTIFICCOG COTTOCOCTT CTCCAAATCT TCVAAAANAT CCTOGTACTG TAAANATTAG	720
	ACTICANAC GITGGICGAG TCTITCNNCC TINCCTACTC NCONGCONIG TCNIANIATI	780
40	TTGANCOCCN TCCAATAAAA AACCCTTING GOOGTCNCAA GNCACCTCCC ACCCTCTTTT	840
	GPPTCCCCNF CCCNNAATGA	860
	(2) INFORMATION FOR SEQ ID NO:547:	
45	(i) SPOUENCE CHARACTERISTICS: (A) LENGTH: 835 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1381RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547;

	GATCATTATA TIATAAAATA TAATAAAGAA TATATTAAA TAATAATAAT AATATGAAAT	60
	ATTATATAA TICTCCATTG GAGCAATTTG AGATTAGAGA TITATTAGGT TTAACATCAC	120
5	CAATAATAGA TITTAGITIT ATTAATATTA CIAATTITOG TITATATCTT ATAATTCTTT	180
	TATTAGTAAT TITTACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTTCTA	240
	ATTGATATTI AAGTCAACAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA	300
10	TIGGIGGIAA AGIATGAGGI TATIATITIC CATTAGITTA TACATTITIT AFTCTIATIT	360
	TTACTATAAA TITAATTAGT ATAATTCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT	420
	TIGEAGTATC AATAAGTATA ATTATTIGAT TAGGICIAAC TATTATTOGT TTITATACIC	480
15	ATGGITTAAA ATTCTTTGGT TTATTTTTAC CACTAGGIAC ACCATTAATT TTAGTCACCA	540
	TTATTAGIAT CAATTGAATT ATTATCATAT TTTOCTAGAC TTATTTCATT AGGTTTAAGA	600
	TTATCACCIA ATATTATACC TOGICATTA TIAATTGITA TITTAOGROG TITATTACTT	660
20	AATCTAAANC CACAAATATT TAACNITTIN TIAAGITONN CONATGAATG CTATTINAGT	720
	AIGINIGITA GAATTINI'AT CITATACONG CITANINIGA AGININAATA CNCONIAINA	780
	AACTATTTAT TOOTTATTAA ATTAACANTT NAACNOONA TTANITINIA TNOTT	835
25	(2) INFORMATION FOR SEQ ID NO:548:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 863 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic)	
35	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1381UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:	
40	GATCATIGIC CAATATICCC CACTGCTGIA TCATATAGAT ATTGATTATA ATTTCTAAAT	60
	CAACGTGATT GTTCTAACTT TAATTAACAA TTATCAATTT TTCCCTAGTT ATTATTTTTT	120
	AATTAACTAA TACCTAAATC ATTATAAGCI TGACTTAAAA CAAATAATTA TTACATTATT	180
45	CPPEATTIAT TATTIAATAT TIAGITAAAT TITAAGITCA TIATICITAA TITTIACTCA	240
	CGAGTACACC ACTUATURAT ACTATURATU AATAATATUA ACGUUGATU COCATGUGUA	300
	ATGICCTIAG TTAGCOCTTA ATCIGAACCA ACATCATGIT CICATTATTA TTAACTATTT	360
50	TTAATTATT TAAATAATAATTA TITAATACCA AAGITATACC ATICCAACCT ATCAAATCAT	420
	AAAGATITAT AATAOCTCAA ATATTACACT TTAAACCACT CAGTCAAACT TTCTTAATAT	480
	ATATACTITA TATATICATUR CAMANDURA COMPANIA COMPANIA	
	ATATACCITA TATATGGITT CATAATITAC TTATAATATA TAGTATATAA TITAATGATA	540

	ALCICCIAAA IGATAAAGAA GIATAATATA TAAATATTAA TATTAAAGIA TITAATGAAT	660
5	ATTATTATTA TITATTIAT TATTATTITI ATTIAGIAAA TAAATAAATA TITOCACTIA	720
J	TIGAAATATA GGITCTINGA TIAGAAATAA OONAINATAA TGINOCATIG ACTATTAAAT	780
	AVIGIOCION CINGACITOC CIATTINOCN INGANAMIC NGAANATOAG AANANAGATT	840
10	CCNANAINTT TAATININCCC CCA	863
	(2) INFORMATION FOR SEQ ID NO:549:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 845 base pairs (B) TYPE: nucleic acid	
15	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1382RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:	
25	GATCICACAC GIGACTAAAA TCACTAACAC CACGIGACTT CGIGCACGIG GCATCGICCC	60
	ATTICTOTOGO TOGOTAGCAT TOTOGOCOGO CATOTOTOTO AGGOCACTOC GCAGOTGACO	120
30	ACCCUCTACC ACCCCAGCCT TCACCACAGA CGCCAACCTC AATCCCTATC TACCCTTTCA	180
30	GCIGGAATIT CITACCOCA TCCGATTAAT TCCTTTTTIG GCTTCCTTTT GCCCCTCTTT	240
	TICCAGIGGG TIGCTTCCIG AAAACAGGGA GCTAGCTICC CGIAGIACGT AACAGTCGIA	300
35	GAGGETTAGE CATOSCTGAG CTCGAGACCC GETGATGCAA TGTGCACAAC CCTGGTCTGC	360
	OCAMANCOCO CAUGAAGATT GAAAGTATOC AGGAGTGCAG COCAGGGTCA TGOGAGACAG	420
	AATGGGCCAG AAAAAGCGAA AAAATGGACG ACGCTTTTAT ATATATATGT AGCCAGGCCG	480
40	GOCGITICCCA GAACOOGACC CGACACAACT TGITGITACAA TTICTATCIG CAAGGAATCA	540
	AATACAAAAT GGAATCTAGA TIGGGATGGC TAACTGGTTT GAACTAGGAC ACTGGTTCTG	600
	CATTGAGAAG AACTCCATCA TCCGGACAAT GGTCCTAAGA CCAACCACCC AGANACTING	660
45	TOGANCTIAA AAAGGNOOGI TGAACATOCT GACAATGAAC TICTOOCNOG GTOCTACAAT	720
	TINCCACCATIC GETGATCINAA NACCCINNAAT TOGAGATIINT NOONGITAAC NITIGGCCTTIG	780
	CITIGAANCC AAGINOCIGA AINAAAIGIN CCINICGAAA NITANIACCN TOOOCIIACCC	840
50	AAANC	845

	(2) INFORMATION FOR SEQ ID NO:550:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 862 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
	(34.40)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGL382UP	
0.0		
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:	
25	GATCTATAAC AGGTOCCAAG TTGGCAGATT TGTTTCAGGG GCTCGACGAT GTAGAGTCCA	60
		-
	GIAGAATOCT CIGUAACCCC AGAGCATACT TIGOGOGAAA GICITIATCT GITGAAATCA	120
30	ACTOSOCIAT COSCITTICAT CCTGTCCCCC ACGTTCATCC CTTTCTTCAT COCCTTGTCC	180
	AGUATCUGGI TGGTAAGCUC AAUGAGCUCC GCAUGACCAC GUCCCATATT GUTTUGAAAA	240
35	TAGCACCCAG AACCACCCAT COCCCCATCG AACCCCCCAA ATACTTCCCC ATCCCTCACT	300
	GIGACAGITA TAGTAAATOG TOCAGATTAG GICTIGCTAC CAATATICCT GEOGITATAT	360
40		
40	CTGCAGAGAT AAAGGCAGCT TTTCGCATGC TATGCTGCCC CGCAAAGGAA CTGCGTGGTA	420
	TAGECGITCA GITTETTAAA CIGAAGCAGG CATOCATTTE TEAAATOOOC OGICAGETEA	480
45	Compression movements and accomments are	
	GETTTCCATT TOGTACAATC AGACCTTTAA CAACTCCAAA GAATCGTATC ACAGCGTCGG	540
	TENCECEPATE CALCULATIONS CHEMINATIVE TO COMMENT OF THE COMMENT OF	
	TTACAGAATT GCCACCTGTA GTTTATAAAA GGGCCACTCC TATTAAGGAT TTTTTTTGACC	600
50	GOCACAAGAG GACTCAGATT CACCATCAGC TGATTCACTC ACATGATGTC TGCGTCAGCC	
	CONTRACTOR OF TOTAL CAPITATION OF TOTAL CAPITA	660
	TIGICOCAGI CATICCIOGI CCATTACCIA CGAICTICCC CAAAAATOON AAAAAACAIT	220
		720
55	GACNATOINA AACCAGACIT CITINIIGON ATICCCAAAA AAATIGOOM GNOCCCNOGI	780
		, QV

	TRIVATCOCAN CATGCCCTTA AAATTIAGAT CCTTGACCCT ACTCCDANTT GNINCCCNAA	840
5	AAAAAACTA TCAATGININ CT	862
	(2) INFORMATION FOR SEQ ID NO:551:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 823 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: UNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1384RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:	
30	GATCTOCATC GCGTCCACCG TGCACTGGGC GGTCGTGGGC GGTCACGGAA AACTCGGCG	60
	ACTOGGICAT GGTGCCGGCA AGCGTCTCGT AGCGGATGGG CACCACCTTC GCAAAGTAGG	120
35	AAAAGAAGIG GCTATGGCCG TTGGGAACCT CCATGGCCCG GCCATTGAGC GGCCCGCCGT	180
	TOCCOGCAAT TTCGGGCCCA AAGGAGAGAC TATGGATCAC GTGGTTGAAG GAGAGATGCG	240
40	OGTGTTCCTT GTACAACCAA TOGTCGTCGG OCTGCCCCTT CCCAACCTCC CCACACCCC	300
	GEOGRAGIE AATGITICCCE TEAACGCGCT TEAGCTICCCC GETGCCAGCG ACGCGGCATC	360
45	OCTOGRIGAT CIGCIOCTOC AGGOOCTOOG TGTAGCCCTC GCGCTTGCAC TGCTCAAAGC	420
	CITTOCCATC GAAAGIGGCC CAGITCATCT CTGCGTACCC CGCGCCACC TCCCCGCACG	480
50	TOTGACAGOA CACGOGOTICG CTGCGCGGCA GGTTCTCGTT CTGGTCCTGG TCGCGTGCGC	540
	CATACACOOC CACAGTAGTC THOSTOSTCT GTAGACOOCA ACGTCTOOCC ACTOGGAATT	600
65	OCTOCTICOC CAOGICOGIC CNIGITIGIC CACCNITITI OCTIGATOCT OCTOCAACNA	660

	THE PROPERTY OF THE PROPERTY O	720
5	TATATONAAC COCACTOONC TOTOCTOCCG TOCTTCAANC ACTGNOCGTC TOCCTCCCCA	780
	NITECCICCI ANCAAANACN CGIICACAAC ACONCVIAIN CCI	823
10	(2) INFORMATION FOR SEQ ID NO:552:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 849 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(a) Total Linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1384UP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:	
	GATCACTTIC TTICICTCTC CACCATAAAT COCCTCCCTA CACACTITIA CCACTCTTC	60
35	TIGOCIGAGA COGGACAGGI CAATCICAGA GITTITACIA TICATIAGIG AGIAGATIGA	120
	COCGTAGTTA TTATCAAAGG CCACCOGGGA ATTGTTAAAG AAGTTGGAAA CAGATGATTT	180
40	CGACATOGIA TAGITCIGIA GCITAATTAG AACGGGCAGG TCTGAGCIGI CCGGCACGGG	240
	AGTACTGTTT TGAATGGGTG GCACAGGCAG TGGCGGTTGG GGCGTGACCA TGCCAAGCTG	300
4 5	TECCECCECT GTCAGGCCCG CTGGTACTGG AGCCCGCCACG CTTATCCGCCG GGTCTGCTGG	360
	TGTCCGCCAT TTCCAAATAC GGTTGTTGCA CGCTCCTACG TATTTTTTCGC GCTCCGCTGG	420
50	GCTCATCTTC TTCTCGGTCA AAGCAGGGTC GAAGITCAGA ATACCCTTAC TCTTGGTCTC	480
	CTCTGCAATC ATGTGCAACG TTTGCGCCAT CTTCCCCCAGC TTGTGGTCAT AGGCCGCCAG	540
55	GICGCCCGAG TICCGGATCA CCIGCGCITT CATGCCAAAG TIAACGAAAT ICTIGIAACA	600

	GUGINULACE CASCECTICC CAASCESTAC CECASUSCAA ATCSTTTICC TECTOSTACT	660
5	TETTETENAT ATTERATIONA ACAGGECCCC CAATAANCCT GTCCCACCGG CCCCGTTCCT	720
	GANNAAACCA GCATCACACC GCNAAAAAAC GGGCCCCACN CGTCGTCATC NAACTTACCC	780
10	CTOCACACTG NATATOCANA GCATACACCT TETETANICCC GIGINICIGA AANINCNAAG	840
	CCCCCACCT	849
15	(2) INFORMATION FOR SEQ ID NO:553:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 862 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1385RP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:	
	CATOGACCTC GTCATCATGG GCAAGCAGGC CACGGACAGC GACAACAACA ACACCGGGCA	60
40	CATICATIONE COCCUTTATION ACTICOCCICA COCCUACIONAC COCCOCCUTTO TITENOCTICA	120
	COCCACTOCC ACCOCTOCCA COCTCACCOC CGACGTCGAC CCCCCCCACC ACCTCGTCAC	180
45	TOCCOCCETE CCACTOGTEG TCACCACGGA CCTGCCCCTC AACACGCCCC CCTACGTCAC	240
	GCTGCCCAAC AAGATGAAGG CGAAGAAGAA GCCGATGCCG AAGCTCAACC TCGCCGCGTT	300
50	CCCCCGCCCCC CACTCCCCCCCCCCAA TCTCCTCCCCC TTCCCACCAGC CCCCCCCCCC	360
	COCCOCADACTICA COCTOCOTOCIA COCACACTICO COCAAACTICA COCACCOCAA	420
55	GOCCGITTAA CACCTATATA AACTAACAGC COCTATTICC TOOGCGCACG CAGCGTCCCG	480

	CTCTCCASCA CCCCCSCCCC CTGCTTGCCCC AGGTACGTCT GCTCGTACCA CCCCTCCCAC	540
5	TOCCOGCCCT GCGCCCCCCCCCTTACC CTCTTCCACC ACGCCCCCCC ACTCCTCCTC	600
	CCACGCCGCG AGGITGCTCC CCCGGTCGCT GCCGCCGCG CTATCTTGCA ACNCCGCCAG	660
10	CTTGCAGTTT CGCCCGCCCC CCCCGCATGT NNCCCCNCCAA CNCNTTTTTA CACNGGATNT	720
	TNCCONFFIG TINICCNINN NITCONCCCC GIOGRANICON TITIOCONFIG CITGANAATG	780
15	CTANCCAACC COCCAATITG ATMONGCCCC COCAAAATMA ACTITICCACT TIGOOGAGAC	840
	CCCGCCCTGT NCCCTTNFTT AA	862
20	(2) INFORMATION FOR SEQ ID NO:554:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 851 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1385UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:	
40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:554: GATCCTTGAG GGCTGGTTCC TGGGCTTGGA GCCCGCGGCCCCC GAGGCCGAGC TGGGCCGCCCC	60
		60 120
40 45	GATCCTTGAG GGCTGGTTCC TGGGGCTTGGA GCCCGCGGGC GAGGGCGAGC TGGGGCGCGC	
45	GATCCTTCAG GECTGGTTCC TGGGCTTGGA GCCCGCGGC GAGGCCGAGC TGGGCCGCGC GGCCGGGACC TACGGCGCGG CCGCGCTGGG CGAGGTCAAC GCGGGCGTGG AGGACTACTC	120
	GATCCTTCAG GECTGGTTCC TGGECTTCGA GCCCGCGCC GAGGCCCAGC TCGGCCGCCC GGCCGGGACC TACGGCGCGG CCGCGCTCGG CGAGGTCAAC GCGGCGCTGG AGGACTACTC TGCGTGTCTG TGGCGCGCG CTGGCGTGCC CTGGGTGGCC ATGGTGTTCG ACGCCCAGGT	120
45	GATCCTTGAG GECTGGTTCC TGGGCTTGGA GCCCGCGGCC GAGGCCGAGC TGGGCCGCCC GGCCGGGACC TACGGCGGCG CCGCGCTGGG CGAGGTCAAC GCGGCGAGC TGGGCCAGGT TGGCGTGTCTG TGGCCGCCGC CTGGCGTGGC CTGGGTGGG	120 180 240

	GOTGONICA CALCGARANG TIALGIRIGI TARXCALANG ANTAIGIANT COUNGICIA	420
5	TACTTOCTOG TOCCAGATOT OCTOCCAGGG GATGAGATAG COCCTICTOGT GOCCCTTGTC	480
	2000000000 2000000000 2000000000 2000000	540
10	COCCOTOGAC GOCACCACOC TOCOCOCAG CTCCTCACCT COCCCCCAG CAACCCCTCC	600
	GICTOCOCCT GOCGCCCCCC CAACGCCTGC AGTCGCCCCA ACGCTGCCCCA NCACGTTCGT	660
15	COCCOCNETICE ACTOCNOCOG ACTITNITIANA CACTOCTOCT TICCTOGRAT COTTIGNACINA	720
	NEGENSTIGE CETTINENAE TNINATGANE COCCEAAACE CETNITIENG GGETGOGGGC	780
20	NCCCOGCCCC NANNOTCTOG CONGGITINAG TGTCCTTNAC CCTNCCCCTT TNCNTTAACC	840
	GINIANNIIN N	851
25	(2) INFORMATION FOR SEQ ID NO:555:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 857 base pairs	
30		
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1386RP	
45	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:555:	
	GATCGCACGI CATTITIACCT ACAGGCTGGG CITTITGAAGA AGACGCCTGC ATGGTACAAT	60
50	GIOGIAGOCA GGATOCCACO TGIGACCAAG TTOOCCAGAG AACOGAAGOT GCATGACOCA	120
	GTTAGCGGCA AGTACAAGGG CGAGCTGGAT ATAATGACGG ATAGATTAAA CAGAAACACA	180
5 5	GAGACGTACA AGACACGCGC TGGGAGTTCC GACCGGCAGA CGGCCGCGGT GCACAAGCCT	240

	ICHAMBERGE GERFLARESA GGACAAGETG CGGTGGETGT TTTTCCAGCA GCAICCCTGG	300
5	GAGCTIGTOGC GGCCGAAGGT GCTGGTGGAG AACATGGGAA ATGAGCAGTA CGACTGGTGG	360
	COGATOTTOC AGCTAGOCAA OCCOCTTCAC OCTGAGTCTG TGGTOCAGCG GACOCTGTAT	420
10	CTIGCTIGAAGT COCCCCCA CCCCCCACATG CTIGCCCCCAT ACGACCAGOC GCCCTTTICAG	480
	TICTATOGIC IGAGGATGCA GCAGGAGCIG GAGGAGCAAA TAGOGITACGA GGAGGCCACG	540
15	ATGGTTGGCG CTGTGTTCAA GACAACCGCT GTGGAGCACG GTCTGCAGCA AGAGCAGAAG	600
	GICCICGACA GTOGAAACAA GACTITIGITG CCCCGGTTTGC CCTGATTTTT GCNAAAAAAA	660
20	ACTICTACAAA GCAGTICCNTG GGCCNAACCC ACCGAAGAAA AAGAAGAACC AGGACNNTGC	720
	CGAACCCNAA GACNCCACCI GIGNACICCN TIGCCAACIT IGIIAIAAAT ICIIACNNII	780
25	TTATTCCCTT NGTACAATNC NANNTACTGT TNIGTCCCAT CATGIGCCCC AACAGGTTCC	840
	CCCCVITGGA NAAANGC	857
30	(2) INFORMATION FOR SEQ ID NO:556:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 856 base pairs	
-	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
40		
	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1386UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:	
	GATCCATGCC TOGITATAAC TGAGCAGAAG TGTGCATGCG AACAGAGGC TTTCCTTGTT	60
5 5	CCTTGCCAGT TCCCCCCATTC CCCAAGTTGC ACTGCAAAAT GTGAATCATT GATGTCTTGT	120

	colection coloction managed recollect countries characters	100
5	TCTAGGCGCC GCCGTGAGAG TCCAGATGAT GAATCTGAAG TTGAGGCCCA GCACGTGTGC	240
	TTAAAAGATT GTAATCGGGT GCTGCTTTGT GGTATCCACA TGTGCAATTA CAAATGCCAT	300
О	GCAGGCAAAT GTCCTCCCTG CTTAGAATCA GATTCCAATG ACCTTATCTG TCCCTGTGGT	360
	AAGACAATOG TACCAGCCCC TGTCCGTTGT GGAACAAAGC TCCCTCGCTG CACTCATCCA	420
15	TGTCGAAACT COCTOCTOGA TACTTGGCCC TGCGGACACA GTCCACCTTC GCATAATTGT	480
	CATCCCTTAG ATGAACCTTG CCCCCATGTA CCATCACAGT CAAGAAAACT TGTCGCTGCG	540
20	GIAAAAACGA GATCAGGACA TICTGCTACA ATGATGATTG TCGTGTTCGA GACCGTGTAA	600
	GAAGCCATGT CCTATTGCAA TCACTTCTGC CAATINCCTG TCATTCCCAT GGCAATGCCA	660
25	GCAAACTIGT TAGCAAGOOT GIGGICNACC ACCGAAAGOO GCACNIGITT GITAGGGAAA	720
	TECNTESCAT NOCENATIONOT GAATCOCTET NONAAAAAAA AANCNOOGTIC CETTESTOCAT	780
30	CNCCACCAAT MIGGNIGATT TOCTOGAAGA GAANGTTOOG ACACCNOCCC GTOCTONAAG	840
	AATGTCCAAT CINICGN	856
35	(2) INFORMATION FOR SEQ ID NO:557:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 830 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1387RP	
50		

(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:557:

825

	GALCAALCAL ICGIGIGCCT ATALATAGSA ACCAAAAAGC CTICIGCCCT GGTCCTCAAG	60
5	TAGIATIGIA TAAGITIGGA ATCCTTGIAC GOGGITGCCT TCCGCGCACC TTTCATATTT	120
	TOGGTAAAAG COTOCACAAG GITTOCTATIOT TUATOCTITGA AGITIGICTOC ACAGGACTOC	180
10	CACAAGAACG CCCCAGCAAG CITCTTATCT TICACGIATT CCTTCTTTAT TITCATTGAA	240
	TOCACATTGT CGTAGACCAC AAGAGTTTTA GTATTAGGAT CGTAGCTATA TOCAGAGACC	300
15	CAAACATIGT CAAACTICTC TGGGCCGTGA GCTAGCCGCA ATTGGTTGTA TAGCCACATA	360
	CCCGGTTCCC CFTCTGATCC TCCGCCTACA CCAGAATATT TCTGGCCAAT TAGTTGTTCA	420
20	CCATCOCCCC GAACGITICGT GAAGCCACGG CCATACGCTG CCATCCCCAG TGCAATTITT	480
	CTTGGGCTGA CCTTAAATTG TTCGGTCATC ATGAGTATCG CATCATGTGC ATTCAACTCA	540
25	TCAAAGITGT CAATACCCAT ATCTTCATAC CCACOCTTAT CTAGGTGCGA TTGTACCGCG	600
20	AATTOGIAGO ATTIGIACAAG TIGCIATOGI AGOCTIGITOG CICTOACCAT GCACOGTOGI	660
30	ATCGIATGIC ATCATATCON CATOCTGAAA ACTGITICACT CNCAACCOGA AATGCAATNI	720
35	CTGAAGAAGC NGOCTGCCAG CTINATTGAA CCGTCCTGIN TCCCCGGGCC CNANATNITT	780
	CCATCIONNI GITNECAGOG GINCTITINNA AAACTOGNIC GUNCHOCA	830
40	(2) INFORMATION FOR SEQ ID NO:558:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 857 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1387UP	

(xi)	SECUENCE	DESCRIPTION:	SEN	TD	NO:558
1/-/	SECOMME	DESCRIPTION:	ಾಬ	ш	MO: 336:

5	GATCACCACA ACACAGAAC	C ACGCAACGCT	, vevecacile	CCIGITCITI	TGCTTGCACA	60
	CGTCCABCCC AGAGGACGA	T TACACCGCCG	TCAGGGFTCG	CTAGTCTCCG	OCAOCACAGG	120
o	CTCCTTATCA CATTITICCA	T TTTCACGCTC	GCACATGTCA	CAAATAACCA	AATACATCCC	180
	CAAAAGCACG CTTTTTCTC	T GCCCGITCII	TCTCATCGCG	TCAGACTICG	TACTOGCTAT	240
15	GAGCGCCAAC GCCACGCCC	G CAGOGAGCTC	ATCTACAGGC	ATCGGGTCGC	GOCCCACGCC	300
	TCTGCAGCGG CTGCGGCAC	C TOGIAGOGCA	. TOGAGATOOG	GCAAGAGGCC	CCTCACCTCC	360
20	ACTTACGAGC ATCGAAGAC	T TTACTAGGAG	ATGACAGOGC	CTGCACGTCC	CTGAGGCTAG	420
	CCTCCCCAGC CGGGCGGG	C OCTTOGIATA	. OGGITTACAT	ACCAGAATCG	CACGAATATT	480
25	TOCTCTAGGC AACTGCAGC	G ACGGAAGGGG	CTTCATGCGA	AATCCTTGCA	cceccesere	540
	CCGTATATAA GGTGACGCA	G CTGCGCAGCT	' 09000335CA	TGCTAACCAC	CACAGGATGT	600
30	OCACTOCTOC OCCATTATI	T ACGACAAGCC	: GGCGTCGACG	GTCGGTGCAC	AGGCAGGACA	660
	CCTGGCGGAA ATCCCAANT	C GTTGAACAAG	GGAACTGGTG	CAGCNGGCGC	AATCTACAAG	720
35	AGTTGTTGAN GOOGGCCGT	C ACATTIGOCO	TINCACTGAC	CCTGTCNCGA	TCCANGAACA	780
	GGNCTGGCAT MTCCCANAA	C CTCCCCACAG	CIGINGACIT	GAACTOONGC	CTACCTTGAT	840
40	TTOCANNOCA GAAAAAN					857

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 base pairs

(B) TYPE: nucleic acid

(C) STRANDELNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL	SOURCE:
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(A) ORGANISM: PAG1388RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

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•	•

	GATCCACCCA AATTCGTCTG TOCTGCACCA GCTTTCCCCAA CAGTCTCCGA GGTAATCAGG
15	CTACIGOGIT CCTATITIAT GOOCITCAAT AACTCITIAT ACTIAATITA GAOGITAACT
	TCCACATCCG GTATTTTTCA CATCTGAGAT ACTGGCAAGC ACGGCTAGCT TTAGGAGAAC

20

TGTATCCCAT GACTIGIGGA CAGGGGCTTT ATGAAAAAAC GCCIGICCGT GTAAGGATAT

AGAAAACATA CIGAGATOGC TITTIGITOCT GAATCAGACA TICITAGGIT ACATTITGGG 300 CCIGOCIGIA CAAGOCACTA ATATGAAGAT AGAGITATAG COCGIGAGAA GGAAAGOCTC 360

25

CACTGGGTGT TGCATGGGAT TTCAGGGTCG TGATAATAAT GCCAGGCAAT CATATAGATT 420

30

ACCACGAGGG AAACATCAAC GCTATTTAAG GTCATCCTTT TTGACATCTG TCGAGGAAGT 480

35

CCACAACTCC AATGACCTGA TTACTGCOCA GCAATTCCGT CCTCGAAAGT TGGCACGTCG 600

COGAATACCT GIAAGCCCAA CTCTACAAGA TCCCCCCGTC TCCAAGACCA ATCCTAAGCA

ACTIGACTIGGT TITTCTGCCCCA GAGATICAATIC NATTIGATICON TINATICCCTTA CATICNICCOGA 660

40

CITINGAAAA COCAAATTAA AATTOOGNAN NOCAAAATOC NOCGATTONC CACOCTIGAA 720

CTACCCACNE GGECCTATTA TITTATAATT GONNACAANN CCCGATCCCC CGNNAACCON 780

45

GTAAANOGAA AACCCCCCGG NVFTCGCACC NVCNTTTINC T 821

(2) INFORMATION FOR SEQ ID NO:560:

50

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(A) LENGTH: 838 base pairs

55

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) Original Source: (A) Organism: pag1388UP	
10	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:560:	
15	GATCCAGCGG CTTGGTAGCA TGCTGGCCGA GGAGTTGGGC TGTTCTGGTT TTGCGCGCTG	60
	ASSCICACIT ATASSICOOG ACTICGATIG CCACTIGIGG CCAAGACTIG CITCITTACA	120
20	TAGCTAAATG CCACTGATCA TATAGACTGC TTATTCCTGC TTAACTGCCT CAACGTTCCA	180
	TACCATCTCC GCGUACTCCT CUATCCACCG GTCACTGCTG AAGAAGCCAA CGTTGGCCGAC	240
25	GGACAGGATC GACTTCTOGA GCCAGGCCCG GCGGTCGCCG TGGTAGACCCAG	300
	ASCOTOSCAG GOTATOTAGG AGTOCAAATO GTOSCTCACO AGGTAGTAGT COCCGTOCTG	360
30	GEOGROGERG TOCACCAGAG GTTGGARIFTC ACGCAGGTCC TGAGGGGARA ATGCGCCCGA	420
	GGAGAGOGTC TCCAGTACGC GAGCAATGGG GGCTGGCAAC TCTTGGCGGT GATACCGGTG	480
35	CCGGTAGCOG AGGTCTTCGA CATCTTCTGC GAGATTACCA AAGAGGAAGA TGTTGTCTTC	540
	GCCGATCTCG CGTGTCATCT CGACGTTGGC GCCATGGACG GTGCCGATAA TGAGACACCA	600
40	TICATAACCA ACTICATGIT NGAATICCON GAACCICATT ACCOCCIGIC AAANGIGCIC	660
	ACTAATOGGA ACNOGGANAA TATTOGCCCG GAANATGIAT CCCGAATGAA ACCCCTCAGA	720
45	AATACNATCC CICTCITANA CACNOCCCNC TIATTACCTA TAINGCIGCC MITTTACCCG	780
	GCCCTINCCC CNAAAANACC TIGAGAACNC CCCCTNININ GGNOCCGIN CCNITTIA	838
50	(2) INFORMATION FOR SEQ ID NO:561:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 826 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) Original Source: (A) Organism: Pagl389RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:	
	CATCITCTTT TIGAACCCCA CAGACACAAA CIGIGAIGGA GIOCIGGAGA COCCAGCTTI	60
20	GCACCACTIC CITTICITAG ACCOGCIAGI CITTITICCIA GGIGIATGIC TETCCITOGI	120
	GOOGHGITTIG CICACAATIG CCITTAGCIC TICGACGACA AICTITIGIGG ATAACCITTIG	180
25	GCCATCTAAT CAGCCCTTTT CAATTGCACC TTTGATCCAA CATCTTCCAT TCCAAACGAT	240
	ATTOGICACC ACCAACATAT TAGTOGAGIT ATCTTTCCCC CATGATAAGT AGAATCTGGT	300
<i>30</i>	ATGIATTICA AACOCACCIC COGAGGGIAC ATCIGGOGIC TICGITATCT GCTCCACTAC	360
	TATGTGAGAG TTCACATUGC AATGTAGGAT TYTTTCCTGG ATCAAGCATC GOGTCTGCTT	420
35	AGGACCAACA GGATTGITTA ATGCCTTGAT ATATTCATAT TCCCTCACAT TATCTGAGAA	480
	TICAGACGGI ATAGCIGAAA TATIATGATI AGCCIGIITT TCTAATATCT TITIGCAAGIA	540
40	GGACGIGICC TCACCAAATA ACAGCTTGIA CACGACACCC AATGGIGCTG CGATGGAATC	600
	GAATCATCAA CAATAACATC TCCTGGFTGC TCGTATAGGT GTTCTTCGTC GGAGGANGCT	660
45	ACTAGOGOGA TATTNOTAAA TATTAACANA CANTTOTTGA CTGTTNGAAC TGCCNCGTAC	720
	THEATTMINT ANAMOCTONN ANTESTACOG THOMACNOTT THEAGANTIN ANCOCTONA	780
50	TECNITICENE GIGANITINE ATCICCCCTE MICTATACIG ATACNI	826
	(2) INFORMATION FOR SEQ ID NO:562:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGIH: 839 base pairs

(B)	TYPE: nucleic acid
(C)	STRANDEDNESS: single
(D)	TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(2) INFORMATION FOR SEQ ID NO:563:

(A) ORGANISM: PAG1389UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GATCCGTCGC ACTITICAACA TIGIGAACGA CITICACACCG GAAGAAGAGG CTGCCATCCG	60
CCGTGAGAAC GAGTGGGCCC AGGACCOCTA GCCACGGCCC GCCTCTATGT ACCATAAGTA	120
CCCCATATCT ACCOCTGCCG GCCCCGCCCCC CCCCCGCCCC ACCGTTGCGT GCCAGCAGCT	180
CCTCTCCCCA CTATCCCTCC CAACCTACCA AACCATCCTC CTTTATCTCC TCCCCCCCC	240
GCTGGTTACA ATTAACCOCC CCAGGTCATC GGTAGACGGA GCTAGCTACT CGTTGTCCTG	300
TAAGTGAGTT AACOCACAAG GOGAACTATT CGTGTGGTCA GGCAGCAGAG ACOCTGCAGG	360
ACATACTACG AGITATTTCT CATAACTAAA CATTTTTGAA ACCTPTGTTG CCCCCAG	420
GTCGTTTCCC AAAACCCCCC GCAATAAACA GCCAGCAGGG GTAGATCCTC TTCTCAGCCA	480
CAGGCTAGCA AGGATGCCAG AACAGCGGGAA GCGGTCGCGG TGGCTCAGAG AGAGCGCGG	540
COCACTITIC AAGAAGCATA COOOGGAAGG GOOOGGAA GOOOGGGG ACAGTGCCAA	600
ACACCICTIAC GACCCGAATG GGCAACCGCG GANCGGGCCC GAGCGGTNAT TTCAAGTTGG	660
COCNOCCAAC COCCCEANTIT NAAACCOCTC TNTAGACAAA AACTIGICCA GITCNCACCC	720
GINGITTACC AANNININAA TCTCCNCCCC NOOSINGGIG GCCNGAACCC CCNCIGOCIT	780
ACGEGERACEA CATETETICOC CCCCCTCCCA TTAAANACCC CENCNCCTTT INTCTENCC	839

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 740 base pairs	
5	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(:i) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1390RP	
75		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:	
	GATCAAGTAA TCAATCAGTT AATAATATTA AGAATATAAT ATGTAGACAT TTAGTCTAGT	60
25	CTATTAATTA TTAATTATTT TGTAATTIGT TGTTAATTTG TTGATATTTT ATTGATTTTG	120
	TICACATITI GITGACATGI TGATATGITA TAAAATATAA TITAATATTA TITTATATAA	180
30	TTATTATTAT TATCTAGICA TAGACTCATA TAAATATGAA TATATTCCAT TATTAATTGT	240
	TTAGGATAAA CATAAATTAA TATAATAACT TATTTTTAAG TTCAATAAAT ATGTTCATAT	300
35	TTATATGATT AATTCATAAC GTATTCGATA TAAATATCTC ATACCCTTTT ATGAATTAAT	360
	TAAGCGGTAT TAAATTATTC TCATTGGATT AAGTTATTAT TTAATTTATG TTCCTAACAA	420
40	TTAATTGATT CCATAAATAT CGATATTTAT TATTATTTAT TAAAATATTA ATGATAATAT	480
	TGTAATACTT CAATTATTTT ATCAAATGOC AAGTAATCTA TTAATCNITT AATACGATTG	540
45	ATAAGAAAGA AAAGAATATC ATCTATOGTA TAATATATTT CAAGTATGAC CTCTTCAATA	600
	TAATTAGAAG TITAAACTIG TAGAGAATTA AGAATTAAAT AIGAGICTTA CATTAAACCT	660
50	GATATGAACC TITAATCTAC TTATTIGITT AACCGITGAA GAGAGAATAG TTAATCINAG	720
	TATNACITAT ATATTGATAC	740
	(2) INFORMATION FOR SEQ ID NO:564:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 773 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1390UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:	
20		
	GATCAAACTA AGAAACCTAA TAAACTAATA GAACCTATTA GATAAATTAT AGAAATTTCA	60
25	CCAAATACAG GITTTTTAGA ATAAGITGAT ACAATATGIG ATATTATACC AAATAGIGGI	120
	ACAATTATAA TATATACTTC AGGATGACCA AAGAATCAAA ATAAATGTTG ATATAAAATA	180
30	GGATCACCAC CACCITGIAC TICAAAGAAT GATGIATTAA AATITCIATC TATTAATAAT	240
	ATAGTAACAC CAGCTGATAA TACTGGTAAT GATATTAATA ATATAACAGC AGIAATTAAA	300
3 5	ATTGATCATA GAAATAAAGG TATTTTATGT AAAGTTATAC CATTAGTTCT TATATTTAAA	360
	GCTGTAACAA TAAAATTAAT AAGTCCTAAT AATGAAGAAA TAGTAGTTAA ATGTAAAGAG	420
40	AAAATAGCTA AATCAACACA AGCACCACAA TGTCATTCAA TAGAACATAA AGCAGCATAA	480
	ACAGTICAAC CAGTACCTAG ACCAGATICA ACTATAGTAG ATGITAATAA ACAAATTAAT	540
45	AGTOGTOGTA ATAGTCAAAAA TGAAAATATTA TITAATCTAG CAAATGATAT ATCAGAAGCA	600
	CCAATTATTA ATGGTAAATA ATAATTACCA AAACCACCAA TTAATATAGG TATTACTAAA	660
50	AAGATACTA TTAAAATAAG ATGICCAGIA ACTAATACAT TAAATAATTG ATTTTGACCT	720
	TGIAAATATT GITGACAGGT GCTGATAATT CTATTCTAAT AATAAATGAT ATA	773
55	(2) INFORMATION FOR SEQ ID NO:565:	

	(A) LENGTH: 749 base pairs	
5	(B) TYPE: mucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGI391RP	
	W. Contract. PROIDTING	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:	
20		
	GATCHTTTIG CTCCAGGITA TICCCTTCTT GGACACATTT ACGAAGTGTA TITTICAAGAC	60
	CTGACTCGCG CATTTAGGTG TTACGTTAAA GCCTVTGAGC TAGATGCCGG CGACCTGGTC	120
25		
	OCTOCTARAT ACATOCTOCA ATACTATACT CACCIGIOCA ATTOOCAGO: GOCGOCCAAC	180
	ATCTUTGACC GTGTAATCAA GAATGATATG CATCTCAATT CCGTCAACTG GCCGTACAGA	240
30	GITCIOGGIG TITATTATIT GGAGCITCAA CAGGAGGCIG AATOGATOGA ATOGITCCAA	
	OTTO CONTROL OF THE PROPERTY O	300
	TOTOCITTAC GCATTGATTC GTCTCATGTT GACGCCATGGA TAGGCCTGGG ACAGGCGTAC	360
35	GCCGCATGIG GCAGAATCGA AGCCTCGATC AAGGTTTITG AAAGGGCATT AGAGCTGTCT	
	AAAGCATT ACACCIGICT	420
	CCAGAACATA AGIATOCAGG GITATTCCTG GCTATATCAT TATGCCAGCT TTCAGAATTC	480
40		
40	GAAAAAGIC TOGAGGCCCT GAGAAAACTT GIGAATAAGI ATOCACAAGA AGCTATCTTC	540
	AAAGAAAGAC TAAGTGCAAC GITGGTGGAG CATGCTTIGC AGTTCTTCGA CCAAGGTTAC	600
	The state of the s	600
45	CIGATAAAAG COOCAACITIG COCTOCTGAG GIGATATOGA TCATAGAAGG CATTGIATICT	660
	GAACAGGIAG AATATACAAC CAATATGIGG ATTACTTTAT CAAAGGCTTT GAATATTITIT	720
	3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.	720
50	ATTICCACGC GTICTCAGTT CGACAACTT	749
	(2) INFORMATION FOR SEQ ID NO:566:	
55		

	(A) LENGTH: 767 base pairs	
5	(B) TYPE: nucleic acid	
,	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1391UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:	
20	GATUGUUGU CAGATTIGTOC AGAACGTIGCT TIGCACTAGGG TICTUTTACGA CAAAGGACTA	60
25	CATOCAGICG TIGGCITCOG AIGITICIGI GAAIGAIGIG COGIOCAIGI TIGICAACCI	120
	GETTGAACTA GOCTTTCIGG TCCCGCTTTC CAACGIGCAC TACATGCCAC TGGCCGATCT	180
30	ATGGGATGIG CTCTACAAGA AGGAATACAA TGCTATTCCA AAGAATTCGA CGTTGTCAGA	240
	TOCCAACAAA COTOCAGAAA CAAAGGCGAA GACGAAGGTT CAGTTCAATA CGTTGCTGAA	300
<i>35</i>	GAATGICGAA ATGAGCAACG TACTAATGAC TGATATGCAG ACTTCAATGA GACGTGTCCA	360
	AGACAATCTT CCTCIAACAT TTAACTTCGG CCGGTACATG AAGCACCGGC GTTCTCGGCA	420
40	OCTIGIAÇÃO TITOCACOIT OCCORGIGOS GASCOTACCA GOCATGATOT ATAASOTOSC	480
	ACTIGAAGATA ACCIGAACAAT GTGCCCIGTIGC GCTTTCAGAT CCGCTATIGTIG ACACAGGCCT	540
45	AATOCAGGAA CITGAGGAGC AACTGGCTAT TCAGGAAGAT ATGGCGCTAG ACGATGAGAA	600
	GCTACCOCC GITACATTCA ATGCGGIGGA CATATCCAGA AACITIACCAA ATAACATGGA	660
50	CCTACGTGGC ACACTGACTT CTATGCCAAG AAGATCACCA GAACGTTGCA COCACCAAGG	720
	TCAATCCCAT AAGCGGNIGA AGGCTGAAGA TGGGATGGCT GTAGCAG	767
55	(2) INFORMATION FOR SEQ ID NO:567:	

	(A) LENGTH: 753 base pairs	
5	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1392RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:	
20	CATCOCCACC ACCGTCACCC COCTCCCCCC CACCACCCCC TICCTCACCT ACCCGTCCCA	60
	CGICACCACC ACCITICACICG GCATATOCCC GATACOCTACG GACTACOCCA CATACAGAG	120
25	CTTCACCAAC TOCTCCTCTA CGAAGOGGGA GCTCTCGTGA ACGATCATGT ACGGGTCCTG	180
	OCCOCARGOS TICOCOSCOS COCIOSCATO GICATICORAS TOCICIOCOR GOCACOCCOS	240
3 0	COSTABOSCO ACCITICATOO COSCAASOCA CTOGAASTIG TIGAGGTOCA GOOCGETOGT	300
	GIGCOGGCAG TIGCCCCACA TCAGGGCAAC GIGAGICGCA CGIGACGICA GCACCCAACGI	360
35	TEACACCACG ATCCCCCCICA GCCCCACCAG CCCCCAAACG CTCTGTGAGT CCACCTGCCG	420
	CASCISCOSTIC TICASCISCOS CICTOTOCAS CICCACCITOC ACCISCOSCA GCCCCCCCCC	480
40	GICCICCOCC COCACCOCC CCATCCOCCC COCTATITICC GICACCCCT GCICAAACAC	540
	GOOCACCOOK TOCACAGOCT COTCOCOCAC AGITTICIACA GOOCCTCGIT GIACCAATCA	600
45	CATOCTOCCT CITICACCCC ACCOCTACC CCCCACCACC ACCITICATOC CCAACTCCTC	660
	OCCATATAAN NAACCOCCCC TONAACCAAA CTOONGCACA AANONOONGA AGAGOGCACC	720
50	NCCTCCGANC GCTCGTTGCG CGCCCGCCTC CTC	753
	(2) INFORMATION FOR SEQ ID NO:568:	
55		

	(A) LENGIH: 752 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1393RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:	
	CATCACCICAT TOCCCCAAGT ANTOCCICAAC AGTCGTCAAN TCTCACATAT CTCTTCCAAA	60
25	TECTAGOCIC TEGEGECTTE AACTAACCAT TACTTCTAAT ACCTGCCTAG CTGCCTCCAA	120
	ATCCGGATCC AAAAAAGCAA TATTTATACA TAACTATACA CGAAATCTCA GTTCATCGCT	180
30	ACCTACCTCA TOGTATOCOG GACTGOGAGA GGAACTCAAT GCTGTGGAAC CCTTGGAATA	240
	TOGCAGOCTIC GOCCATGITG ACCAAGGACT COCCTGGGCC AAACATGCGG ATGCCACNIA	300
35	CONCOUNTE TO TO TO TO THE TOTAL TO TO THE TOTAL CANDOD CAALA AACTOCCACT	360
	TCAGCAGGCC GTCGGAGGGT CGGTTGTCCT CGAAGGTCAA CTTGACGCAC CCATTGACTT	420
40	COCCACTICT ACCETCTIGT AGTACETICC GTOCGAACCC CTIGIOCCCAG CGIATATCCG	480
	GAGCGTCTCC NANGTGTAGG ACTCATCGAC GAAGAGCCAG AAGTACATGG CAAGCTGGAT	540
45	GATGICAACG CGCTTGCTGA AGAAGACGTC TATGGTGTGT GGCTGGCAGC CGTGGCTTTG	600
	CCANAANGIG GCGGGGITAT CATCCNAAGG CGITTTOCAT GGGGIANCOG GCCTTGAANG	660
50	AAGAAGGCTT CCANTAGGCC AACNAAGTGA TATCNACTTA CCCTGGTTCT CCAATGTTTG	720
	CAAGCCCNCC TGITATTING NCCAGAAAAG AC	752
	(2) Thirdenia fricas trop and and account	

	(A) LENGTH: 773 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1393UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569;	
	GATCCAGGAT ATCATOCCCA AAATOCTTGA AGCCGCTGCA AAGCGCCTCG TGCAAATCAA	60
25	GAATCIGCAC ACGGCAGAGA ACTTACTCTT CGIATTITIGC TACCIGACTT CTATTGATGC	120
	GCGGCAGACA GTGGACTTTC TTTCATCAAC GATCATCGAT GAAGGCGGCC GTACCGCCCT	180
30	CCAGOCTATC GTTCCGCGTT GGCTAGAAGC ATTCGAGGTT CTCCGCGGAG AACATAAAAT	240
	CAAAGAGAAC ATTTTATCCC TITCCAAGCT TTTCTTCCTT GAGGATCCCC GTATAGCGGG	300
35	CATCACGGTC AATGGGGATC TGATTCCCCA CGATGGCGAC ATCATAATCA CCCGCTCCAT	360
	GOCCAAGAAA ATGCCTGATA AGIACACGCA GATCTCCGCG GCCGAGAAGA TAGTCAAGCT	420
40	CITTGITGCA GAACTAGCCT TCCAGCAAAA CCAGCCTGAC CCTGGCCGTT ACCCTAAAGA	480
	COSCICIOSC CCIOCICACC CACATGACIC CGAGGGAGAC TCACCIGATG AAGACIGGGA	540
4 5	GGATGICGAT GACATOCTTG ACTACGAAAA ATTGCGGGAG TACGGGGATG ATAGTGACAT	600
50	TGACGACACG GTGACAGCCT TTTATTCACA AGTAACATCG AAGAGGATGT AACCACTCTC	660
	CTTACTCAAT TCTTCAAGGA AGCOGTTGCC AGAAATGCCT CTGGCTTCCA GGAGATCTAT	720
55	AGCAGGCTCA CTGAACAAGA GAAGAAGAGC TATCTGCATG CATGGTATAG GAT	773
	(2) INFORMATION FOR SEQ ID NO:570:	

	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 755 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1394RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:	
	GATCTCGACG ATTACCOCCT ATGATTATAT CCCAGCAACA TGGGCACACG CCGCCACACAC	60
25	ACACATGATA CTGGTCGGTG ATTCGCTGGC AATGTCCACG CTGGGTCATG TGTCCACGGT	120
	CCACCTCCAT CTCCACCACT TOXAATACCA CCTCCCCCTCC CTCTCTACAC CACCACCCTC	180
30	GICCITIATA ATTOCAÇATA TOCCATATOG TAGCTITGAG CGAANCATIG AOCAGOGAGI	240
	ACAGACOGOG ATCICOCTTA TGAAGACATC CAGCAGGGTG GGTGCTGTTA ACCTCGAGGT	300
35	TGGCGCGGAA GAAAACGACT ACTGTCTTGA GCTTGCCGCA GAGCTCTGCA GGCGCGGGAT	360
	CCCAGTAATG GCCCATGTCN GCCTGACCCC GCAGCGCATG CATGCATTGG GCCGGTTACAA	420
40	GGTTCACCGC GCAAAGCACT TGGGCCAGGC GCTGGCGGGG TACCACCGGG CTAAAGATCT	480
	GCAGGCTGCA GGCTGTTTTT CCATCGTCAT CGAATGCATT CCAACTAAAC TAGCCGGTAT	540
45	CATAACCGAG AAACTCAGTA TACCTACTAT TGGCATTGGC GCGGGCCCCC AGACAAGCGG	600
	GCAGGTGCTC GTACAGTCGG ATCTGCTGGG CATGTTGCCA NXXAAGGCCC CAAAATTTTG	660
50	TOCNGAATTC COCOGACTTC CNCNGGGACG CCATANGTTC CTTGTGCCCC CTATGTTCAA	720
	AANGIGOOCA NGOCNICTIC CONAAAGING GOGCA	755
	(2) THEOREM TO COLUMN TO AN EXT	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 773 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEUNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1394UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:	
	GATCGAACTC CATGAAGGAG CGTAATGGCC TCGTGCAGCT GCACCGCACT GGGTGCGTAC	60
25	ATAGCCCCAT GTAGCAATGC GCCCATAACG ATTCCCCAAAA CCTCACTCCC CTCCCCCCTCT	120
	ACCITICACIT CAACCIGGCG CAGCAGCGIT GCIAITAGGCT GITGIGGCGA CAACGICGAC	180
30	ACTICAGITG CAGIAGGAGC AGGIAGCATA CGACIAGITA TATCGAACTG GIGCCOGIAA	240
	TGAGGATGAG GGTCAATTTC TGGCTCCGAG CGCTGGCTAG CACCACAATT ATCACCAAGT	300
35	CCATACCTCC ATGCAATTCT GAGATCTTGG CTACGTGCGA CCGGTTTTGC ACCCCCTCCG	360
	SCIAAGITT SCACCGIGAC CITCGATICC TOCTGGGAAA TOOCAGATIT CITTACCICT	420
40	TTACETETEC CCTECAATAT CCCCCCCAC TCCTTCCCAT ACTCACTGTT CACCCTCATC	480
	ACCACCACAT GOGTATTCCC TCCCCGCTGT GCGCCGCCAC TTTCCGCCGC GTTATGTGCT	540
45	SCIECCISCS CISCAAAGAS CITICCAAST ACCGAIGCAA AGICIGIACC CCCITGITCI	600
	TCCACCAGAA GCATCTGGCC CATTGGCAAG CCCATATGCC CTAGGAGCCG ATCCATATCT	660
50	OCACAACCCG TOGATGITGT GOGATOCGAA GTAACCGOGG ACCGGACGCAA GCCCGGATGC	720
	GACTIGOCTIGE CINCCTCACTIG TTGGATGCCA ACCTCTCCAC GCCTCTINGAA AINC	773
55	(2) INFORMATION FOR SEQ ID NO:572:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 746 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1396RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:	
	GATCAATCAT TCTAGAGCTG GAGCAAAGGA TACCTATAGG CTTGCCTCGT CATTGGCCCC	60
25	THICATTAIT ACATACCCAT OGITOCACAG OGIGICACAT TOTGCCATIC GAGAGCAGGA	120
	CACCCAAGIT TICAAACAGA ACAGCCICGI TCICTIGGIA AAAGITIGGAC CITCIAACGG	180
30	TOTOCICATO GAMOCOGICO TOGOCACIGA GEACCITICAG GEOCITICAG GIGOCITICA	240
	TGIAGICGIT GAGCATAGCA ACCOGGIGGI COOCAAGCIT ATTGAAAAAT TGGIACTTGI	300
35	TESCRETEGA CCTGANCTEC ACCCCAGC AGITECCTCT TCTTTTCCAG CGTTCCCAGC	360
	TROOBERIOGA CETEBERIGET GACTETIETTE AATTETETEA CEAGCACCAT CECETETTEG	420
40	GCAAGGGACT TTTGGGGGGA GGCGGGTTGG GCATCCTTAA CCGGGACAGG TGGCAGGGG	480
	ATGTCCAACA CCAGTTCCCC GTACCTCCAC CTCTTCTCCA CCTCCATCCT GTACTTCATC	540
45	COCACOSSO GEATESCETT CATCTOSSCE TICACACCTG GOOCACCTCC GTCACCTTCA	600
	OGTACTICOG AGGCICIOGG GOODOGCCA GCAACTIAAC GAICAIGGCG TCCACCTIGA	660
50	TGACAACTIG TCGTCGTTCT GCGTGCTCTT GCCGTTGCCG CTNGGGTCTG CCACNAAGAA	720
	CTCTTGAACA GGATTTCTTG TNAACC	746
<i>55</i>	(2) INFORMATION FOR SEQ ID NO:573:	

	(A) LENGIH: 772 base pairs	
5	(B) TYPE: mucleic acid	
	(C) STRANDHINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1396UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:	
	GATOBETTAC TTAGAGGGAG TOCAAGACCT GECCTGACTT ATCTTAGGET TATTAGCTAT	60
2 5	GACOGGIGIG TICOGATTIC TGICCAAGOG TITAGATGCC ATCAACICCC TGAATTCOCA	120
	CUACITIGOS TIGICOSTOS ATGAACAGAA GOCCATGACT TICGITGAGC GIATTAGATA	180
30	CTACAATTOG ACGITTGAGG GGATCIGIGT GGICCIGCIC GGGCTGATGT ATGCCGIGTA	240
	CGTGGCGGG ACCAAACTAA ACGAGCGGG CTCGCACCGT CTGTTCGAAC AGCTGAACAA	300
35	GITCITCIGG GAGGAGCIGC AGITIGCGCG CGIGGGITTI TCGICCUGGG ACAAGGGACG	360
	GCTGCCATAC ATCAGCGATC GGAATGGCAC ATGGTGCACC GCATTCGCTA CGGGGGCCAC	420
40	GIGIGIOGAC CATATIGIOG TGAAGOCTCA CTACCCOGGG COCTICAACC CIGIOGOOCT	480
	CCTGGTGGAG AACCTGCTGG GGATGTTCTT COCGCAGGTG GTGGACCGCA CGGCGATGAG	540
45	TITICICAGE TGACOCTICAC COCCAACGGG AAGTOCACGA AGCACGAGAA CAGCGGGGTT	600
	CAGGOGACGG AGGACGGGCT GAACCGGTTC CGGTTCATCG CGTCGATCGT CCACAAGAAC	660
50	GRANCIEROS CARCORANTE CUCHICAR CONTRACTOR DE CONTRACTOR	
	CAAACTCTCC CATGCAANIA CICITCATGT CCGANAACAA CCACTGAACA AC	772
55	(2) INFORMATION FOR SEQ ID NO:574:	

	(A) LENGTH: 753 base pairs	
	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(with outstand occupant)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1397RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:	
20	GATCCCATTA TICTACAGCA AATATTACAC GGCCGGGGGA CCCTCGACAA TGCAGAATTC	60
	CATOCATACA CAAAACATAT TACTACAAAG CITTCAAAAG GIGICICICC CACAGACOCA	120
25	TITCTAGGCG CACTCAAGGT TTACATTCTC AATTGCAGTT TGAAACGTTT ACGCTTGCAG	180
	AAAOCACAOG TTATACTTCT TGATAAAATT OCGATATTCA TCAATACAAA TGIGGTCCAT	240
30	GIGICIGIOG AATOGATACA TAOGATACIG AAAAGITTAG CIGAATATIT TATIGATGCC	300
	AAGGAATATA AGGGACTCAA CAAGGTGGTC AATATTTCAT TCAAGGCATA TGTGATGTAT	360
35	AAGCATGAAA GCCTTATACG ACTTGCAGCA GATCTCGAAT TATTTCTCTT TATGTCCGTC	420
40	AAACAGGACT GGTCAATGIT TACCAAGITC GAGAAGITTA TITICTIGTOOC TICAGGAGAC	480
40	ATCICAGIAT COCTOTTIGA ACAGIGITIC ANIGITIATG TIATGITCOC GGATCCCICA	540
45	THOCCCOCC TATOCCATCT CHCCTHCAAC AACHCCHTGA AGHGTTTCAA GAAATHOCGA	600
43	CTAACTAGIT ACACAGACTT TAAGGCATCG TCCGAGCCAA TGCTAGTGIT GGTATACAGT	660
50	GGATTTGTTT CTGATATTTT TACAATACCT TATAATGGCT GGGCTCCGCT ATGGAAAATG	720
	TTATTCATOG CATTAAATOG OGTCTATAAA TTG	753
55	(2) INFORMATION FOR SEQ ID NO:575:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 767 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1397UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:	
	GATUTGAAAT ATTOCTCACC CCCACCGTGA CUTATGTAGA TGAACGTGCT GGAGTTCGTG	60
25	ATCATTCTCA CGAATTCATC CTCTTCTGCC TTTGAGCCCAG TTACTATCCG TGTTGAACCC	120
	AAGTOGCAAC AAAGTOTOGT AAAATGTTCT TTAAAGCOCA GTTCAGTOCT GGTCAAGTOC	180
30	CCATGCGGET TTAAAACAAT GGAAAGICIG CTGICTAGET TAATCTTTGG AGACATCICT	240
	CCTCTGAATT TAGTTAGTAG CTCGTGAAGG AAATTTATOG ATOGTACOCG CCTCACAGAA	300
35	GCATCGGAAA ATATACTGAG AGATTCCCAT GGAACCAAAC TGCATTCGGA GCTTATTACC	360
	ACAAACCTGT GTCCTAACCT TGGCGCCTCT GGTGCCTTGG CATGATAGTC GTGAATTAGT	420
40	TOCTOAAGTT GAATATGTAT GAGATGAACG TOAATCTCAT CATAGGCATT TTCTTCGCCA	480
	TOGAAAAGCA ATATGICAAA GATGAAGTAT ATCAAGTCCT CCATGAATIC CACCITCTIT	540
45	TOGTGAGGAA GOGCATCOCA ATCCACCTTT AAAAATAACT CTAATATGAA ATCGTCCACC	600
	TGPTAGAACA TAGACOSGIT TCCATACTGT CTTCTTGTTG GAAGATTTGT TGTAAAACCT	660
50	TIGAAATCCT AATTIGAATA NIGCAAAATG GITITATCCA ACTGITITIG GNIGAAGAAA	720
	COGCINGAATO COATATOCAG ATCTCATGOG GOGCINICNAT CTACATC	767
55	(2) INFORMATION FOR SEQ ID NO:576:	

	(A) LENGTH: 774 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1398UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:	
20		
	GATCGCTCTT CTTTGAAAGA ATATGTAGGC ACCCTCTCCT ATCTTGCGCC GGAATTGCTT	60
	CGCTGCAAAG ATATGAAGAC GATGACACCT GCAGAAGCAG AAAGAATCCC AGAGTACGGT	120
25	CCACCACTOG ACATATOGGC TOTTGGTGTC CTCTGCTACT TCATGATGAG TGGCTATATG	180
	CARCASICO ACATATOCCE TETTOSTOTE CICTOCTACT TEATORICANO TOCCIATATO	180
	CCGTTCGATT GCCAAGACGA TGCCCGAAACT AGTGACTGCA TCTTGAAGGG TGACTATTAC	240
3 0		
50	GITGACGAGG AACCTCGTGC CAACGCCAAT GAGAGCTATA ACAGCTGCTG GAACTTCATG	300
	CASCOCTOCT TTACGATOGA TGATAATATC COGCCOCCCG CACACGAACT CATGOGCCAC	360
35		
	SCATICATOC SOCAATACIT CCAATOSOCT GOSSCCAATG ACTICOCATC TATCCCOCTA	420
	CTCGAGAGAT CAAGATCCTC GAACTCCCTG CACCACTTAG CGCCGCCATC ACGCCGCCACCG	480
40	TITATOTOGT CTGGCCTGCC GGTTATTAAC GAGCGCCCTG TGCCACGTGT TGGCTCGCGT	540
	Transfers crossroce astratival distractor receivant rescreeds	340
	GASCOCAATT TOCATAAGIT GCGGGATACT TIGCGGAAGA CCTTTCCCTC ACTICGCTTG	600
45		
45	AACCTATGCG CTTTGTTGCT CAAGCGAATA CTCCTAATCC TAATAAGAAG AACTCTACTT	660
	TIGITOTICA GOCAGOTOCT COCACGOGGA GIOTAATGAA TOGGIGITIC ACGICACACC	720
50		
	GGAAAGTAAT CCAACCTCAA TACGCCAGTC CTTTGGCGCA GAAGCTGCGG CCAA	774
	(0) 7	
	(2) INFORMATION FOR SEQ ID NO:577:	

	(A) LENGTH: 756 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1399RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:	
20	GATCATTACT COCAGAAACT GAGATGITAG GCOCACCAAA CTCTTTTCTT TGATGAGATA	60
25	COGGAGGATG CCCTCGGAGA ACCAGAACAA TGCAGCAAAA GOCACGAAGA ATGCCAAGGA	120
	GAAAAGCACG CATCOCTOCA TATGCAGTOC CACCCCATAG TAGTTCCTTG COCCATATOC	180
30	CIGOGGCAG AGIGIATOTA AGOTTOTICA AATACOCTON AATATIGOGA AAGIGATATT	240
	GETGETCATE GAAGCCAGGE AAACCGCTGC CAACTCATTC TITICCCAGGT GACCCACAAC	300
35	TAATOCACAT ACAACCOGAA ACATCTOCTC AAGCAGAAAT GTAAATATGA GOGGCACOGA	360
	GTAACACAGA AGCACCAGAC TCTCGGACTT CACGGTGGCT GGTTCGTCGT CGAGATCCTC	420
40	GCACCCTCGG AACGCGCTGG ACGCGCCCCCCTTGCTGCCA ATGCAGTAGT AAGACACCTT	480
	TOGGGGCOGT AGAACACGCA CITICIGCCTT GTCCGACGGC AGITIGCTGCT TAACCCGATG	540
45	CATGAAGTGA GIGTAGTGCA CCATGTCTOG CGCGGCCCC TCCACATCGA CGGCCACGAT	600
	GICCICODOS CIGCOSITIAA CAGIOGAGIA COGOCGINOS IGCICCICCA ANATOCAGIO	660
50	TACATTOAGT GCAGAGGACG GCCCGCCTCA CTCGCAAGCG TCGACGGCAG CGAGACTGTC	720
	COCGACAGET CTCCTCCGTC AAGCACGCCC TCCTCC	756
55	(2) INFORMATION FOR SEQ ID NO:578:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 775 base pairs	
5	(B) TYPE: nucleic acid	
5	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1399UP	
15		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:578:	
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 576:	
20	CATCTIGIAC GACGGCCGC CAAGAATCGG TGCCATCGIT TCCAACAGAC AGTTCCAGTT	60
		00
	TGACGGCCCA CCACCACAGG CTGGCTCCAT CTACGCCAAG GGTTGGGCCC TAACCGAGGA	120
25		
	GOCCAACTIG GOCCTAGGIG ACAGCGACGI CTICIACCAN IGICIGICOG GCAACTICIA	180
	CAACCTATAT GACCAGAACA TOGCACCACA ATGCTCTOCA ATTAAGCTCC AGGCAATCAA	240
30		
	ATTOGTOCAC AACTOCTGAA CAGOCACAAA GGTATATAGT GCATATATTG TATTAGTTAA	300
35	ACTAGGAATT TTTGTTGGCA GCTAGACTGC CCTAGGTGGA TTTCTCGTTG CGGATCCTGG	360
	GCTGCCGCTG GCGCTGACGC ACAAGAGCAA CTGCACAACT ACTGGGCGTAC CGCATGCCTC	420
	COCCCCO COCOGREGO MEMAGRICAN COCACAMET ACTOGOGIAE COCATOCOC	420
	CTTGTGCATT TTTGCCGCGG TGGACGTCGC TGACGTCAGC GTGGCACGTG ATCATAATAT	480
40		•00
	GTCCCGGGCC AGGCCCCTAT TGTGGCGGAC AGGAATGCAT GCGGAGGTGC AAAATGGTGC	540
	AAAATOGTGC CCCATGCAAC TCTAGGCCCC AGCTGAAACA AGATTACCTG GGCAGOCTAA	600
45		
	ATTIGUAGOG GCTGCCTGGC AGCCCACATG TGTATTGTGC TTTTTACAGTT CTTGCTGCGG	660
50	CTGTCCAATA CACCCGATCG CGACTTTGCT CCGCACGCGC CACTAGGCCT GCGCGACAAA	720
	AACTGCAGGC GCGCCGGCGT GAATGGCGCC GCACGATGTG CTGCCGCCGA ATTCC	775

(2) INFORMATION FOR SEQ ID NO:579:

	(A) LENGIH: 757 base pairs	
_	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1400RP	
15		
	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:	
20	GATOCIGICA AATATOOOCA ATACCAAGCA GCCGCGTGTT GTAGAGCATG TGGTTGAACT	60
25	CAAACCCTCA AGCAGCCGGG TITTGGACTG TGCACAGGAG ATATTGTCTC CATTTCCACA	120
	GICCAAGAAC AAGCCCAGGC CGGGGGACIG GAATTGICCC TCTTGIGGIT TTTCTAACTT	180
30	CCAACGGCGC ATTGCATGCT TOOGGTGCTC CTTCCCAGCC ACTAGTGCAG TGACGGTCAG	240
	CAAGCTGTAC AAGCCACAGC AGCAACGCCA TTATCAGAAC OCACACCACG TCCCATCGAA	300
35	ACAACAGGIG CAGCACCCGC AGATTCACGA CCAAGACACA CAGCAGCATT CTCAACATTT	360
	CAACATCCAG CAGATGCCGC AGCAACTCCA AATGCAACAG CAAGCGCACG GUACCGTTCA	420
40	ACCESSIONAGE ACCATOCACO ACTACAACOA CACOCCTCAG CACOCCTTAC ACCOCCITATO	480
	TOOCTOCTAC CAACAGCAGC AGGCGAAGTC ACAGCAGCAG TACCAGATGA ATCAGCAACA	540
4 5	GETGCAGATG ATCOCTOGCG ACOCCAGAGA COGTTATAACC GETACAACAA AATGGTGCAG	600
	GOCAACOGGC AGAACOGTAA TYCTYGTACG GAAATGGCTC CCTGGGCAGT AGCAACGTGC	660
50	CCTTCAGAGC TOGOGACTOG AAGTOCTTCA ACTGTTCTTA CCATAATTTT GCCAAGAATA	720
	TIGITIGICT COCTUCIOST AATOCAAAGA COCCCAT	75 7
55	(2) INFORMATION FOR SEQ ID NO:580:	

	(A) LENGTH: 775 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1400UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:	
	CATCOSCOOG TACTICAGGI CATTCTCCTC CACCACCACC ACCAGCTGCC COGGCCCGCG	60
25	CTCATACAGC TGGTACGCCA CGCGAACATG TCGCTCCGCC TGCCGCCACAT CCGCCTCGTA	120
	CAACTGATCC GCAGCCACCA GCCGGTCGC GCACTGGCGG CCGCCGGGCTT GCGTCAGCGT	180
30	CCCCACTAGC TGCGCGACCG GTGTGAGCTG CACCATCTCA GGGGGCATCA GCCAGCTCAG	240
	CGTCGATGCC ACCACCAGTG CGGCCGAGTA CCGCTGGCGG AGCTTCCCGC TGAACTCGAC	300
<i>35</i>	CTGCGGCTCG GCCCCGGGA GAAGCGAATG CGGGTCCATA GCGCCCAGGC AGTCCAGTTG	360
	GIGTOTGGGA AGACGOTCAG ATTGCCATTG TYTGAACTGT OCACAGTTAG AACTTGCACT	420
40	ATGCTACCIC COCCGCCCCT CCGCCACCCC ATAGTCACAT ACTATCATCC TCACACAACT	480
	CAGTACTICC TCCCAGTCCC AACTCAACCT AACGAGTACC AGACTTCGTT TTCCCTGTTG	540
45	CTGTATGCAT TOCAATGGTT TGTATAATCG AAAAATTGTT CAGTTGCTCA GCACATCTCA	600
	TACAAGCAGG AACAAGAGGG AGTCGCGAGC CAAAGACCTIC TTAGGCATTA GTATCGGTAG	660
50	CTAGGATGTC GCCAGAACAG TTGCGACAAG TACACGCAGT TGCAGGGCGA ATTGGAGGAG	720
	CTOGTOGTGA CAGACAGAAG CTOGAGACOC AGCTGCAGGA GAACAAGATC GTGAA	775
55	(2) INFORMATION FOR SEQ ID NO:581:	

	(A) LENGTH: 723 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLCGY: linear	
10	(ii) MOLECULE TYPE: DNA (genemic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1401RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:	
20	CATCTTGTTG TTGCCAATAC CCTGTCTTAC GTTGAAAAGA AGTGTCTCTG AGGTGTCCAT	60
25	CAACAAAAT ATTACCAGTT ACAACACCCA COOGAACTOT ATTGGCCAAA ACATOCAACA	120
	ATGICGICIT ACCTOCACCT GAATAACCCA TCACACCAGT CAAAGTCCCA GOCTITACCC	180
30	AACCATCCAC GITGGITAGG ATCCTCCTGG TITCATTCTT AATCTGTATA TCATAGCAGA	240
	CATCICGCCA GIGGAAAAIG CIATCAGAAC CAAITCICIG AATAAGITGG COOGAITIGGI	300
35	CACTROCTAT AGRACTAGAT TOCTRITOCTG GTGCATTACC AAATTCTATG TOGCAGTTGA	360
	TOSCUTTET ATTRICCTET TITATTTTCT TCAAAGTIGA CCFTAGGAAT ACAGCCATTT	420
40	CACCITITIG CATCCCACIT TIATTATACI CAATTAAGAT CAGATAAACA CCTAAGAAGA	480
	AAAATOCATA AGCAAGAACG ATCCCCCCAAT TCATCCACTT GITTFIGGIG TIGIAACCAT	540
45	AASCAAACTC TATGTAACGG GTCCCATTTA CAAAGCTCTG ACCAGGAACT GCTCCCACCG	600
	ACAAGCAGAC TITATTOGAA ATAGGGAATC CCTCATAGAA ACTACCATOG GGTACCATTC	660
50	GAGAACATTC GAATATOCGT COGTCAAATT CATTCGCAAC CATGGCTTCC ATGATGCGTG	720
	CGA COCA	723
55	(2) INFORMATION FOR SEQ ID NO:582:	

	(A) LENGTH: 720 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLCGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1401UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:	
20	GATCIOCIGA GATTAAGCCT TOGTTGTCTG ATTTGTTTTC TATTTGGAAG TCTGCAGGAG	60
25	CAGOCTTICA AATAGAGTIC TTATGITATT TAACGTOOGG GTAACGAGTA TACAAGCATA	120
	TGITTATCCG TATCCTAGIT ATATCCTTTG AAGAGGTGGT CTGCAGCTGG CGGTCTATTT	180
30	TATTITATIT TITCATTICA CTAAGACTIT ACATTITITI TITAAATTAT TITTITIGGG	240
	CTARGACTOT GAACAGOGAT TITTAGAAAAA AGCGAAAAACG TICAGGAGGC CTCAGCTACA	300
35	TGATATCCCA GSCCTIGIAT TIGIGAGACT GCACTCCCGG GCTAGGITGF GACCAAGAGT	360
	TCACGIGOGG CGGCGIGCGC ATTGCAGGGC TTCACAGTGI GGTTAATTTA ACAATTTATA	420
40	CACAATAGAG ATGCCCGAGC TTAATCAACT GTOGGGGGGG CCAAATTOGA TTTTTTGGAG	480
	TTTGTCGATT TTCACACCAG ACGAGAAACC AGGACAGGCG GCCGCGCCCA GGCAGTCCCC	540
45	OCTOCAGOCO TGAGCOGACA CAGAGAGAAA ATACAGGAAG ATGAATACTG ATAATCIACA	600
	GATTICATTC ATATCTCATT CATCCOCTGA TTATCAATGA AAGTACCCAA TGATCCATGA	660
50	ASCCACTAGA TOTTAGTATA TITTATTAAA TATATOCACC TTTGTTATOC AATCICTGTT	720
	(2) INFORMATION FOR SEQ ID NO:583:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 719 base pairs

	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1402RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:	
20	GATCAGGAGC CCATCAAGGC GCCTAAAAAAT CGCATCCCCG CTGTCGGTTT TCCCCGACTAC	60
	GCCGCIGITIC CTICAAATAC AATTACTOCT GTAGTTOCTC CTGTCATGCT GGTTCAAATG	120
25	THECOGCOCC AAACCCHICTIC CCHCCTICAAA GEACCTICAAA GERGETICACC TGETTCCCCC	180
	ACTACTAGOG TOTOCAACOG TOTTIGAGOO CAAAAACACOG AGGOOGATTA CATTICCOGTO	240
30	ASCORDED ACCITAGAAG ACCITCCCCIG ATGGGAGITC ATGCTCTTAC TGCGGGTGTG	300
	GIRATAGIAC TOACCACCAC TOCTUGACCA AAGOOGGACCA GGGGGIAGOG CTGCCATCTG	360
35	TIGITOCCIC CIGCGACGIG CITCTAACIG TOCCAAACGC AGCIGIGCCT GITGCTCCIG	420
	GIBCGOCTICC ACCITIGOCCA AGAGCTCCGG ATCATCATGC AACATCTCCA GCACCTCCAA	480
40	THRESCOCCT AMSCEMENTS ACTIONSCIPE CARSTOCICE ATTRICTOCAT SCHICATEAT	540
	CACCTOCAGA TOGASCTOCT CCAGAATCIC GCGCTTCGCT ATCTCGTATT TTATCCGCTC	600
45	CETCTCCTCE CTCTCACCCC CCACCCCCCC CTCCTCCCCA CCCACCCCCC TGTATTCCTC	660
	GICGOCCAGG CANASCITOGT GCCGCCCACTT CCGTIGTCCCC ACCTGGTAAT ATGCCCGCCC	719
50	(2) INFORMATION FOR SEQ ID NO:584:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 726 base pairs	
55	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1402UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:	
	CATCAAGITA TOGITGATCA AASOGICAAT ACCCITITICI CIAAGCATGI GCCAGGITTIC	60
20	CTTCGCCGCC CGTAGGTATG GTTTCCCCGTA CAACGCAATG AACCAGTAGG CATAGTGGTT	120
	GAAGTACTOT GOCATOCATT CAAAGACACO AACAACGGCA TOCAAGATTA ACCACAAGCA	180
?5	CTGCATCCAC CCACTGTCGG ATTATCCCGGA AATTAATCCCA TTGCGAAGCA GCTGAATTAAT	240
	CTGCCGCAGT AGTTGAATCA GAGACACAAT CAGCGAGCCA AAGCAAATGG ACCCAAAGGA	300
30	AGTGGTCAAC GCTCTCTTTA ATGAGCCCAAA AGCTGGCCAA CGTGGCCATGC CTTGGTCCCA	360
	CITICGAAAAA TAGTACCAGC AGCCGTAGAT GCCCGCGATG GTGCAATGAA TCACATTCCT	420
35	GATGACCICA GAAATGTAGA ATCCACAGAA GAAAACGAGT ACCAAAAATAC CAATTAACIT	480
	TOCACCIGAG CAAGAGCCAC CAGATACATO GCAGCCACCA TICIOGCICI TOCGGICATA	540
ю	CITTATETAG GTCGCAACCA ACACTACAGA GAATATEACA GAGAACGCAG CCGACACAAT	600
	GETACCTAAT AATGACACAA GOCACGTOTG TGGATGTTTC TTCATAACTG ACATGACGGT	660
15	ACGCAAGACA GCGACACTAA ATGCAATCCT TGAGCGCATT AACCAGTAGC ACACCGCCGT	720
	CAGAAT	726
50	(2) INFORMATION FOR SEQ ID NO:585:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 731 base pairs	
-	(B) TYPE: mucleic acid	

(C) STRANDEINESS: single (D) TOPOLOGY: linear

-		
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1403RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:	
	GATOCGITOC TIGAGAAGCA CCTAAAGCCT GAACTOCTGG CAGAAGCGAT CAAGGGAACC	60
20	TOTTOGRAGG GIAAAGITAG TATTAACTIG GIAGAOGGAT TOGRACCACIC GIATTACTIC	120
	GTCAGCACGT TCGTGCCGGA ACACGCAAAG TACCATGCAG AAAAGTTGGG TCTAGTTTGA	180
2 5	GATTICACCI TOCOCCIGIT AATTOGIATA TACTTACATA TITAGICATA TGACGGCTTC	240
	AAGTACTOTG ATTOTGCATT ATAAGTGCAG COCAATGOCA GCCTCCCGCCA GTAATGCCAA	300
30	COCAAACIGA ATTIOCCOGT AGITCAACCT TOOCCOGTIG CAGCACOCGI ATOCTCOGAG	360
	CAGACTCAAA CGICOCTATT TOOCGGGIAT CIACAGCCTC GTCGGGATCT CCCTGCCCAA	420
35	GACAGCCACA GATATCACTC TOCAGCCCCC AGGAGTAGAG TTCACCTTIG TOGGITAGAG	480
	CTAGGITGIG GTAGTCTCCC GCAGATACAG CAATAAACTT CTGGCCTTGT TCCAAATTCA	540
40	TCTTCATGAA TGAGTCCTCG ACGATATCAC CATTATTCAC CTTCAGGGTG TATGTGCTAT	600
	TCTCGGTACA TAAAACCAGT GTCATGCAAG ATGCCTCAAT CTTCGTTTAA CCGTCCATCA	660
45	AATGGCAAAT CAACGGTTTT TGAAACGCCA TGAGTGTATA TCCACAGTTT GCGCCCATTG	720
	Tragiaaigi a	731
50	(2) INFORMATION FOR SEQ ID NO:586:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGIH: 717 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1403UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:	
	GATCTCAATA TCAACCAACT TETGACETCG CTTAAAAACAC CATATOOGGA GGACATTAIG	6(
20	TOCATCACCG TGTACAAGGA CAATGITTTT GOCACGCACA AGCAGGGCAT TACGGGGTTC	120
	CACCAAGGGA ACGIGAACTT CTGGAATGCT CACCAGGGAC TGGTCTTGAG TAGGGAAATA	180
25	TTGCGCAACA GCTGTACCAG TAATCGTATA GATCGGATGG TTACTGGCGG AAATGATGGG	240
	TCATTAGOGT TGTGGAATAT TAACGAATGG CTGAACGGTA CAGCGTCCCC GGGTGGATCA	300
30	GCCCCGACCG AAGAACACIC GCTTCCCTCT GGCCAGCGCC GAAAITICTTG GACCCAGTAT	360
	CAACAAATCC AGITIAGATAA CGATCACATG ATTGCAACAC TGCGGGAATT CATTAGITAC	420
35	CAGACTIGITT COCCAACTOOC AGAGCCCCCAA AATATCATCG ATTCCCCTIAG GTGTCCCAAAC	480
	TICCIGCAAA ATCICITCAC TAAGCTCGGT GCTAACCATT GTGGGCTTAT ACCIGICAGT	540
40	ACAGGCAGCA ACCCGGTGGT TCTCGCGCAG TTCAAGGGCA ATGCAGCGGC GCCCAAACGC	600
	ATACTATEGT ATOCCCACTA CGATGTGATA TCCGCGGACC ACCGTGGCAG TGGGACAACG	660
45	ACCCITCACG CTCACTTGOG AAAATGOGTA TCTTAAGOGA AGAGGOGTGT TGATAAC	717
	(2) INFORMATION FOR SEQ ID NO:587:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 710 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1404RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:	
15	GATCTGCAAC GITACTGATT ATCCTGTAAG CCCTCTTTTG GGTTAAAACA TCCTGTGAGT	60
	TAACAGTOGT GITGAACATA GAAAATAAAG CAGIGTATGA TGATOCTOGA ACAACOCTOG	120
20	ACATAACCAC CACAACATCT AGAAGTGTGG CACTCATTTT TGGCTGGCCC TTCACAGGTT	180
	GOCTAGACOC CTCCTTATCC ATGOCATCTT TTAGTAATOC OCATACGTTA TCAAACGTGT	240
25	TAGACAGGIT TICCGCAGAA GIAATTIICA AGIATGCCTC GAIGGITICC AAAATAIIAGC	300
	TCCGAGOGIT GGGTGCAGTC TGCGTGTAGA CATTGAAAAG AACGGCCAAC ATAITGGGCG	360
30	ATTICIOSCA GAGGIATICI AIGITITICI CCCCTICIGI CCCCCCAAT TOCTGICCCA	420
	TAATAATGIC GICCITATAC GCACCATCIC TGTATAGAAG ATTACTIGIG ACCAAGACCT	480
35	TCAATCCATT GCATATGACA GIACGCAGIT CAATTCTGGA ATAAAGIAGG GACGCTAACT	540
	CTGCAGCAAA CTCATCCGTG AATACATCGT TUAGATCTTT TGGAAGAACG CAGAACTGAG	600
40	GGAAGGTAGA CCACAATTGG TCAACAACAG TCTGAAGTAA TGTGCACTGG ATAGACTCCT	660
	TATCCAGTTT CICAATOGTG GACTCGAAAT GACGAATOGT AGGAATAAAT	710
45	(2) INFORMATION FOR SEQ ID NO:588:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
50	(B) TYPE: mucleic acid	
	(C) STRANDFINESS: single (D) TOPOLOGY: linear	
5 5	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIGINAL	SOURCE:
/	A. MATERIA	

(A)	ORGANISM:	PAG14	04UP

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(xi)	SEQUENCE	DESCRIPTION:	SEQ	\mathbf{I}	NO:588:
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GATUTICASC AAGATCASCA CCACTIGACS CACTACAAGA ASTACCOSCA CTOOCGSTGS	60
CAGGCCAAGC GCAGGCTGGC CGGCTGCGAG TCAGGAAAAG TCGGAGCAGG TCGTACAGGA	120
COOCCAAAAC GCCCAGCCCC TCCCCCAACCT CCCCCACCCTCA CCCCCCCCCC	180
GGGCAAGATG AGCTACTACC GGCAGCTCCA GGGAAGCGTG AGCTCGTTGC TCAGTTCTGT	240
GICOCAACTA ACGACGICCA CCCGGGGGCC AGAATGCGAC TICACIGAGC AGITCATCAC	300
CTTACTOGIG AACACCTACC ACGACATGTG TCTGCATGCA ACCGTCACAC CGTTGGACAA	360
GACTIAACCOG CCATCTGCTT TTCTCAACAA GGTACCGGT GCTGCGGTGG AGCGTTCTGA	420
GCAGCAGACC ATCCCCATCC GACCTCCCCC CCATAAATCC TTGTTGACCT CCACCCCCAA	480
GCGGCTTCTA CAGGAAATAA AGCGGGGAGAC CGAGGACGTT CCACAGGGGT CCGTGGGCTC	540
OGTOSCCIGT TOCATGAACC ACOSCACCCT ACACCGCGAT CTAACCTCCG CTTTTGCACA	600
GCAGGGCGAT TICTICIACT GGCATOCGGA CTTCCAACIG TICCAAGGCA TCAGGGCAAA	660
ACTICIAACC GACACTOGAG ACATCTCOOG CAAAAATACC CCATGTCTTT GGATC	715

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDETNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1405RP

	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:	
10	GATCTFTCAT ACTTTCGGGT TCGTGCTATA TAACTAAGAT TGGACAGAAC TGCAAGGGCC	60
	ACAGAGGAAG AGCTGCTGCA TITOCACATTA GOCAGGAACA GCGAATGTCT ACAAATGCAC	120
15	ACTACACACT ACCOCTOTCA COCCATOCCA ATCTCAGATG COCACAGCAA COCACCAGT	180
	TCTTTGCCCA TGCCCCTGTA CTCGCAGCGG GGCCCAGATG GGCTGCTAAC CATTAATGCG	240
20	ASCOCIATAS OCTOSOCIAT GOCCOCCAS COGGIGATAC CTOCACTCAT GCACCAGGIG	300
	GCGGTCGACA AGCACGCTCA TATCATGCCA GGCTCGTACG CGCTGCGACA GAGCTCGCCC	360
25	CAGGTCACGG CCATTATGGG CCAGTTAGCG ATGCTGAAGA AGTCGATATT CCAGTCGCTG	420
	AACGGCCAGT TCACCCACGCA GCAATACAAC AGCATCTACC AACATTTCAG TCAACTGCTG	480
30	GOGTOCCTOC CACOGCOCGT OGAGCCATCT GCAGCGCAGC COCAGCTGCG ACTGCCGTCG	540
	ATATCTCAAA TTATGCCGGG AACAGAGGCC CAGGAAGTCC AACGTACCTT CATCATAGCA	600
35	TOCTOCCAGT CACAGOGGG CCAGOCGTAC ATCTCGCCCC CGTTAAGCTC CACAATGTCT	660
	ACCCACCOCC TTTCACCOCC CATGTOCGTA CCCAAACCCA ACTACTOCCT GACCACCAAC	720
40	AAGAAIGIT	729
	(2) INFORMATION FOR SEQ ID NO:590:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
50	(D) TOPOLOGY: linear	
	(D) AUFCHASI: LIPSHI	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1405UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:	
10	GATCCAAATA ACACCACGGT TITICATCCCC GGGTTGTCTT CGCTCGTGAC TGAGGATGAG	60
	CTACGGGCTT ACTICCAGCC ATTCGGACAG ATTAGTCTACG TGAAAATCCC GGTCGGCAAA	120
15	OCATOCOSCT TIGICCACIA COTOGATOSC ACITOCOCAG ACAACOCGAT COCCAACATG	180
	CAAGGATTIC CAATTOGTAA TICGAGGGTG CCCCTCTCAT CCCCCAGGGAG CCCAAACCAA	240
20	ACAGOOGCTA TGCAGCAGGC GTTTGCCATA GCACTACAGC AGCAGCAGCA GCAGCAGCAG	300
	CAGCAGCAGC AAGCCCGCCC GCAGCATTCC CAGCAACATC AGTATCAGCA TCAACAGCAT	360
25	CAACAGCAGC CTCAACATGT CATTTCTGCA CAGCCGTTGC TGCAGCAGCA ATTGCAACTA	420
	CAATTICCCT ATCAGCATCA ACCTGCCATG CCGCAGGCCT ACGGTTACAC ATTIGGACTCG	480
30	TIGAGOGGA COGGITOGAA ACATGITCOA ATGCAGGGIT TICITTOCGG TAATATOGGO	540
	TICCAACCIT CTACGGCAAT TGATAGCTCT CCAGCAACGA CCTTGCTTCC CAACCITTCT	600
35	TOSTIGGACT ACTORGOSTS TOCACCTICO ACGICAGOST TOACTITICA COCACGAACT	660
	CTTTAGOCAC AGCTTTCACA ACATOGOCTA GATTCTCAAC AATOGCAGOG TGTOC	715
40	(2) INFORMATION FOR SEQ ID NO:591:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 699 base pairs	
73	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1406RP

5	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:591:	
	GATCTCCTTC CAGTGACGCT GATGCACAAC TGCGGACCTC AGCCCGCGTG CCTCACGTGA	60
10	CCACAGTOGA CATTITICTICA GITTAGCOCTIC GITTAGCTTA GCTATAGCAG GGATGOCACC	120
	ACTIAGGOGO TOCTOCOGNA COAGATACISA TONAGCOGOO CANATTOCAT AGAATOCTOC	180
15	CTCGCTGAGC CGCCGTCATA GGGAAACGAC CAAAGGTTCC GTCTGCCGCA TCGTATGTAT	240
	GIGICIGIGI ACGAGGACCG AAAAGITGAC TITTAACGAA GIAGATTITI TIATTAGATA	300
20	TTTAACCACG TATGCGTTAA CGAGCACCTT GCAAGGCGTA TACCAAGGCT CTGTGCGCTT	360
	ATCATTAGCA GGGCGACATG TCAGAATCCT TGCTACAGAC AGTGGTGGGG TACGTGCAGT	420
25	TOGTOCTOCA CCACTICATG GOGTIGICGI GCACGCAGCA GCIGICCATA GIAATAGTOG	480
	CACCATTCAT ATACTCOCTG GRETOGCAGA CGFTATATTC ATTCAGGAAG CATAGAGTAC	540
30	CGCTAGTGCC GTTCATGGTA CCCTGGGTGG GTTCCGCGCT CGCGTATGGG AGGGCTCGGT	600
	ACGAGITITIT TOOCAAGIGC AOCAGAAGIA TOOCGATGIG TITIOCGITCA TOCTOCTOCG	660
35	CONTRICATE ACCEPTATO TERRESACIAA COROCACCIA	699
	(2) INFORMATION FOR SEQ ID NO:592:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 709 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1406UP	

(207)	SEQUENCE	DESCRIPTION:	SDQ	\mathbf{m}	NO:592	:
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5	CATCTTCATT AGAACGCGCG GATTAGTCAA AAAGTGCCGG AATGTTCCAT CCACTAGGCC	60
	ATCIGCCTIC ACCCACGEAT TGCAAATGCA GACAACGITT ATTAGAATTA TACCGATTGC	120
D	CCAAACGTOG CCTGCAGCAG TAGGAGCTOG GAGCTCACCA CCGAGCGATC CGCGCTCGGG	180
	TOCCATETAG TAAGACCAGC CTACOCAGAC ATTOGGGGGG AGCTCCGGCA CGGCTGTOGC	240
15	CAGCCCCAAA TOGCATACAT GIACGITGIA CCATTIGICC AGAAGAATGI TCTCCGCCIT	300
	TAGGTCGCAA TGATAGACGC CGAGTCGGTIG GCAGTAGAAA ATAACCTCGC ACAGCTGCAG	360
20	GAAGACCITC TTAATCAGTA GOCCATCCTT AGCAAAGACT TOCTOGITGA CAATGOCTGA	420
	GAAAAGGTOG CACGTGATGT AATCCATAAC AATAAATGIT GCCAGGCTTG ACTCCATCAC	480
25	CTGATGTATG GTAACCACAT GTTCGTGGGT GTGCACAGTC ADGTGCATCA GCAGCTCCTT	540
	ATAATGTOOC GOGTOOGCCA GCTOCTCTTG GGATAATGTC COCATOGATT CCAGGTCCAC	600
30	AGATGGTAGA TACAGCOGGT TCTGGAAAGA TTGAAGAAGT GGTACAGCTG GGTGCGCAAA	660
	ATTGTCGACC GOCCIGACGC CTCGTCTGCG CTGCCCCTGT GCTGCTTCA	709
35	(2) INFORMATION FOR SEQ ID NO:593:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 707 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1407RP 50
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

	CATCAACCAG ATAACTATCT TAAAGAACAA CCCCAAAAATG CGCAAAACCAC ACCACGGGTC	60
5	CITCOGTGAT AGACTGATAG AGATACAGAA AGTAACTTCT GTGTCAAGCG AACCGGAGCT	120
	COOCHTHINA CACCTICOCA ACASCISCOC CCATGOCATA GCACTCTTIG ACTICCTCTA	180
10	GTTGCTTTCC ACTAAACACC GCTCCGATGT TTCACAGAAC AGGTTTAATA TCGGCAACCA	240
	ANGNOCAGET TACACTCAGA GAATCACAGT GTOGAAACAC COOCTATTCA ATGAGGCATT	300
15	COCCCAAGIC GETTICITITE GITTOGATIG CCATTOGCTA GIAATCCACC AAATCCTCCG	360
	CTGCTCACCC ATGGGATCGC TAGATGCCCCA GGATGAGACT GITICAGGITTA GGCAGGTGTT	420
20	GUATGOGOGG CCAGAGGGAA ACCCAAUGAC TITTGCATAGA ACAAACCCGC CATCACCCAT	480
	GICTIGOGCT GTATAGAGAC TAAGGTATCT GACGATCCCT TAGGGACTCT CTGCACGGCT	540
25	OGACISADOCC ATTIGAACCTC TITACIGAACTG CACAAACCTA CTCGAACTCT GITTOCAGAC	600
	TTCTTTCTGT TTGTCTTCAA CIGCTTTCGC ATGAAGTACC CCCCAGGCTA TTTTTCTTAC	660
30	CCGCCIGGIG THIGICIATA TACCCGGITG TATHTHICA TAAAAAA	707
	(2) INFORMATION FOR SEQ ID NO:594:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 571 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1407UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:	
	GAICTICTAA TIIITYYTTAITA COOCCAAAC ACTTAICEAN	
55	CATOGROGAA TITOGGRATA GOGGCCAAAG ACTAATOGAA CCATOTAGRA GORGGRACOT	60

	GCCCAAGTTT CCCTCAGGAT AGCAGAAGCT CGTATCAGTT TTATGAGGTA AAGCGAATGA	120
5	TTAGAGGTAC CGGGGTTGAA ATGACCTTGA CCTATTCTCA AACTTTAAAT ATGTAAGAAG	180
	TCCTTGTTGC TTAATTGAAC GIGGACATAT GAATGAAGAG CTTTTAGTGG GCCATTTTTG	240
10	GTAAGCAGAA CTGGCCATGC GGGATCAACC GAACGTGCAG TTAAGGTGCC AGAATACACG	300
	CTCATCAGAC ACCACAAAAG GTGTTAGTTC ATCTAGACAG CCGGACGGTG GYCATGGAAG	360
15	TCCGAATCCG CTAAGGAGIG TGTAACAACT CACCGGCCGA ATGAACTACC CCTGAAAATG	420
	GATOGOCCIC AAGOGIGITA COTATACTOC ACOGICAGOG CAAATATGAC GOCCTGACGA	480
20	GTAGGCAGGC GTGGAGGCTCA GTGACAAGGC TTTAGGCTGTA AAGCTGGGTC GAACGGCCTC	540
	TAGTOCAÇAT CTTOGTOGTA GTAGCAAATA T	571
25	(2) INFORMATION FOR SEQ ID NO:595:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 658 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1408RP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:	
	CATCCCCCTT ACCAAGCAAT TACAGGAGAC AGAAAAGAAG GATAATAATT TACCACAGAA	60
50	CTCCAAGCCT GACAGACCAG CGATTIACAT TCTGAGTCAC ATGACAGCAG ACTCTCTTTG	120
	CTTTGGAGCT TCAATAAGCA CCAATATGAA TATGAATAGT TTTAGATGCT TTGTATAATT	180
55	ACCACTATTA ACTITATOTT GATTAATATT TATTATTTTG TTATTTTATT ATTTTATTAT	240

	TATIATITA TITATITATUT TATIATITA TITATITATŲ ATUTATIAT TUTATITATU	300
5	TTATTTATT ATTATTTATT TATTTATTAT TTATTTATT ATTITATTTA TTATTTAT	360
	TGPTGITIG TITATTATIT TPTTATTTAT TACCPPTTA TTTTATGTTA TTTTATTTTA	420
10	TTTTATTTT ACTIVISTATA TAATATTATA TEATATCATA GTATAGITAT ATTATGGTGA	480
	CTTTATTCAT TATATAGATT GTATTTIGIG AACATAATAT ATATOCTATT TCTATTTCTA	540
15	APPLIATED APPLATED APPLIATED APPLIATED APPLIATED APPLIATED	600
	THE THE THE ATTENTED THE ATTENTED THE THE THE THE THE THE THE THE TARTET TO THE TREE THE THE THE THE THE THE THE THE THE T	658
20	(2) INFORMATION FOR SEQ ID NO:596:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 722 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1408UP	
40	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:596:	
	GATCCCCCIT CCATCGAAGA GOGTACTGTT TGATTATOGT GATTTCTTCG TGTCCGTTCG	60
45	ACATTCAAGT GCATAGTTGG AGGTTACCGA TAACTTACAT TTTCTTATAA ACGGTTACCC	120
	TACGICTICG COGTIGGOGG ATATACTICAT TAACAGTIGG ACAGCCTIGG COGGATACTG	180
50	TGAATGCCTT CTCTTCAACA TTATTTGAAT ATGCAAAGGT TATTTAAATT AAGTAACACA	240
	CTTGTGCTTA TATATTCAAT TGTTCCAAGC GCGCCATCCA ACATGGCGAT TCTCATCTAG	30
55	TTIGAGAACT TOOGTCTATT CITATTCTGT GTACOOCAAC GGTATTAGGA GAGACTTOGA	36

	GITTITIGGAA CITICAAAGTC AATACITICAT CATOGTAAGT AGCAGTTACT TGGCCTAAAC	420
5	CAGTOCCCAC CTYTGTAGGG AGCCTGATTG TTCGCCGAAA CTCCGGGTTTT GTGGGTTCTC	480
	CASTASTOCA COCCTOTGIA TICTCATOCG TATTAATOGC TGOCACGACA ATAGAAAGAA	540
10	CIGCATCATT CATGICTCGA TCCACOCCAA TATCIATGIG GTCTTCACAC ATTACCCCAG	600
	GAACTCTGAT GIOGATCTCA TAGOCGTCCG AACGCTCCAA AATTAATAAT GAAGGAAGAA	660
15	CGICAGAATT TOCGCCCGAG ACCTIGIATT CTGAACTAGC TCCCACACTC TCACCTTTGT	720
	GT	722
20	(2) INFORMATION FOR SEQ ID NO:597:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(b) Robotton Illiear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1409RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:	
40		
70	GATCCTGGCT ATCTACCTGC TGCTGGGCGC CCTGCACGCC ATACTAGGGC GCACATTCAG	60
	COGNITIANTS TATISTICGANT ATCCCCCAGT AGAAAACCCA COTINCATISTIS ACAACAAGGC	120
45	CACCOGACTA ACCAATITAC ACAACCOCCG CTATTITACAG COCTGCCCTG ATCCCCATGA	180
	GTACTIOGAT TOOGCTICCA TOOGCAGTOG TACACGOOCT GTACCTICCTA TOCOCAGCAT	240
50	TIGIGGCACA ATOCAAGCIG ATATAGGATA CAGACATOCA GCAAGACGCI GGAIGGATOG	300
55	GINGTATCCC TCTOCTCCAT CAATACGCTA TCGCGGGCCG GCAGCITAIT GICACGIGAT	360

	TEGETATETY GIOCALEACE CAGACATATG TTGCTGAGCC TOCCTCAGCT ATATAAGCGT	420
5	CGAAGAAGGG CGCGAGTCGA ATACATGTCT CTCGCCGCTGT GTGCCTCGTG CAGTCCTCCG	480
	OGATETOGIC AACTUICATA AACCGITOCT TESCAACTAT COGTACAGAG CITECUTITI	540
10	TOGTTGATTC COORDICATT ACCOCRACAC AGTCAGACCA GATTGAATCT AATCTTCCAA	600
	ACCOTAACGA ACCOCTOCGT GOCGCTOCCG CAAATAACGC AGGGCCTGTG GAGTATGTGG	6 6 0
15	AGOCACTITA TOCGITTCAG CCCCAACACC CTGGITGACC TAGACTICAA	710
	(2) INFORMATION FOR SEQ ID NO:598:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1409UP	
	THE PROPERTY OF	
35		
	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:	
4 0	GATCOGOGAC CAGAAAACCA CACAACTOGT CCTTGAGOCG GOGGTGGOCG TATTAGOCTGC	60
	TACTGTCTCT TCTTGTCGTA GCTGTGGCCT ACGGCTCTGC GTGCGTAACC GCTGGCATGT	120
4 5	GOCTICATURE CAGARARIAT GATGICTICAR COGRAGITICE RATATIGICE TGFTCCCTGG	180
	TOGITICIDOS CTACOGIGIT OCACACCIOS TITOSOCOCO TOTOTOAGAC CIGIACOCOC	240
50	GOCOGATAAC GIACTICACA TCICTATICC TITACGIGGI AITTAATATI CCATGIGCOG	300
	TECCTCCCAA CATCCAGACE CTTTTGGTTT GCAGGTTTAT TTGGGGGGTC CTGTCGTCGT	360
55	CTGGACTATG CCTAGTCCCC GCCTCTCTCG CCGATATGTT TCCAGCCCAC CTGCGTGCGT	420

	ICACCAICOC GITCITIGCA TITIGCACAT ANGCAGGICU GGIATITIGUG CCACTITATAA	480
5	ACGGATTCAT CGCTGTCCGC ACAGAGAGGC TTGACCTTAT CTTTTGGGTC AACATGGCGT	540
	TAGCCOGAGC TGPTTGGCTG TTAGTCOCAC TGGTGCCCGA AACATATGCG CCAATTATTT	600
10	TGAAACGGCG CGCAGAGAAG CTGAGGAAAC TAACAGGCAA CCAGAATATA ATGACAGAAC	660
	AGGAAGCACA GGGACTICTCC CTGTCGGCAT GGTGCAGACT TGTCTACTGA GACCG	715
15	(2) INFORMATION FOR SEQ ID NO:599:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 709 base pairs	
20	(B) TYPE: nucleic acid	
20	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1410RP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:	
35	GATCAATTOG TCACATTTOG OGTATGCAAT TTCTACCATC TCCTCTTTOG TAGCCTTTAA	60
40	TICCACTCCT GGIGTAACAT CACTAATGCC AATAGAAAAG CCTCTATTTC CCAGATAGCG	120
	CGCACAAAGC TTTGCCATCC TATTCATAGC CTGCGTTGCT TCTTGTGGCC CGAAATCTCT	180
45	CAGAATAGTA TAGAATACGG AATGITTCTT ACCATCACCA AGCACAGACT TATCCATGAC	240
	ACCAGACAGA ATATTAGAGC CTCTGATAAC TACATAACCA TCATTAGCAG ACATCTCATT	300
50	TOGATAGGOC TEATTCTTAG GOCCAATATA AACCTTATTC TITTCCATCCA AATTAATAAT	360
	AACGGGAGAT TICTIGITCG GITTTATCAA TAGAGAGAAG AGGIGITTIC CAGICCATAA	420
55	GINGIGIGGI COCNIANTIG CAGGOGGOGG TATGICANAC TOCAGGITICC CGICAGACAT	480

	CATASAASC ATTIGGACAA AAGTIGGGGG GTOGAAGAAG GAGTCTTTGT GAGAAATCAA	540
5	ATATCATCCA CTCATCAAAT CCTOCCTACC TOCAATCATC CCTTCACCCC ATTTCCCACT	600
	CAATAAATIG TTTTICACAC CCATAAGGIT GATIOCTTCC GGGCGAGCCT CTTCCGTTTG	660
10	AGGAACATOC AAGTICATTT CGTCACCATC AAAATCGGCG TTGTAGGGG	709
	(2) INFORMATION FOR SEQ ID NO:600:	
15	(5) CONTRACTOR OF THE CONTRACT	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 727 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPOLOGY: linear	
	(b) Toronosi: Timear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25		
	(VI) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1410UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:	
35	CATCTGAGCC CTAGCATCTT COGTTGGAAG CGGGAACTCT ATTTTCCTAT CCAAACGACC	50
	GENACOCAGA AGOGCTOGAT CANOGACATC GACTCTATTC GTAGCAGCCA AGACTTTTAC	120
40	CCTATOSTCA GAACCAAAGC CATCTAGTIG GITTIAGCAAC TCAAGCATGG TICTCTGCAC	180
	CICICIATCA COGGACTICI COGAGICAAA ACOCITAGII CCAATAGCAT CCAACICATC	240
45	GATGAAGATA ATGGTAGGTG CCTTTTCCTT CGCCAAGGCA AAGGCGTCGC GGACCAGCTT	300
	COCACCITCA CCTATGAACA TCTGGACCAA CTGCGGAGGGGGGGGGG	360
50	ATTOCTOTEA OCCOCACAGO CTCTTCCCAG AAGCCTCTTG CCCGTIACCCG GTGGACCATA	420
	CATCAGAGCA CCTTTCGGTG CCCTAATACC CATATCCTTG AACTTGTCTG CCTGCTTCAT	480
55	GEGTAACACE ATTOCTTOCA CTAGTTOCTC GATCTGCTTG TCTAGCCCAC CAACGTCCCA	540

	GIANGITICE GIACCETIGE CATOCACTIC CATASCITTIC ACTOTAGAGE CAAACTOOGA	600
5	AGGAAGOGTA TOCAAGATCA OGTAOGAGTC CITTOTTCACA COCACCAGGT CGTTCGGCTT	660
	CAACTOCTTA AGGGTCCACT AGCCCAACCA TOGOGAGAAA AACOGTTTGT OGCGACGAAG	720
10	TITCACA	727
	(2) INFORMATION FOR SEQ ID NO:601:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPCLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1411RP	
30	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:601:	
35	GATICAAATOC CCTTCCCTTT CAACAATTIC ACGIACITIT TCACICTCTT TTCAAAGITC	60
35	TITICATCIT TOCATCACIG TACITGITGS CIATCOGICT CICCOCCAATA TITIAGCITTA	120
40	GATGGAAITT ACCACCCACT TAGAGCTGCA TTCCCAAACA ACTOGACTCG TCGAAAGAAC	180
40	CTTAGATGGC ACTAGCACCC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCCTGTTCC	240
45	AAGGAACATA GACAGGGACT AGCAACCAAG GTACTITICTT CAAATTACAA CTUGGACGCC	300
	GAAGGOCCCA GATTICAAAT TIGAGCITTIT GCCCCTTCAC TCGCCGTTAC TAAGGCAATC	360
50	COGGITOGIT TCTTTTCCIC COCITATICA TATOCTTAMA TICAGCOGGI AMICCIACCI	420
	CATTICACET CAAACTTICG CAATACTATT COCCTCGAAG CCCTTGTTTG TCCTACCTTC	480
	TTCAAGCCCC ACCTCCACTC CACCATCTGG TCGAAACCTA ATACGCAGTG TAGAAACTAG	540

	CICAGACCOC AGICCOCCCA AGITICCOCCC ATOGCCACCA TITTICAAGIT AACCTIGICT	600
5	TACGACCGAG TATCACTCAT TACCAAACCC GAGGGTTTGA GAACGAAATG ACGCTCAAAC	660
	AGGCATGCCC CTGGAATACC AGAGGACGCA ATGTGCGTTC AAAGATTGGA TGATTCACGA	720
10		
	(2) INFORMATION FOR SEQ ID NO: 602:	
	(1) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 717 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1411UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:	
	CATCCTCACA TACCTTAGIC TCTATACACC CCAAGACATG CGTCATGCCG CGTTTGTTCT	60
35	ATGCAAAGTC ATTGGGTTTC CCTCTGGGGG CGCATACAAC ACCTGCCTAA CCTGAACAGT	120
	CTCATCCTOG GCATCTAGCS ATCCCATGGG TGAGCAGCGG AGGATTTGGT GCATTACTAG	180
40	CCAATGGCAA TCCAAACCAA AGAAACCGAC TTGGGGGAAT GCCTCATTGA ATAGCCGGTG	240
	THTOGACACT GTGATTCTCT GAGTGTAACC TOCTCTTTOG TTGCCGATAT TAAACCTGTT	300
45	CTGTGAAACA TOGGAGOGGT GTTTAGTOGA AAGCAACTAG AGGAACTCAA AGAGTGCTAT	360
	OSCATOCOGO CAGCTOTTOC GAAGGTOTAA AAACCCCAGC TOCOGTTOCC TTGACACAGA	420
50	AGITACTITO TGIATOTOTA TOAGICIATO ACCGAAGGAC CGIOGIGIGO TITICOCATT	480
	THEOGRAPH TOTTHAGAT AGPTATICIES THEATECTEC CAGRAGICAT ATECTTORICE	540
55	CAAAGATTAA GCCATGCATG TCTAAGTATA AGCAATTTAT ACAGTGAAAC TGCGAATGGC	600

	TOATTAAATO AGITATOGIT TATTIGATAG TROCTITIACT ACATOGATAT CIGIOGIAAT	660
5	TCTAGAGCIA ATACATOCTT AAAATCTCAC CTTTTGGAAG AGATGTATTA TAGAATA	717
	(2) INFORMATION FOR SEQ ID NO:603:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 710 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDFINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1412RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:	
30	GATCIGGAAC CAGGATGACT GICTGGCAGT TAACTGGGGC GACCAGATTC GCTTCCTACA	60
	CAACTICIGC TOCOGIGOCC ACGGIATTIC CATCOOGICT GITGOCCACA AGAAGGGCGA	120
35	CTCAGTCACC AACTTCCTOG CACAGGACAA CCAGGTCGTIC GAGTCGGACA ACGGTCTAAG	180
	AATCAAGACT TICGTGGGGG CCATTGGCAA GGTGGACAAC ATCAAGTTCA TCAACAACAA	240
40	GGICAACAAC ATCCGCAAGT TCGCTATCGT CATCCAGGGC GACTACAAGG ACGGCACCAC	300
	CACCECCACC CCAACCECCE GCTECCCAAT CACCAACCTA GACCTCAGAG CCAACACCEC	360
45	TAACACCGIC COCAACOCCA CCAACCICAA CATTCTCCTC AACAATOCGT CTAACTGCAC	420
	CTTCCCCCAC AACAACATTT TGGGCAAGAC CTTCCCAGGC TGCTCTGGCG CACCTAACGG	480
50	CATCAAGTOC TAAGCOCCTT TITTTTTTTT GOCTGCGCCT CGAAACTATT ACTATCAACA	540
	TTGGCGTCCA COGCCACTAC AAAAGCATCG GGTCTATCCC ATTATAACAT TAAAATCTCA	600
5 5	GITGATATTA TATTTTACAT TOGAATGICC TTAGGGCTIT TITTATATTAT ATAAACITTA	660

	GATTAAAAAA ACCAGGTACA AGCAGATCAA CGAAGCTTTT CGGCCAGCCA	710
5	(2) INFORMATION FOR SEQ ID NO:604:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 728 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: INA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG141ZUP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:	
	CATOCAACGA GATAAACAGA GGIATIGGIT GITATCACAA ACATATAATC CTGGGGATAC	60
30	AACGCTGTCA AACTCTGGGC CTTCTGCTTT GTGTCTAGAT TCCTTTTGCA GGCTTGAGAA	120
	TRACCIGIAC RATITITIGA IGIGGITAGI RACAGACOCA TCARCCATAT CATCOCACAA	180
35	AGTICGGITT CITTOCCCTG CAAGCOOGAA TOCGCCTICA TTACTICCCG AATCITCTCC	240
	ATGAGICGAT GGTCTCGGCG TIGAAGCTIG TAGIGICAAA GGTTCTATTC TTGGAGAAGG	300
40	TICTATCICT ATTITITICIC COCAGAAAGA ATCATTICAC ATCCAATATC TIGIAACTIC	360
	CCTOSCATGT AATCTTTCAA TAGCGGGGTT TCGGTACAAG CTGCTACCTG CCACATTATT	420
45	ATTIAACGAT TCTTCTCGTC CGTGAACGTG ACGTATAACG TGGACGCTAT TGGGTTTCTT	480
	TICCAACATA GGITGITCAT CAAATGAGAG GTAAAATGGT TCCTGCTGGG AACGCGACGA	540
50	AGGCTOCTTT ACTITIAAGIC TTAACAAGGC GTCAACATAT ICTTTTTGAA TOGTTCTAGA	600
	AGRICUTAÇA AAATCCATAT TOCGICTTAG ATCICACTCC TGAACGCCTT TGTCTAGITT	660
55	CTCATCCCCC AGTGGTAAAT CTGAACGAGG GACAAAGTAC ATGCAACTGT CCTCATCATT	720

	GIAAGICA	728
5	(2) INFORMATION FOR SEQ ID NO:605:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 732 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
15		
,,,	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAGI413RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:	
	GATCTOCTOG GAGTGACTCA OGAAGCTTTG TCAGTACCTG GAATGAAAAA ACAGTCTCTG	60
30	ACAGAGOGG GAAGCTGOGC CTGATGGTGG TTACAGOGGA CCAGTTCAAA GAATATGAAC	120
	AATTGAAGAC TGTCAGCCCC AAGGATCAAC TTGCTCAGCA GGCGAAGGAG CTAGATATGG	180
35	TOCTANTICA TOCTOCTGAA CTATACCAAT TAACAACCAA AGTITICOCAT GCACTGTCTG	240
	CCCATTICAA CICIGACTIT GICTIGAGCA ACCACATCAT TCTIGAGAAT CCTCATACTT	300
40	ATGGITTAAC GGPTCTTCAA ACGGAAGAGT ATCTTCAATT ACAGAGTAGT TTGGAGAGAG	360
	AACAGGTAAC GTOCTACAAC ATTIGCOGAGA AAGCAACTAC AATTIGGCTAC GTTGCACTTC	420
45	CAAGAACCGA GTACGATGAA CTTGTAGCTT COCAAGCTTC TACGAAAGAA CAGAATTTTG	480
	AGGTATACGC GGCGGAAAAT GGCAAGGTCA TAGTGGATAA ATCTGAGTAT CACGATTTCA	540
50	AGATCAAAGC TATCCCAGIG ATTICACCAT TOCCTCAAAT GAGCAAAGAG CAGATGGTIG	600
	AAAAGOOCAA GGAACTIGGA AIGGIAGCIT TOCICATIGA CGAGIAIGAG AAGITAAAGA	660
55	OCCCTATTIC CGATAACOCT TIGAATOCAA CAGCGAAGOG ACCGIGGAAA GCITGITCIC	720

	CTAAAGGAGA GT	732
5	(2) INFORMATION FOR SEQ ID NO:606:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 721 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1413UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:	
	GATCCACTT TAGGICCACT TCAAACIGGA TITTCGGGIA CTCCCCCCAC ACCACCGICA	60
30	AGICATOSSC ATAGATOSAC TCAAGCACIT CCAGCTOCTG CITITIGCTCC TOCTGATAGT	120
	CCATACCTAT CCCCTCGACC AACTATGAGC CCACGCCCAG CTTAGGGCTA GACCGTTACA	180
35	OCTOCAGGIG ACCGICCOGG GGACCATOCG CTATCOCTOG CCAAATTITT CGCCTATACC	240
	ACCACTTATE TTACCCEGTC TATAGREETE CTCTCCCACC TCACTGATGC TGCTGTCCCG	300
40	COGGGACTICC TOCCTCGTICC CCCCAAATICC CCACCOCTCT GAACGCTCGT TCCATCTCCC	360
	TCACGOGITG ACCGAACGGG AATTGCGCGC GCCGAGAAAT CTTGGCGAAC CATGCTGCAC	420
45	GTAGCCTTAC TGCCAAAATT AAGCCGTCAA ATGGCTGGCT ATCCTTCCAC GCACGCCCAT	480
	AGTCACCTGA AGCTGGCTGG AACAGTGGTC ACGCAGCTTT CTGACGCATA CCAGGAACAG	540
50	GIGOCCCAGC CCCAGOCCAA COGIGOGICA TTAIGICACC GACTITIGGI GGATTACGIA	600
	AATCTGGGTG CATGCCTGGC ACGACAGCGC GCATCGCACC CCAAGACAAA CGTGCCACAC	660
55	CCATTCAATA TIAGAGGACT TIGCTGCACA CCCTAATCAT CCGTTGGGTT GTGAGATACG	720

	С	721
5	(2) INFORMATION FOR SEQ ID NO:607:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 729 base pairs	
10	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1414RP	
	(ari) (TOO TOO TOO TOO TOO TOO TOO TOO TOO TO	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:	
	GATCCGTAAT CCACTTTAGC TICCGTGTCG CATCATCGAC ACGTGGAAAT GCTCGCTTGT	60
30	COGCOGNOTO AAAACGAGTO AGATGIOCAG AGAGGOTIGAA GTOCAACATT TIIAACCACOG	120
	CTGAAGACOG GGAATAGTAG GGCAACGTAG TTCCGCGAAC TTCAGTTTTG TTTTTCTTTTA	180
35	ATTEANTOCA CTACACCAAA AAAAGCTCAA CAACAGTOCC AATTAGTTCT GCTAGAACAT	240
	GCAAACACGT TAGTGATCAG TAAGTATGTG TACTGGTGTA CTGGTCCTGC ACTGCAAAGT	300
40	TCGCGICACA ACTAGCTGIG AACCATGGIT TGAAAAAAA TAATGATAAT GATICCGCCC	360
	AGGATOGAAC TOGGGACGTT CTGCGTGTTA AGCAGATGCC ATAACCGACT AGACCACGGA	420
45	ACCACCTATA AGCCCTTAAT TATACTCAGA TACTAGTGAC CATTITICTAG TCACATGATG	480
	CTAGTTICCT GAATAAAAGA TOCACGTCAT TACCAAATCT GTATTTACTA GGTAAAATGC	540
50	CTTOGICAAT AAGIACGTAG ATATTATATA TGIATACATA TOCATTTTAG ATOCAATAAA	600
	ACCICIANTA TGIATGOGOG COGAGCITTA ACCCAGIGIG TTTTCCCGATT GITTTGIOGA	660
55	TOCAATOGIC TITOCATAAA AGCCIGACIT TCATCITTITI CGIOCITOGA TGITAACTIC	720

	CAACICIGA	729
5	(2) INFORMATION FOR SEQ ID NO:608:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 639 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1414UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:	
	GATICTICOCCC CIGCOCCAAAAAA GCAGAGACCCC CCCCGTTCCCC	60
30	CCCCCCACTG CGCCCGTTGC ACAAGACATA TATGTCGGTA TATAAGACCG CGCGTGCCCC	120
	GIGGCTOCCC TOCAGAACCC CCCGTCCCCC CCCCGCCACA GATTTCTAAT ACTCTCCGTT	180
35	TICITITIC AGOCCIOGI ATATAASITC OCCCIGIGIC COCCCOGITC	240
	GCCAGGGAGA TAGGGGAGCA TTCCGCAGGA GCCGTCTGTA GCCGGACCAG TACGACAGGG	300
40	ACGCAGGACA CAAAGCAGOC GACGGCGAGT GOGCGGGATC AGCAGCGCAC AGCGAGCCAG	360
	GOSTATAAGA GCCGCGGTAC GAGGCGGCTG GTAGGTATAG GGCCAGATGG AGGTGGGTGC	420
45	TAACOGCATT TTTCIOCACC AGAACGACTC TGCGGAGACG ATCAAGCTGG AGATGTCGCC	480
	TETCOCCOCT TCCCCCACCC CACCCACCCC CATCCCCATTC CCCACCCCCC ACCACCACCT	540
50	GACGAAGTOC ATCAGCGACC TGAACATCTT CCATCTGCTG CACAACAACC CGCCGTCGAG	600
	TICOGACGAC AACAAGGAGG GIGGGGGGGG GGCGGCTGC	639
55	(2) INFORMATION FOR SEQ ID NO:609:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 688 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1415RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:	
	CATOGICGIT CIGITATOCA AACGITCGIT CCTAGAACAT TOCCCCAGGI TCAAAGTAGC	60
25	CACAGCATGA TACGAATTCT GOGATTATCG GCTACATTAC CTAACTTCTT CGACGICGCA	120
	CACTITITIOG GOGITAACAG ACATGIGOGA ATGTTTTATT TICATCAATC GITCCGICCA	180
30	AAACCCTTAG AACAGCAGCT GCTTGGTTGC AGAGGCAAGG CGGGCAGCAA ACAAGGAAGG	240
	GAAAATATTG ATAAGGITTIC ATATGAAAAG CITTATGAAC ATGTCTTAAA TGGCTCCCAG	300
35	GICATGGITT TIGIGCACTC AAGGAAGGAT ACTGIGGGGA CTGCGGGGAA TIACALTICT	360
	TPIGCCCAAG CCAACCAACA GICCGATGIT TICCTAAGTA GCGATCAAAG CGITACCAAG	420
40	TITTCCCGAG ACATCICCAA ACATAAGGAT AGAGATATGA AGGAGCTCTT CCAACATGGG	480
	TTTGGIATAC ATCATGCTGG TATGTCTCGA TCTGATAGAA ATCTAACAGA AAAGATGTTC	540
45	AAAGAGGGAG CTATTAATGT GCTTATCTGT ACAGCGACGC TGGCCTGGGG TGTGAACTTA	600
	CCCCCTGATG TTGTCTTGAT AAACOCAACT CAGATATMTG ACTCTAAAAA ACGTCGTTTT	660
50	ATAGATTICG CGATTCTGAT GTGATACA (2) INFORMATION FOR GEO. TO NO. 610	688
	(2) INFORMATION FOR SEQ ID NO:610:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 703 base pairs

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1415UP	
	Transpire Transpire	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:	
20	GATCATCAGG AGFICGICAC CTTGGAAACC AATTGCGAAC CACAATTCCT TCTGAGCCTT	60
	TOGANATTIG TOACACCANA CICIGANACO GICTITGIAN CITTOATTAT GOOGGANIOC	120
25	TACAAGTGTC AACTTATCAG GGTTGGATTG GTCCTTAAAA TGTACCTTAT CCAGAACAGG	180
	AAGCATOGAG GCTTCACGTA TAAACTTATC TTTCGCCGCT CCTTGAATGT TATGCACGCG	240
30	GCACACTGAG CACAACGCAG CATAGCCCAT COGACCTAGC TTCTCCAACG TCAGCATCTC	300
	GCCACTATAC TCATAGOGAA AGCCATCATC CCCCAATAAT TCGGGGIUIA AGCGTTGIAG	360
35	CGTAATTCCA GCCAAAGCAG TCACCGGGTT GTCCTCATAC CATGITCCCT GCTTAATGCA	420
	CIGCATOSCT TTAATCATAG TCATAACIGI CCIGAGGIAC CCAGATICGC TIGCAATAIC	480
40	GATATACCCC TGTACAATAC GTACCCCTG GTCCACAACT CACATCCTAT CTTCGTAATA	540
	ATCIGCAATT GCTAAGICAG CICTACTTAG GTAAGCTTGT AAAAGCAAAA AGGCTTTGAC	600
45	ATGGGGGTCC CATATTGGTA ACTUTTGTTC TCCTGTAAAA GTACTTTCAA CGGAATATCT	660
	AAGAGITICI GACATITCAA CATICAIGAT AGICICGCCC CCC	703
50	(2) INFORMATION FOR SEQ ID NO:611:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
5 5	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1416RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:	
	GATCATCATT ATTTOCTOCG TICGTOCCGA CCATTCGAAG GOCGOGGICG GITTICTTGAA	60
20	GGATITICAGG CGIATGAATG TTGCTCTCAC CAGAGCAAAG GCCAGTCTCT GGATCCTGGG	120
	TCACCATAAA TCTTTATACA AGAACAAGCT ATGGATGCAT TTGATTTCAG ATGCCAAAGG	180
25	GCGTGACTGC CTCCAAATGC CATGTCCGGG CTTCCTTGAT CCAGGGAACA GAGCCGCCCA	240
	GGATGCTCTT CATAGGTTCA AAAATCACCA TAATTATATC GAGAACGCAG ATGATTATGG	300
30	GCCTGAACCG GTGATGACTA AATCAAGAGG ACGCAATAGA TCATCCAGAA AACGCAAACA	360
	TATOGAAGAT AATCCAGATG ATAACTACGA TCCCGTTOCT GAATTCAAGA AGGAAAATCA	420
35	AAGAGAAAGC AACACAGGCA COGGTGGTTA COGTGCGGAT ACATCTAACC ACAGATTGGC	480
	ACCTOCTAGG AACGATAGCA AGAAGGCCAA GACGTOCTOC AATGCCGCCG GTATTTCCGA	540
40	GOCTACTICA GAGGATGGIG ATCGAGGICA GAAAGGACAT GGAACTAAGA AGAAGTCTIC	600
	CATATTOGGG AATTITTATGC CCCCAGTTGA TGACGCGACC CCTGCTGCCC ATGTGTACGA	660
45	CCCTAAGGAA CGCAAGCCCA AGAATGCTGC ATCCGCTTAA GCGGCTGGCC TTGGCGAAC	718
	(2) INFORMATION FOR SEQ ID NO: 612:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: INA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1416UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:	
15	GATCTTOCCC OGCAAGACCA OGAAGTCGTT GTACGTCAAC COGCCCCGCG TCTTGGAGTC	60
	CATCAACTOC TOCACOGGAC AGOOGGTCCT TCTCGGGCGIA OGTCGCCAGG TGCTGCAGTG	120
20	COGREGOTION GICTOTERA GICATTOCON TITIGITICON GIGCTATICAA CAGAAGCAGT	180
	CAACACTAAA CCCAAGCTCT CAAGTTGACC CATCCATCAA GTAACTATCC CGAACAGACG	240
25	CCGGTAAACC CAGCTGGCAT TIGGCGCATC TAGAAAACCT ATTTATACTG CAGCTCATCG	300
	CTGCAAACTT TTCACGTAAA AGAAACGATG ATCCAGCGGG GGCCAAAAAG CAATGGGCCT	360
30	GCGCCGCACG ATGCGAGCCC TACCGCCGGC CAGCACCAGG TAGGAGCTGT CAGGGGCCTA	4 20
	CAACGOGGG ACGCTAGACG GGCTCCTCGG GGGCCGCCCC AGGCGTTCCCA CGCCCGCCTC	480
35	GCAGCAGCAG GCGTGCCAGG CCCACCAAAAA GACCGACCAG CCAGCGCAGC AGTCTGTAGA	540
	CGGCGGGGAG CAGGGGAACG GCCAGGAATA CAGTCCAGAG CAGGGGGGAG AGCAGCAGGA	600
40	AGITGAACAC GCCGTCCATG CCCACGCGCG CACAAACGGG AACAGCGCCA GCGCGCGC	660
	GCAGAGCGC TGCAGGAATG CGACGACGGA CAGGAACGGC AGGATAGGAC TA	712
45	(2) INFORMATION FOR SEQ ID NO:613:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
50	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: INA (genomic)	

(vi) ORIGINAL	SOURCE:
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(A) ORGANISM: PAG1417RP

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10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:	
,,,	CATCCCCTTG GCGTCGTCGT TGACCAGGTA GCGGCGCTGT AGCCCCAAGA AGCCGGACAT	60
15	COORTICICAL GOOGTICGICA GOOGACOOC CATICATIGOOC GOOCTIACTICS AGATICACOCG	120
	CCGGTACAGG GGCCAGTCCT TGTGGATTCC GACGCCGGGC GGGTAGCGGG TGCCCAGCAC	180
20	GAACGGATGT GTGCGTAGTG AGTCCAGAAG CAGCGGTACG CTCTCTGGCG GATGCTGCAG	240
	GICCOCGICC ATGCACACCA GGTACTCOCC CTTGGCCTCG TAGAAGCCCT TGAGCACCGC	300
25	ACTOGACAGO COGOCOCTOGT COGTOCOCAC GATGATOCOC ACGITIGITAGO COTOCTTICOC	360
	CAGOGOCIOC ACCICTICCA CAGACCOGIC CIGOGAGITIG TOGICGACAA AGATCAGCIC	420
30	AGICTICITG GAGICCOCCT TACCCAGCOC GOCAAACAGC CGCGIGGCAA GCGCCTTGAT	480
	GITGOCCCTT TOCTOCTIACC COCCACCAC CACACACTCT CCATOCTCAT COCCCTOCTA	540
35	TEGRICCITIAA TETAGTEAGT AGCEAACETC GETAGCTETT TOOCAAATAA GTGAGGCCTE	600
	CGCGCCTAAT GTOGTGTCCT TATCGTTGCT TTTTGGTTCG TGTCACCGGG TTACCCGGCC	660
40	ACCAGGCTAG ACAGGGAGAC COGCOGTIGAG CAGCOCACGA CCAAGAAGCG CTIGTA	7 15
	(2) INFORMATION FOR SEQ ID NO:614:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
50	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1417UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:	
10	CATICTOCGTA GGTAGTAGAT GAATTGAGGG TATAGGGAAA AGTTTGGTGC CAAGCGGAAG	60
	CACCOGGGT COCCCTTGTT GIAGICGGCG TACTTCTGGC AAAGCTTGAT CAAAGTTCTA	120
15	TUGATUCACO GGATGACGTO AGOGOCATOA TOGGAATOTG COTTATOGAC TGCAACACGO	180
	GCCATTAGTA CAGCAGCOGC CTCCTGGTCA AAGGAAGCAG CGATTGCCGG GTTACCGAAT	240
20	GCCAACATCT GGTTAGCAAC TGTAGTCACT CTGACACGGT TGGTTACCAGA TGCATGCTGG	300
	TATOCAGIAA TCAATTOGGI GTATOCCAAT TITTOGTCTGT CCCCCATGAG GCTGGCAGTT	360
25	GCAGCGGTAT TTGCAATCTC CAAAAAGATA GCGTAAGAGT GGTGAGGGCT CAAGCAAGGC	420
	ATTITICCATE TAGAAGTOOC COCCAATACOG ATTICIGAAT COCTCACGIT CIGIOCATCA	480
30	ACCITAACCC COCAACCATC COCAATCAGT COCTGCACCT TTAGATCTOC ACTGGTTTTA	540
	ATECACATEG AAGCATTGAA COCCATEGIT AGGIACCCIC CTCATCTTTA GAAAACAGIC	600
35	TGATGAAAGA TTGCTTGAAG ATGCCCGTCG AGAATGCGTC AGTCAACAAC AAAACACCAC	660
	CAGIOGAGIC OGICAACITIC TICATCICAG ACATACAACC IOGICOGIAGC ATCCA	715
40	(2) INFORMATION FOR SEQ ID NO:615:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 728 base pairs	
43	(B) TYPE: mucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: INA (genamic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1418RP

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	(AI) SEQUENCE DESCRIPTION: SEQ ID NO:615:	
5	GATCCGCGAG ATTCATCGTG GACCCGCCAC AGGCAATTAC TATAACAACA TCCTGCGGTG	60
10	TTAAAGGACC TAACTCACCC TCAAGTATTT CACGATGATA TCCTAGATGA ACACCTGCCC	120
	CACACOCIOG TICOGITACA ATATIOCICT CITCOGCAAA ATITAAACAT GICTGTACTA	180
	CAGOGAGCIG GICAAGCACA ACAGATITIG TCCTGTATIT TIGGGCGTAA CICAGAGTAA	240
15	GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACOCT TTTAGGATTC ATGGAAACGT	300
	TOCTIOCOCAG CAGCAAAGAT CTGTOCAAAA CCTCOCACCC CTCTGTTTCC ACTGCTACAA	360
20	CAGGGATAGA GICTGCCAAA CCATGITTCT CCAGCCCATA TACAATCCCA TTATATAAACC	420
25	CCCCCCCCACC TACCCTCCAG ACGATACCTT TCACCCTCTC CAATTCCACG CCTTCCAGAT	480
25	OCAGTOCTIC TACTACTICA TCTACCATTG TEGCATOCCC TECCCAGATG AGTOCGITGT	540
30	CGAATGGAIG TOCATATATC GGAGCGACTT TTTCTAAATT CACATTCCCC ATCAACTCGG	600
	AACGTAAGTA GTCATCGCTC TCTTTCAATA CACTTCCCAT TGATATCACA TCTGCCCCG	660
35	TTGACCGIAT COGCTCTACC ATCCGCCGIC GAGTAGTTTC AGGCACTACC ACTGTGCAAG	720
	GTATCCTA	728
40	(2) INFORMATION FOR SEQ ID NO:616:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE	

(A) ORGANISM: PAG1418UP

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:	
	GATCATCIGC GIGCGATACT GGCAAAAAAT GAGAGACAGC ATGATGAAAA TATAGITAAT	60
10	AAGATATTOC ATGATATAAG CACAGOCGOG TTTCGTCGAA GAGGAAAGGG TGCACTTGAT	120
	CTOGAAATGA GTGAAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA	180
15	CITTIGAAAC AAAAGATATT GGAAAAIGGT GATACTAGCA AGCTOGTATC TAACCCCAAG	240
	TOATACOCCT TITTTCAGAC GATOGIOGAC GATGITACTG AAGCATCAIT TOGAAATACA	300
20	TTTCATCCCA ATATACATCA AAAAACACAT CCATCTCCTG CAGGTCGGAA AATTGTCATA	360
	TCACAACAAT TIGIAAAGGA AACCCTGTCA TICTTGTCGA GCAACAGTGG CGACTCAGAA	420
25	ATCCCTGCAG AAACTAAATC TATTTCATCC AGCACAGTTIG AACGTGAAGA AATTCAAGAC	480
	CTICCATACA TIGAAGCAAA ATAGTAACAT TAAACATTIG AAAGGAATCI AGAACITCCT	540
30	OCTOAGATOG CTGAACTCAG CAGTGGAGAT GAAGGTGATT ACGGCTTTTC TTTTAGATAGA	600
	TICOCTCTOC COCAAAAAGT TTAATAATOG AACTAACGTC GACGATAAGT TTAAAAGTOG	660
35	CACCAAGGCA GTGCGAATICT TAAAGGCAAT AAGACAATTG GCGGTCAAAA GCC	71.
	(2) INFORMATION FOR SEQ ID NO:617:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 723 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single	
-0	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1419RP	

Ivi V	CTEY'S DESCRIPTION	DESCRIPTION:	and the	-	370 (17
(AL)	SEQUENCE	DESCRIPTION:	ಶಾಲ	ш	NO:61/:

GATCT0000GA	GICICATOGA	AACGTATTCG	ATGAGGCTTG	GTGGTGGCAG	GCGGCTCCTC	60
OCTOGATTOG	CCACCTCCTG	ATGACTICGC	ACTICICOGG	GCCCCAAAAT	TOGTGTCAGA	120
CAGTOGGCGT	TGGCGTTGAA	GC1GCCGCTG	TTOCTGCACA	CGTGGTGGCG	CCCTTABCTG	180
AATAOGTAAC	0C103C0CG C	TCTCCCGCGC	ATCCAGGTAT	TCTTCGAGGC	TETCETIC	240
CCCCATGICT	GAGATATCTG	GAGCACCGCG	AGCATTCTGA	TACACGTGGC	CCGAAGATGT	300
TTGCTTCGCG	GIGAAGICIC	CCTCAAACCC	GTAGAAGTCA	TOGGGGTATT	CTCCATCCGG	360
CATTGTCATT	GTAGIAGIOG	TCTCCACATA	GCGTACGCCA	TIGAIGIGCT	TCACCGTCTG	420
GCGAGTCACG	GICCGIGIAC	GECCCTGCAG	GICCITOGIT	TCCGTCGTCT	TCACCGITAT	480
CGTATTGCCA	GCTGCGACAG	CAGGAGGGCC	AAAGCCGTTG	TTCCTCCCIA	OCCAATTCGC	540
GCGTCGTTGC	GAGCTCATAC	TGTAAGTCCG	CCCACGCCCA	CCCAGGTAGC	TGGGCCGAGC	600
AGCICCTAGC	CACCCCCTCC	GCCCGTIACCC	AGTCAGTGAC	TCASTCCCCC	CCATCCCAAC	660
CCCIGGICTT	CCCACTCACC	CAACCCACCC	CGCCGCAGAC	GACAAGCCGC	TGCCTGTTGA	720
ATA						723

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1419UP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:			
5	CATCOSTOCC COCCTOCOTA COCATAGOGO CCAGOTICOCO CAGOTICACTO	60		
	CGCCCAAACC GCACCTGCAC CTGAACCGAG CCTGCAGCCC ACGAAGGAAC GCCACGCTIAC	120		
10	ATGTGCCCGT GCAGAGCACC GCCCTTGTCT TGCGGGGCTG AAGTGACTGT GGCAGGCTCC	180		
	GCAGGACATA TOTTTTTAAT GAGCTIGTIC ATGCGCACAT TOTCACOGTIC GOGCTACOGT	240		
15	ASCETUCOUC TUTGICACUG TETCACUTOC TOCCAAAACA AACAAATUGG GAUGGGCCCG	300		
	CATOCAGIAA TTACCTCCTC CCGAAGOCAA COCCTTOGTT TIGITTIACGT TOGCCAGAGA	360		
20	TTTTCTCTTT COORTGEATT ACCTCACCCC TCATCCCCCC COCACAGGIG CCTGCCCTGA	420		
	CAGITCTTCG AATATIAGAT GCIGGIATGC GOOCACGCCT AGGCCAACGG ATTGTAGTTT	480		
25	ATTGITTOGI CACACCCCCC TAGAGGGCCG AGCTACAGGA TCGCCGATGI GCCGTGACGG	540		
30	ACAGCGICAA CGITACGATC TCAACGGICG CICGIGCGGG CCCGICIGIG GTAGGCGITG	600		
30	AGATACOCIT AGGATGAAAG CACGAAAATT AAGGITGIOG TAAAAACACA AAGTCAACTG	660		
35	GOGITTICCGA ATGOGITAGA GTGCCATCGT AATGGCGGAC GCAGAGTGTC CATGGTGCGA	720		
	G	721		
40	(2) INFORMATION FOR SEQ ID NO:619:			
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 721 base pairs			
45	(B) TYPE: nucleic acid			
70	(C) STRANDFINESS: single			
	(D) TOPOLOGY: linear			
50	(ii) MOLECULE TYPE: DNA (genomic)			
	(vi) ORIGINAL SOURCE:			

(A) ORGANISM: PAG1420RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:	
5	GATCAATTCA AGGITGCTTT COCAGACATC TACOCTGTTT TOCAAAAGAT COCTCAGCAG	60
	CACCCCGACT ACCAAGTGAC TGTCACGGGT CACTCACTGG GTGGGGGTTTA TGCCTACTTG	120
10	ATOCOCCITOS ACCITOCACET ACTIOSCOCAC AACCCACATG TGATICACCTA COCCOCCCTG	180
	CGTATGGGTA ACCCTGACCT CAACAAATGG TACGACAAGG TGTTGGACAA CGTCAAGAAG	240
15	GTOGAGGACT TGAAAAAACGG CGGAAACCCCA AGAAACGCCT ACATCCGTGT GGTTCAGAGC	3 00
	CGTGACATTG TECCTATGGT TCCAACTGGC CCTATCTACA CGCACGGGG TATCCTATTT	360
20	ACCATCACTG ACGTOGACAG CGAAGTACCT CTACAATCCG GCGTCAGACT TGATGGCTGT	420
	AACACCAAGC TAAAGCAGTT GGTCGGCGAC ATCCTCTTCA GCGGGAAGTT GCTAAGCTTG	480
25	GROCGICTOC TGAACCACAA CAAATTITTIC AGAACAATGG CITTIGCCATG CACTGATAAT	540
	TCCTTGAAGC TATAATTCCG AGGAAGTAAT GAATTTTAAG TACGGAACGT GCAGTCGCTG	600
30	CAGICTICIG CCICTICCIT ATOCCCIATA TAGITAATIT GATGITCIGI TCIATITITIT	660
	TACATTITICC AAACACIGOG AATGCCACCT TGTAGATGIT GITCCCAAGA TGGATATITA	720
35	G	721
	(2) INFORMATION FOR SEQ ID NO:620:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 626 base pairs	
	(B) TYPE: mucleic acid	
45	(C) STRANDEINESS: single	
₩	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1420UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:	
5	CATCOSTOSC CACOCOCOCA CCAAGOCCAA GTOCATOGTG GTTGTGGCCG GCCTGCAGGT	60
	CTTOGAGATT GACATGAAGA AGCTGGCGAA CACCTTCGGC TCCAAGTTCG CGACGGCTTC	120
10	CTCTGTGTCC AAGAACGTCG AGAAGAAAGA GGAGGTCGTG GTTCAAGGCG ACATCGCCGA	180
	CGAGGICGAG GCCTACATCC ACGCGCTGCT AGAGGAGAAG GGGATGAAGG GIGTCAAGGT	240
15	CGAGCAGATA GACGCTGCCA AGAAGAAGAA GAAGAGGGG ACGACGACGA CGCCGCCCCC	300
	GICGIGAAGA GCGGGICCOG ACAIGIGIAT CAGAITICGIA TGIAGIGAIT AATGAITIQCC	360
20	CCGATTICCA GIGICITACC AGTCCAAGAG GACAGGIGIC TOOCATGCIT GCACATIGCT	420
	GOOGTOTOOG TOGGGACCAT CAGOCTOGAG ATOGATOTAA TIGAATOOGC GOTTAACCTG	480
25	CGTOCTOCOG GACOCOGGET ATTTOCCAGT GOCACCGAGG AATTGGACAG AGTOCTAAAA	540
	CIGCACIACO GASTGACATA CCATOCOTTT GACCOGOGCA CCAAGCOGTC GGIGTGGGAA	600
30	GICTOCTOGC GGAGGCCGAG AAGATC	626
	(2) INFORMATION FOR SEQ ID NO:621:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 582 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1421RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:	
	GATCCUTCAG TUCCCCATCT TGCCTTCACA GCCAGGATGG ACCAMICAGUA ACCAMICAGUA	

	ALGOGITTE ATTIGICITE TEAGLACIF ATTAICTCIC TOSTTETACA TECTACITIGE	120
5	TTTATCGITA CUIGGGIATG TATGGCATCT TAAATTTIAT CCACTCIAGI ATTTTTATGA	180
	CTGTGTAAAC TAATGAAAAA TAATGAATCG AAGTCTCGTT TACCTAGAGC TGATTATCCC	240
10	ACATGOGTAC TATOGGOGTG CCACCGCAAT TATGTATCTA TOCTACAGAT AATCCTTTCT	300
	ATTAGCAGTT CTCACGAAAC GTCTCAGTTG CCACTCGACG TCAGCATCCT TGTTCTCCAA	360
15	GGTGCCCAGT GTCAGCTCGT AGAGCTTCAT TTCGAACCGT GGTCCCACCT CCGCCAAITTC	420
	AACTCCATCT CTCGTCTTGA CGTATACGTG CTGCCCCACA CTAATGAAAT CGCCCCCGCTT	480
20	OCCAPATOR ATCACCCTAC COCTETCTT CITEACTCCC COCCCAACA TGTCCTTCAC	540
	TATTITIAACG ACCCGITGCC CCAATGGAGT ATTGAAATTA TC	582
25	(2) INFORMATION FOR SEQ ID NO:622:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1152 base pairs	
30	(B) TYFE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1421UP	
40		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:622:	
45	GATCATCATA COGTIGTOCAA CATOGOCCCAC GGAACCACCA GTCACTTGAA GTGGAACGCA	60
	GGTAACATAC GCGATGGCCT CCACGACGAC TTGGCCAGCT TCAAGGACGC AGTCGTGCAC	120
50	TOTOTOAGET TOGGCAGOGG COAGTOGGGC GACTACOGGC ACCAGTOGTC CATGITTCGGC	180
5 5	AACOGTITCTG CTCCCAGTCC CAAGTCCCCG TCCTCCTTCG CTCCCCCCAC TCACTCCCCCC	240
33		

	CATULACTAC TCGACCACCE COCCCACCCC COCCCCACC COCCTICACCA CCCCACCTCC	300
5	TOSTICOGOS GOCACASCOS CACOSASCAT TOSGGOCOST OSTOSTITOS GOCOCACOCO	360
	COCCACACOC GOCACACTOS CTCGCCACCOC TOCTGCTTTC GCCGCCCACGC ACCGCACGCC	420
10	CGCACCGACG GCACCTGGCT CAACGCACAC CGCGACCGCT CGTGGTTICGG TCGCGAGAAA	480
	CACGCCACCC TOCACCACTC CCACCCTCTC TTCCCCCAATC GCCCCCCTCT CCGCCGTCCAC	540
15	ACCACGOGOT AGGOGOGGAC GOCOGCOGGA AGGTOGACGA CATCAAGGAG GCAGGTGCAG	600
	ACCTOSSOCS CTCOSCOSCAG GOCAAGSTOS ACGACTTCAA GOAGGOCGGC GCTGACCTOG	660
20	GICOCTCTOC CCAGGACCOC CTCCAGCOCG CCCTTGCCCGA CCCCAAGCAG ACCCTCTCAG	720
	COCCOCCIO CACOGICICO GOCCOCCOCO CCTCCOCTICO TECCOCCICT COCCACOCCO	780
25	CCICGICOGC COCCGACAAG ACCCAGTCCC TCTTCAACTG GGGCTACAAC AAGGCCGAAA	840
	AGTOGAAGGC CATOGCCATC GGCGAGTACG ACAAGGCCAA CAAGGACTAC CAGCAGGCCC	900
30	TOGACOCCTA CAACOGCTOC AAGOOCCTOC TOGCOGACOG CGACCAGCAC CITIOGCACOG	960
	GOOTOGAGAG COCCCAGGOC CAGGTGCGTIG ACTIGTGGCGA CAAGCTGGAC GCCATCTGCG	1020
35	COGAGTITOGA CCACTIACOCO COCGAGAACA TOTOCGACAT CINCOGOCON CTOGACCACO	1080
	AGGACOGOGA TTOCOGOGOT TOCOGOCOTOT TTAGCTGGTT COGCTTCAAG GOCOGOCTGT	1140
40	CGAAATOGAC CT	1152
	(2) INFORMATION FOR SEQ ID NO: 623:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1422RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:	
0	GATCCGTGTC CTGGGGCTGG TCGAGAACAT GAGCGGCTTT GTGTGCCCAT CGTGCGAAAA	60
	CCAGTOGACC ATCITICAAGC CAACAACAGG TOGTOGTOGC GOCTTGTOGG AGGAGCTGGG	120
15	GATAAAGITC CTTGCAGCCG TGCCGATTGA TCCGCCAATT GCAAGATGCT GCGACTCTGG	180
	CGAAACCTTT TTGGACGCCT ATCCGGACAG TCCAGCGTCG ACCGCCATCA TGCATGTGGT	240
20	AGAGGCTCTC CGTGACGCCG TCGGCGACGT ATAACGCCCC TAGCAGTTCC TGCCAGTGAC	300
	AGACTGATAC CAGTITATAC ATACATACAT ATTIGTAAAA AAGACOCTTA GIGITACGIG	360
25	GATOCCACCO CCCCTTTCAC GTAGATAGTT TCCCCCTGTC CCACCCCCAA TCCAAGTAAT	420
	CIGICITIAA AAGACGGGT CICCAACGCT TGICGATAAT TCICAACGAT GATATGACAG	480
30	ACAACTITIGG ACATGACACA GCAAACGACG GAGAGTICTC GGTGGGAGGC GAAATCCGTG	540
	GOCAGGACOG GCAGAACOOG GACCAGATOG GAAAGCACCT CITGGITGTG GITGTTGTCA	600
35	AGTOCTATCT GGAGGTACTT CTCAAATACC CCCAGGCCGT GAGTCCAAGT TTCCATCTGT	660
	TGTGCGGGGA AAGTCTCCAA TAATTGACGC AGTGTCTGCA AGTTAGCAGC TGA	713
40	(2) INFORMATION FOR SEQ ID NO: 624:	
	(i) SEQUENCE CHARACTERISTICS:	

45

(A) LENGTH: 642 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) CRGANISM: PAG1422UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:	
5	GATCTCCTAG CCGCCAAGTC GACGACTACA GGCGGGGTTT TTGGGCCAAA GACGGAAACAG	60
	AAGCCCGCAG GCGGCCTTTT CGGACAGAGT AGTGCCGCTC CCAATGCCAC TGGCCGCCGT	120
10	OGTOTOTTOG CTAGCACOGG CAACAGOGGC AGCACOCAAT TGGGTGGGCT GTTCGGCAAC	180
	AGTOCTOCOG COCGTOGTOG CAGTCTTTTT COCCCCCCCTA CAACAACCCA	240
15	TOCACCIOGI TOGGAAATCT CITTOGGAAA CCTAATGACA COGCACCOOC AGCTOGTOGA	300
	GGICTITICA GCAATCOGCC GAACACAGCC ACCACAAATA CCGITTCTIC CACTAACAGT	360
20	CTTTTTACCA ATAATCAGGG AAATGGTGCG CAGAATAATG GCCCCCTCTT TGGTGCGAAA	420
	CCTACCOSOG GOCTCTTTOG AAACAGCACC GCTCAGCCAC AGTGCTCGCT TTTTGGAGCT	4 80
25	TCCTCCTCAC AGAATAATCA GCAGCAGCAG CAGCAAACAC AGCAACTGTC CCTTCTGGGT	540
	TOCANTOCAT ATGGOCTIGNA TOTGACTIGGT GITCOTIGTTA CTACCATGGO GGAATCIATA	600
30	ACCOCAGCAA TTACGTCTAA GAAGAAGACG AAGCCTACCG CT	642
	(2) INFORMATION FOR SEQ ID NO: 625:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 719 base pairs	
	(B) TYPE: nucleic acid	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) ORGANISM: PAG1423RP

(vi) ORIGINAL SOURCE:

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	GATOGAACAC AAATTCATCT ACGAACACAA ACTTOGAGOG GTTOGTGTTG GTTATATTGG	60
5	ACAGGAACAT TGACCTACCT TCAATGITTG CGCATTCGTG GATCTACCAA TGTTTAGTAT	120
	TIGACGINIT CANTCICTCC AGAAATACGA TITCAGIACC GAATACIGAT GAAAAGGGAC	180
10	AACCCACATA TAAGAAGATG GATATTGAGC CTAAAGACTT CTTTTGGACG ACAAATGCGC	240
	ACTTOCCGTT CCCAGACGCA GTGGAGAATG TCGAAAATGC ATTGGCAGAC TATAAGGCCG	300
15	AGGCGGAAGC GATAACCAGG AAGACAGGCG TTGACAATAT AGGCGATTTA GATCCTAACT	360
	CTCAAAATGA TACTITGCAA ATTCAGGAGG CAGTGAACAA GITGCCGGAA CTGACTGCTA	420
20	GGAAGAATAT CATTGATACA CATATGAATG TICTGGCTGC GTTGTTGAAA GAGCTAGAAA	480
	ATAAAGGGTT GGATTCGTTC TITIGAAATGG AGCAACAAAG TGACTCTGCT AAGGTGAGGC	540
25	AAGCATTCAT GGACGITTTG AAAGATGGCA AGACCAATAA CCTCAAGGAC AAGITTAAGGA	600
	CATACATAAT CATCIATTIG ACTAGTICGG AGAAGCTTCC CGATCAATTC GTCCAACATG	660
30	TTGAGAGTTA CTTCCAAGAT AATAATTICG AAACOCCACC GTTGAAGTAC TCTATAAGT	719
	(2) INFORMATION FOR SEQ ID NO:626:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 719 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(-i) ODICINIA COMPONI	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1423UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:	
55	GATCATOCTG TTGAACTOCA TOCTCATGTC GTCCCATGAG TACACATGAT TGAAGTCAAA	60

	CAAATGTTTG CCCGACTTGA CCTTGCCGCC ACGCAACGTC GCAAACAATC CGTCGCTGGA	120
5	COGNANGICT GOGNTECCTE CHOCCHCAGA GATCOCCCCA COOGTGACCA COACGATGTC	180
	COCACTOTOC TOCACCOCAT ACCORATICAA GICCOCCTICC COCCCCCTCA CCACCTCCCC	240
10	GICACIGACG TAATGOGCTA GCTGAAATAC CGAGTTCGTC GCAGGCCTGT ACGTCAGCCG	300
	COSCUTACIO COCACOSCAS COCOCOSCUT COSCACOSCO GETAACASCI CUTTOSETICI	360
15	CACCICCICG GACACCCICG CCCCCCIGIC CCACGCCICI GICICCIICI ITIIGACCCI	420
	CGACCOCCC GTGATCCCCA GCTTCACCTT CATCCCCAC CCGTACCCCT TCACACCCAT	480
20	ACCACCAGTA GOCTCOGTCA TOCCGCACGT TOCACAAACC TOTGCCGCTT GOTGCACTCG	540
	TEGTTECCCC CCTCCGTCCC GTGTACCCCA CATGAAATGA GTCACCCCCG GCCCAATTTT	600
25	GCCGGCGTTC GCTTTCGACC AATCCGGAAA ACTTATCCCC CGTAAAACAA AGGCAGGACT	660
	TOOGGIGIGG CGATABOOOC TITTIGIOGCA TOOGCTCCIG GTCCCGTTAC GCCTACATT	719
30	(2) INFORMATION FOR SEQ ID NO:627:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1424RP	
45	(A) CREATER: PASI424RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:	
	GATCTCATCT GTATTTGGAA GGGAACGCAC CAGACGGGGG TGACTCGCAG AAGCTGCCAG	60
55	AGGAGAGA AAACATAGAA AATATATTTA TATTATCTAT ATTGAGTTTA CATAAGAATG	120

	TGTCATAATT TTATTGTTTT TAGATTICGA CTTOCGAGTG CCCTGCATAT GACTATCCTT	180
5	TTATTCTAGA TTCAGTOCTA GCTAGTCGCA AGGAAATOGA TATCGTAATT CCCATTTAGA	240
	ACAAGATACA AATTAGOGAA TITTOCOGGAA AAACCGGTCT TATAATACAG CATCATTGCC	300
10	GAATCCATAC CAGTCCTTCA ATTAAACTTC CGAATCAAAA AAGOCCCGGC GCGGTCTCAA	360
	GAATCTTTTC GCCAGTACTC GAATGGTGAC TATCAGCAAG CGACTCTTCA CTACCCGAAA	420
15	CGACCAGTAT ATTICTICTIC ACCAAATGAT TTAACCCTCT CCACACACCCT CTTATTCCCC	480
	TOCTATGTGT TOTGTGCACG COCTGGCCCC GATAAAGAAT GCAGGTCGCC TAATAGTAAT	540
20	TACTAACCET TITTIAAATC CCCCTCTTCC TICAGACCTC TIGAAACCATA ATCCCATTTA	600
	TACCAGATGA ACTOGOCOCA CTATAGTGTC CGTAATTCAG CACTGTGCAT TOOGAGTTAG	660
25	GGTGCGCGAA GTAGCAAATT TGTGTATCCT CCATAATAAG GATATCCAAT GCCAGTATAA	720
	TAGT	724
30	(2) INFORMATION FOR SEQ ID NO:628:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 720 base pairs	
33	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
40		
••	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1424UP	
	(1.7)	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:	
	GATCATCGTA TOCACTCAGT TGTATTCTAG CATAGCCCGT GOGATTGCCG TGATTTCGAA	6
55	CGATGATGAC AGGCAAATCA CCATGAGGAG COGAGGATTC TOOGCTAAAT TOAGCTGCAT	12

	TIGLARCARA GRIGOCOTOT TICTRIGUER COCCUTICAC ACCOCUTAR ARCATGITUG	180
5	AAATGCTGCT COCTCTGCCT TGCGCTGCGT GTGCCCTCAG CCAGACGGTC TGTTTGCTTC	240
	TAATGTGGGG CAGAGTCGTT CTACTCACGT GTTCAGCGTG CTGAATAACT TGCCTATCCT	300
10	TACACCIGCT CACCICAGOC AATOCACGIT TOCAAGICCA ATAGICTACG GOCCCCAAGG	360
	TIGICOCGAA TOCACAGIGA TOOGIAATCT ATTACTACAG COCACTOCAA GOGIACAGAC	420
15	AACCTACAAT GACGCCCGT TGTACAATAA AATCAATTCC GCTTGCTCGA CCGTTAACCC	480
	AAAGCIATAC CGIACCTIGI GICCTICCCI GITTCCATTA GCCGITGCAT GIGCTITTITI	540
20	ACTOTOGATTA CAGAGCCTIT CTGTAGAATG TGTACGTGAA TTTAATACTA GAGAGCTATA	600
	AACCICICIT GITCITGIAA TGICIGITTC AGAAGATAAA AGGIAACACC AGAAAACGAG	660
25	GTACGACCCA ACGCTATTG GACTACGAAC TOGACAAAAA CTAAGAGTCG TAAGTAAGAA	720
30	(2) INFORMATION FOR SEQ ID NO:629:	
J	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1425RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:	
50	GATCAGCICC CACTIBETIE CAACAGTATT CCICAGACIA TCATICHET AGAGCGATIC	60
	TIGIGAAGCA GITGOCCCGG TGTATGAAAC CGCGTGTTTA CCAAGTGGAG GCCTTTGTTC	120
55	ACABATTITIA GITCCITICTO GAACGTATTO GTOGTOCTOG ACAATAAAGT TITIGITIGCTO	180

TANGTIGING ANGTOGICCA ANATATOGIC TITOGOGNGA GEAGCANGOC TOGNGCCCCT GARCAGIGNI CONCINCANC TICTITOCHT MOCHTGCCC TONOCATTAT TOCTATIGIG TOGNGCICH CANTIGOCICA ANGANICICT OCTITOCHGA GARCATOGIC TOGNACCTIT MINITONICA TANGCICCAN ANGANICICT OCTITOCHGA GARCATOGIC CIGANIGHAG ANGANONICA ATANANCATE ANTOCCICC MEGNANTIE TOTANICOGIC CANNIGHTEN TOCNGCHEN TIGICATANA TITIGAACCAG MICHOCNOC GACTIGIACA GERCOCTOGIC GITGIANICUT GCCTIGOGIT GECCANCTIC TITINATIGAC COGANGANGC (i) SEQUENCE CHARACTERISTICS: (A) LEMIN: 711 base pairs (B) TYPE: INcleic acid (C) STRAINENESS: single (D) TOPOLOGY: linear (Xi) ORGANISM: PAGI425UP (Xi) ORGANISM: PAGI425UP (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC COCCICCOCA TACAGITICC CONCRACAC ACCORDING COGANGAC 26 GATCATACAC GACACOGRA GACTITICCC CONCRACAT TOCCOCTOGIC COGANGACC 12 CANIGCATAC ATRANCOSCA CAGNOGOCIC CIGNANICOC GOCTICCICG GCTGOGTINC 18		GACATAGICA GOGICAAAAA CATICACAGG IGIGICATCA TATGOCOOCC GOCTGCCOGA	240
GARCAGIGAT CONCINGANC TICTIOCAGT ACCORDOGG TORGORITAT TOCHNITUTE 420 TGINCTOCTC GASTIGOGGA GATTAGATAT ATCANACIGT TICGATIGTS TIGGACCUTT 480 ATATTCATCA TATGCTCCAA AAGANTCICT GCTTIGOGGA GAGCCTGGGG CTGCATGAGG 540 ACCAGGACC ATANAAGATG AATCCCTGCC AGGACAGTIG TIGTAACCGC CAAATGGTCA 600 TGCAGGGTAG TIGTCATANA TITGAACCAG ATCTGCAGGC GACTTGTACA GGTCCCTGGG 660 GITGINICCT GCCTIGOGGT GGCCAACTIC TITTAATGGAC CAGAACAACC 710 (1) SEQUENCE CHARACTERISTICS: (A) LENTH: 711 base pairs (B) TYPE: Incleic acid (C) SITRAIDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GCCCTGGGCA TACAGTTGCC CAACGACCTT TCCCGCTGGG CCGACAGCAC 12 CAAGGCATAC ATANACGGCA CAGAGGCCTC GGTGAAATGCC GCCTGCGGTTAC 18 CACAGGCATAC ATANACGGCA CAGAGGCCTC GGTGAAATGCC GCCTGCGGTTAC 24	5	GETTETEGES TEAGECTITE TETTEGETTE CEAGTETECA ACCTICEAGA TAGETTTEGA	300
TGRACIGAT CONCINCANC TICITOCAGE ACCORDAGE TRACATION TOCHNITIS 420 TGRACIOCTC GASTIGUCCA GATTAGATAT ATCAAACTGT TICGATTGTG TGGAACCTTT 480 ATATTCATCA TATGCTCCAA AAGANTCTCT GCTTTGCGGA GACCCTGGG CTGCATGAGG 540 ACGAGGAGC ATAAAAGATG AATCCCTGCC AGGACAGTTG TGTAACCGCC CAAATGGTCA 600 TGCAGCGTAG TIGTCATAAA TITGAACCAG ATCTGCACGC GACTTGTACA GGTCCCTGGG 660 GITGTATCCT GCCTTGGGGT CGCCAACTTC TITTAATGGAC CCGAAGAACC 710 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SCURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC CCCCTGCCCA TACAGTTGGC CACCACCAC ACCCCGACA GCCTCCAACG 660 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GCCTCCTGG GCTGGGTTAC 18 CACAGCCACT ACACCCCTCA ATACACCACCGT GCCCGGGCTG CTGCGGTTAC 24		TAAGTTGTAG AAGTCGTCCA AAATATCGTC TTCGCCGAGA GGAGCAACGC TCGAGCCCCT	360
ATATICATICA TATOCTOCAA AAGAATCTCT OCTTTOCOGA GAGCCTOCOG CTGCATGAGG 540 ACCAGCACCA ATAAAAGATG AATOCCTGCC AGGAGAGTTIG TUTAACCGCC CAAATGGTGA 600 TOCAGCGTAG TIGICATAAA TITGAACCAG ATCTGCACCC GACTTGTACA GGTCCCTGCC 660 GITGTATICCT CCCTTGCGGT CCCCAACTTC TITAATGGAC CCGAAGAACC 710 25 (2) INFORMATION FOR SEQ ID NO:630: (i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 35 (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP 45 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC CCCCTGCCCA TACAGTTGCC CACCACCACC ACCCGCACCA GCCTCCAACG 6 CCTAGAGGAC GACACCCCA GCCTTGTGCC CCACGACCTT TCCCCCTGGG CCGACACCAC 12 CAAGCCACT ACACCCCCA ATACCACCTC CCTAAATGCC GCCTCCTGC GCTGGGTTAC 18 CACACCCACT ACACCCCCA ATACCACCTG CCCCGCCCTG CTGGGGTTAC 24	10	GAACAGIGAT CCACIAGAAC TICTTOCAGT ACCUTOCCCG TCAGCATTAT TOCTATTGIG	420
ATATICATCA TATOCCICCA ANGANICICT COTTIGGGA GASCOTOGG CIGARIGAGE ACCACCACC ATMANASATE ANTOCCICCE AGENCACTIC TETANCOGC CANNIGSTEA 600 TOCACOGIAG TIGICATAAA TITGAACCAC ATCIGCACCC GACTIGIACA GGICOCTOGG GITGIATCCT COCTIGGGGT COCCAACTIC TITMATGGAC COGAAGAACC 710 (2) INFORMATION FOR SDQ ID NO:630: (i) SEQUENCE CHARACTERISTICS: (a) LENGTH: 711 base pairs (b) TYFE: nucleic acid (c) STRANDETNESS: single (D) TOFOLOGY: linear 35 (ii) MOLECULE TYFE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP 46 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC COCCTGCGCA TACAGITICGC CACCACCAC ACCCGCACA GOCTICCAACG 66 67 68 69 60 60 60 60 60 60 60 60 60		TGTACTCCTC GAGTTGCGCA GATTAGATAT ATCAAACTGT TTCGATTGTG TGGAACCTTT	480
TOCACCETAG TEGICATANA TITICANCCAG ATCITICACCE GACTIGIACA GETECCIOCE GITGIATOCT COCTIGOGET GECCANCTIC TITIANIGENC COGANGANCE 716 (2) DIFORMATION FOR SEQ ID NO:630: (i) SEQUENCE GERRACTERISTICS: (A) LENSTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI425UP (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GEOGEGGGA TACAGITIGGE CAGCACCAGE ACCESCACA GOTTCCAACG 6 GCTAGAGAC GACACCAGA GUTTGITGGE CEACACCAGE ACCESCACA GOTTCCAACG CAATGCATAC ATAAACCGCA CAGAGGCTIC CETAAATOCC GEOCTICTGG GUTGGTTTAC 18 CACAGCCACT ACACCCCTCA ATACCACCGI GEOGGGCAG GOTGGGTTTAC 24	15	ATATTCATCA TATOCTCCAA AAGAATCTCT OCTTTOCOGA GAOCCTCOCG CTOCATGAGG	540
GTIGIATOCT COUTIGOST COCCAACTIC TITAATGCAC COCAAGAACC (2) INFORMATION FOR SEQ ID NO:630: (i) SEQUENCE CHARACTERISTICS: (ii) STANDEINESS: single (ii) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATGATACAC GOOTIGOSCA TACAGITGGC CAGCACCAC ACCOCGACA GOOTICCAACG COCAAGCCACA ATACACCCCCA CAGCACCCCC GOOCICCTGG GCTGGGTTAC 18 CACAGCCACAC ATACACCCCCA ATACACCCCCC GCCCACCAC GCCCCCCCCC GCTGGGTTAC (A) CACACCCACAC ATACACCCCCCA CACCACCCCC GCCCCCCCCCC		AGGAGGAGCC ATAAAAGATG AATCCCTGCC AGGAGAGTTG TGTAACCGCC CAAATGGTGA	600
25 (2) DEFORMATION FOR SEQ ID NO:630: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPULOGY: linear 35 (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SCURCE: (A) ORGANISM: PAG1425UP 46 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GOOCTGCGCA TACAGITGGC CAGCACCAC ACCOCCACA GOCTCCAACG 6 GCTAGACAC GACACCGCA GCCTTGTCGC CCACGACCTT TOCCGCTGGG CCGACAGCAC 12 CAAGGCATAC ATAAACGGCA CAGAGGCCTC GGTAAATGCC GGCTCCTGG GCTGGGTTAC 18 CACACCCACT ACACCCCTCA ATACCCACCGT GGCCGGCGCACACG TCGATTGCACC 24	20	TECASOGIAS TIGICATAAA TITIGAACCAS ATCTECACOC GACTIGIACA OSTCOCTEGO	660
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ENA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GOOCTGOGGA TACAGTTGGC CAGCACCAG ACCOCCAGG COGNCAGGAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GOOCTCCTAG C18 CACAGCCACT ACAGCCCTCA ATACCACCGT GOOCGGCACA TOGATTGCAC 24		GITGIATOCT COCTICOCCT CCCCAACTIC TITAATCCAC COCAACAACC	710
(A) LENSTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GOOCTGCGCA TACAGTTGGC CAGCACCAC ACCCCGACA GOCTCCAACG CATGAGAGC GACACCCCAG GCCTTGTCGC CCACGACCTT TCCCGCTGGG CCGACAGCAC CAAGCCACT ACAGCCCCCA ATACCACCGT CGCGGCCCTG GCTGGGTTAC 18 CACACCCACT ACAGCCCCCCA ATACCACCGT CGCGGCCCTG CCTGGGTTCCCC 24	25	(2) INFORMATION FOR SEQ ID NO:630:	
(A) LENSTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GOOCTGCGCA TACAGTTGGC CAGCACCAC ACCCCGACA GOCTCCAACG CATGAGAGC GACACCCCAG GCCTTGTCGC CCACGACCTT TCCCGCTGGG CCGACAGCAC CAAGCCACT ACAGCCCCCA ATACCACCGT CGCGGCCCTG GCTGGGTTAC 18 CACACCCACT ACAGCCCCCCA ATACCACCGT CGCGGCCCTG CCTGGGTTCCCC 24		(i) SPOURNER CHARACTERISTICS:	
(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GEOCTGEGGA TACAGITGGE CAGCACCAG ACCUCCACA GEOTTCCAACG 6 GCTAGAGAG GACACCGGA GEOTTGTCGE CEAGCACCAT TOCCGCTGGG CEGACAGCAC 12 CAATGCATAC ATAAAACGGCA CAGAGGCCTC CETAAATGCC GGCTCCTCG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT GECGGCCCTG CTGGCCGACA TCGATTCCAC 24			
(C) STRANDETNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GOOCTGOOCA TACAGITGOC CACCACCAC ACCOSCGACA GOCTCCAACG 6 GCTAGAGACG GACACCGCAG GCCTTGTCCC CCACGACCTT TCCCCCTGGG CCGACAGCAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCCTCCTCG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT GGCCGGCCTG CTGGGCTACA TGGATTCCAC 24	30		
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GEOCTGEOGCA TACAGITGOC CAGCACCACC ACCEGGACA GEOCTGEAACG 6 CCTAGACACC GACACCCCAG GEOCTTGTCGC CEACAGCAT TECCGGTGGG CEGACAGCAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCCTCCTCG GETGGGTTAC 18 CACACCCACT ACACCCCTCA ATACCCACCGT GECCGGCCTG CTCGCCGACA TOGATTCCAC 24			
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1425UP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GOOCTGOOCA TACAGITGOC CAGCACCAGC ACCOCGACA GOCTCCAACG 6 GCTAGAGACG GACACCGCAG GCCTTGTCCC CCACGACCTT TCCCCCTGCG CCGACACCACC 12 CAATCCATAC ATAAACCGCA CAGAGCCTC CGTAAATCCC GCCTCCTCC GCTGCGTTAC 18 CACACCCACT ACACCCCTCA ATACCACCGT CCCCCCCCGC CTCCCCCCCC 24		· · · · · · · · · · · · · · · · · · ·	
(A) ORGANISM: PAG1425UP (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 630: GATCATACAC GCOCTGCGCA TACAGITGCC CAGCACCAGC ACCCGGACA GCCTCCAACG 6 GCTAGAGACA GACACCGCAG GCCTTGTCGC CCACGACCTT TCCCGCTGGG CCGACAGCAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCCTCCTGG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT GCCCGCCCTG CTGGGCTCCAC 224	35	(ii) MOLECULE TYPE: DNA (genomic)	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GCOCTGCGCA TACAGITGOC CAGCACCAGC ACCCGGACA GCCTCCAACG 6 GCTAGAGACA GACACCGCAG GCCTTGTCGC CCACGACCTT TCCCGCTGGG CCGACAGCAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCTCCTCG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT CGCCGGCCTG CTCGCCGACA TCGATTCCAC 24		(vi) ORIGINAL SOURCE:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:630: GATCATACAC GCOCTGCGCA TACAGITGGC CAGCACCAGC ACCCGGACA GCCTCCAACG 6 GCTAGAGACA GACACCGCAG GCCTTGTCGC CCACGACCTT TCCCGCTGGG CCGACAGCAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCCTCCTCG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT GCCCGCCCGC CTGGGCTCCAC 224	40	(A) ORGANISM: PAG1425UP	
GATCATACAC GCOCTGCGCA TACAGTTGGC CAGCACCAGC ACCCGGCACA GCCTCCAACG 6 GCTAGAGACG GACACCGCAG GCCTTGTCGC CCACGACCTT TCCCGCTGGG CCGACAGCAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCTCCTCG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT GGCCGGCCTG CTGGCCGACA TCGATTCCAC 24			
GCTAGAGAGE GACACCOCAG GCCTTGTCGC CCACGACCTT TCCCGCTGGG CCGACAGCAC 12 CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCTCCTCG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT CGCCGCCCTG CTCGCCCACA TCGATTCCAC 24	45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:	
CAATGCATAC ATAAACOGCA CAGAGGCCTC CGTAAATGCC GGCTCCTCG GCTGGGTTAC 18 CACAGCCACT ACAGCCCTCA ATACCACCGT GGCGGGCGCG CTGGGCGACA TGGATTCCAC 24		CATCATACAC COOCTGOGCA TACAGTTGOC CAGCACCAGC ACCOGGGACA GOCTCCAACG	60
CACAGOCACT ACAGOCCTCA ATACCACOGI COCCOCCTG CTOCCCGACA TOGATTCCAC 24	50	COTAGAGAGE GACACOSCAG GOOTTOTOGO COACGACOTT TOCOSCIGOG COGACAGOAC	120
CACAGCCACT ACAGCCCTCA ATACCACCGI COCCOCCTG CTOGCCGACA TOGATTCCAC 24		CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCCTCCTCG GCTGGGTTAC	180
	55	CACAGCCACT ACAGCCCTCA ATACCACCGI COCCOCCTG CTCGCCCACA TCGATTCCAC	240

	CONCURRENCE OCCUPAÇÃO ACACOCCACT TOACOCCCCC AIGOIGACOS TIGICIOCIOS	300
5	TGTAATCGGG AACAAGTTGC GCGCCATCGA GGCAGGCCTC ACCTGGACCC ACGACCACGT	360
	ACCONTICCC CTOCCOCCON TOCATACCOC CCCCTTICCC GACGCTGTCC CAGAACCAGA	420
10	CCTTCCAACC CATCCCGCCT ACACAGCGGT GCTCCAGTCC CTCAGTGACC GCTTACGTCA	480
	TICOGUIGAC CGUGUGCUAC AUCAGUCCUG TOCCOCCGGUC COCATUGAAC TCUACGUATIC	540
15	GCTTGCCCTG CTCGGCCTCT GGATTCTGCA GACACCTCTC GGCTTGCCAA TGCTGCTATT	600
	CAAGTCGCAC TGCCGTCGCA GGAACCTGGG CCGCAGAATG CCTTGAGCCT AATTICTTACA	660
20	TAATCITAAT TOSOCATTOT SCIGOTOGAA CACGAACTOC GOGITAGOOG G	711
	(2) INFORMATION FOR SEQ ID NO:631:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1426RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:	
45	CATCTTCTCT CCCCTCCACG TCACTGCCCC CATGCACCAC GCCATGAACT CCTCCTGCCC	60
	CTCCTGATCG CCCTCGTGCA CTCCTACCCG CCACTGCCCC TCCACAAAACC CCCCCATCTT	120
50	GTTCGCATCC TGCAGCAGCA CCACCACATG CGGAAACCACC GGCTGCCTGG CTGCTTTCGC	180
	TAGCTGAAAC GAAAGAAGAC GCCCTATAGG CGCGCTGCCT AGCATATACA CCCACGGGAC	240
55	ACCCATAACA GCCCTTCTAA CCCTCAACCG AGTCACTGAG AACTGGCGTA GTGCGCATCA	300

	TCCACCTOCC CATTITICAT TCTACTCAAT AATCCTTACA CCCCCAACAC AAAGGCAGCT	360
5	TCACCACCAT TCTGGCTCAA CTAGGAGGGG TGTCGGGGGA ACCAGGAACG CGTTACTGGG	420
	TAACCOGGCA TCTAGTCAAG TCCCCAGTIG CACCCCACTT CITTITIGTGT GITATTCACC	480
10	GTGTAGGATG CTTGTTATAG GGTTGACAGG AGGTATTGCA TGCGGCAAGT CGACGGTGTC	540
	COCCACACTO CACGAGOCAT ACCOGATOCO GGTCATOCAT GOCCATOCCA TTICOSCOCCA	600
15	CATTATGCGC CCCCCCCACC CCCCCTACCA CCCCTOCTOC AACCCTTTICA CCAACCCCTC	660
	CCGCAACTGG TGCACOCGAA CGGGGACCTG AACCGCGCGG CGCTGCGCGC GTGGATCTTC	720
20	CA	722
	(2) INFORMATION FOR SEQ ID NO: 632:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 703 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1426UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:	
45	GATCTCCTCC ACCCCTCCT TGAACCAATC TOCAGAAGAG TGTCCCCCTC GTCAAGAACC	60
	TIGAAGICAA CCTCGGIAAA GIACTITIGGA CCGCAAGCCT CGAGCATGTC GATCAACCGG	120
50	CCCCCCCTCC CAACCACCAT ATTOCCCCTC CTCCCCTCTA GCCATCTCAA ACTTTCAGTC	180
	CCCCACCACCATCAT GACAACCCCA TIGAAACCCC GAACCTICCT GITGCCCTIC	240
5 <i>5</i>	COCATCTCUT TGATCTCGTT GAACATCTGC GCGGCCAAGT CCCTGGTTGG TGCAATCACA	300

	ACAGOCTIGA CATTITOOGA AGGAGOCCCC TOCAAGAGOC GCTGGAACAG CGGCATCAGA	360
5	AACGCAAGIG TCTTACCIGI TCCAGITTIC GCCCGIGCCA CCACAICGIG CTCCGICTGC	420
	ASCATOSCOT TOAGCCTOTT CTOCTOCACO GCTGTTAGTT TATOGAAGCC GCGTGACTGC	480
10	ASCATCTOGT ACAGCTOGTT GCTGAGCAGG CCCTCCTCCA CCAAGGTCCG CGGTGTGCTT	540
	TOGACCOCCE CAGCITICETC GOCCACACGC ACCACCITOGG TETTIGGGGCC GAGGCTGAAT	600
15	COCTOSCICE COSCICCITC TETACISCOS COTOTISCOTT GTOSCITICOS COACATISCOS	660
	CCGCGGGGGAC CACGCTCACC ATCCTCCCTG TCGCTGCCCG GCT	703
20	(2) INFORMATION FOR SEQ ID NO:633:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1427RP	
JO.	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:	
	CATCITICTA TOCOGGAAAG AGTOCATOGA ATACAAGGIG CITICTAGAAG GOCCCTATOG	60
45	AAACACCATT CCGCGGCTTG CTGCTCCTGA CCGGCGCTAC GTGGGGGGCCA GCGCAGGTCT	120
	TESCETASCA SCSETCTACC CACACTTECT CTCTCTGTTG GACAAGGAAA GCCAGTTCAC	180
50	CCATTCATTC TACTOGATTA TAAATGACCT TTCATATCTG CATTGGTTTT COCATGAGCT	240
	GAGGTACCTG GCCCACCOGA ACTGCGACAT CAAAATTATT TACACGAGGA GCAATGAGTC	300
5 5	GOCTAAAGAA CTGACCCCAG ATGTTOCCGA TTCCCGCCTCT GCGAAGTTCG TOGATTCGCT	360

	GONTATURE AGGUTEUTEC TELECUCAÇA TUTCAAAGAG ATOGTOGAAG AGCAGATECT	420
5	OCTOTOGICT ANOCAGOCAC AGGACGICAC GITTATTAGC AGGGGGCCTT CGACCTITAA	480
	TGACCATTIC COCTATOCTG TGAAATCTAG CATCACOGOC AAACTCCAGT GTGATGTCGA	540
10	CCTAGAGCAG GAAAGCTACA CCTGGTAGAT AGATACCATC TTATTAGITA ATTGTACTTA	600
	TITATICCIC TICCIGIAIC TIAAGCAAAT CCCGCCATGT CTCAACCAGC TICTGCATGC	660
15	TITICOCCATT CACCOCTICCO TOCACCACCT CCACACCTAC CTCCTTTTCC C	711
	(2) INFORMATION FOR SEQ ID NO:634:	
2 0	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1427UP	
	(A) CROSNICKI: PASI42/UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:	
40	GATCATCTTG TOCATGCCCT TGGGGCCCAG CGACGITICTG ATCGCATCCG CGACTGCTCT	60
	GGCAGCAATA ATGITCGCCT TTCTCACTTC CTGCGGCTTC TCGCGGTTTT TGAACGTCGC	120
45	ATTICCTOCCA CTICACCTTCG GTCCCATCTT AATATACTTC CTICATTCCGC GCCCCAGAAG	180
	CCTTACTICC TCCTAGAGAA GITAACGTIG TITGITITATG CTGACAACGC CTAAGITACC	240
50	GICAAACCAT CAGATTTITG CCACTOCAAT TICCCTITGGT ACAAACGGAT ACTIGATCCT	300
	TIGATCICCA AGAGCIGITC CATCOGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGCGAA	360
55	AATCGGGGCT CGACAACTTG GGAAATGTCT ACGGAGGACG CGGCGTTAAC AGGGATGGGG	420

	GICALUGCAG ALCICAAAAA AAAATOOOCG TITTICCAGCT GGIATGAGGC GITCAAGGCC	480
5	CACACTOCOSC 6888COGASGT GATTICOSCCC CTIGCCCGAGG AGTTCGTCAG CTTACGTCGAT	540
	CAGCOCCOGA TCAGOCTOGC GCOCCAAGAA GOCTCGAAGT ATTTCTACOG CCAGGAATOG	600
10	AGCCTACGAC GGACGGAGAG TACAGCGACT GGGAAGGCGG CGACAGCGGG AGTGAGCGGT	660
	CGTTCGTGCC GCTGCACCGG TGGCGGAACTT CCCGGAAGTG CACGCGGGG TGAAGCAG	718
15	(2) INFORMATION FOR SEQ ID NO:635:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 723 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1428RP	
30		
	(mi.) CTV Table	
35	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:635:	
	GATCATACAC GCATTGCAGG TATACATTAT AGTGCTCATA ATTATCGGAT TGCAAATAGA	60
40	ATGGGGGCCCT TACCGTAGIA CIGICTIGGT AATGCAGCGA CGCTCAGGCT TAACAAGCTT	120
	TTTGTTCTCC GIGTATTACT AACAAAATAA TTTCCTCGAG CACAGGGAGT AGAGATGAAT	180
45	TACATAATOC ATATOGACAC CTOGTCACOT TOCAGOGACA TTAACATTTC CITATGAATG	240
	COCAATAATG GTOCCTAAAT GATGTOCTTG GTGTAATGCG CATTATAAAA TGTATGTOGA	300
50	TRATATATTG TITGTAGCAT CTAGTAGAAC CATGGTAGCG AGGTCTTTGG CCATACCCTT	360
	CTGAAGAGAG ACATAGCAAC AGIGICTIGI GCAGACAGIC TGCCGTCGAA TGITGCCTTG	420
55	AAGIAACCAT GAGTACCAAG ACTICTICCTTA ATGAAGCCAG AGGGTCCAGA TTTTCGTGAAT	480

	AGIOGGATUG ACTIGAACCA CICGACATOT TOTOGOCTAA AGAACATATA GOGCACTGTG	540
5	ACCACGCOCT TGTGGAACTT GAATGGATGG CCAGTTAATA TGATTCTCTT GGCCAATATC	600
	COTOTICTOCT CIGOCITICAG GAACOTOCCO TOCCCCACGA ACCTICACCCC CITTOCATICA	660
10	GAGGOGITTT CITTGAAGTA GATGGCCGGT GACTGGGTCA GGTCCAAGGG AAGCATGCAT	720
	GIC .	723
15	(2) INFORMATION FOR SEQ ID NO:636:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LEWSIH: 726 base pairs	
20	(B) TYPE: nucleic acid	
	(C) SIRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1428UP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:	
33	GATCAAACCA GAGTGOGAAG COCACACGCG GCACTGGCGG GAGCCCTTAC CGTAGTTTCT	60
40	TOGGTOGGAG AACCAAACGT TTTCGTGAGC CATCTTGTCT GCAATGCGTT AGTACTCTGT	120
40	CIGACGCTT GRAAGGSCTC CGGCCCTGGT GAGCTGCCCA CAGSCTGGGC GTCTGGGGGC	180
45	TOCTCATTOC COGCACCOTA TICTOCTOSC ACOCACACOCT CTAGACCACA CTITOSCOCCA	240
4-5	TOCTOTOCAC ATACGATTAT GCTTTGTCTC TTGGTATTAT CCTTAGATTC GCTAGACTTC	300
50	GACACTATOG TTATCACCAC TGTTGAAGTC TOCTTCGGTT GOCACCCAAA GTCTGGGGAC	360
	TGTAGTTGGA AAGCGCAGTT CGCGGCAAAT CAAGCATCTC ATAATGTGTG GGTGCAACCG	420
55	TIGAATGIGI GOGIGCAACA GICAATIGIA ATITCTITIT TIGATOGAGA GATGOGATGC	480

	GAIGAGCIAG TIGAAAAAIT TTAGTATOOC AAAACTOOCA TOCATATCTG AGATOOCCA	540
5	TCAATTGCGG CAGCTTAGTG TTACACGACC AATCCAGAGG TGGTAATTGG GCTATGCCAG	600
	GICACTOGCA CAGGTCGTCG GTAAAAAAAGG GCCACAAAAAC GTTCAAGTCG AAGCATGCGA	660
10	OCAACOOCOC CITICAAACOG CTGCACAAGG GCAAAGTGCA ACAGGAGACC GCTGCTGCCG	720
	TCAACC	726
15	(2) INFORMATION FOR SEQ ID NO:637:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 712 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1429RP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:	
	CATCAAAGIT TAGCATGTAA ATGTGCAACA AACTATTTAT TACCTCTGCA CTGCCCATGT	60
40	COCTTGARAC COCCGAGGAT CCARACCAGT OCTTTCATAR TOGRATIOCA ARATTGAGTG	120
	CAGIAATIGA TAAGIATCTT GAGAAAAGCC CTCCCGACTT TACCCTAGAT GATTCCTTAA	180
45	TATGITCAAA AGCCTCCGAG TTAATAAAAA GCCTTGCTAC ATCCAAGGTG CATATAGATG	240
	TGATAGATGA GACTAACAGC ACCATTCATA AAAAGCGGAA GCCCAATTTT CGAATCACAT	300
50	CACCCAGAGC AGTATACACA TOCATTIGGA ATGTOGTATT AAGAAAGTTG GATACCGTTG	360
	TOCACCAAGG AAAGGIAGAA ACOGICCAAT CCTTIGATCA GATACTIGAG AATTICCTTA	420
55	TTAACTIGAA AGAAGTOGAC TTTACTCTAT CTGGGGTTGC TCTGATGTAT AGCACTATTG	480

	ACTACTOGAA COCCCACATG ATCCCAGGCT ACGGCAAAGT TACGACTGTA GAGCATTITCC	5 40
5	TOGTOCAGTA TATCTTACAT CGATATGAGG TATTATATGT GOCCOOCGAT GAAAGCCTAC	600
	TAGATAGICT GGTIGGIGCC ACTATTCOGA AGCTATTTGA ATOCATOCAG TCACAGCATG	660
10	ACCACCAGAG CCTOGTAGCG AATAGCCAGG CTGATACCGC ACGAAGAGAT AT	712
	(2) INFORMATION FOR SEQ ID NO:638:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1429UP	
30		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:	
35	GATCAACCGA TAGCGGAAGG CGGACGAGCC TCCCAAAATAG TACTAGGCAG TGGTTGGCTT	60
	TIGITITIAG CIGIGITICA AGAIGICAGC GAGAACAAGC AGGGAGCAG GCGCCICCAG	120
40	GETGATICSCA GETCGCACTA GTATICGATICG AAAGTCCCCCG ACAGCAACAG GETATITTICGA	180
	ACAGCTGAAC TCGCCAAGCA TICAGAAGCT CATGCACTGG GACGCTTCCA CGACAGCACT	240
45	ATTGGAGAGG TIGAAGATGT COCTAGTGAC TTGCGTGGAG TTCACGAAGT TCATAAGAAA	300
	GAAATACTIG CTAGAAGAGG GCCATGCGCA GGAGATGGGC AAGGCTTATA AGAACTICTT	360
50	TCCCGAGGCC CGTGAGTCCA CCTTCCAGAA TACCATACAT AACGTTTTCG AGTATGACCG	420
	AAAACTTGCG CAGGIGAAAC TPICATATGT TOCTGCGITG CAGAAGATGT ACGATGAGTT	480
55	AACGTOGCTT CTTGCATCCA TCACTAAAAT GOGCAAATCC CTCAAGGAGA GCAGTOGGCG	540

	GTTGGAAAAA GAAGTCGCAG ATGCTATACA TAGCGCCGAA AAGGCAAAGG CAAGATATAT	600
5	GICCPIGIOC ATGGATIGOS AGAAGCICAA GCTIGIAGAT CCTGCAAAGA CGAAGITGAC	660
	ATTOCOGGGC TCAAAGACCA CTCGAGAGCA GGAAGAGGAC TTATTAGAAA GATTGATA	718
10	(2) INFORMATION FOR SEQ ID NO:639:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 730 base pairs	
15	(B) TYPE: mucleic acid	
	(C) STRANDHINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1430RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:	
	GATOSCAGAG AGACACAATG TCCCTGTGCC CACTITIGTCT ATGCTTTATC ATTTATTGAT	60
35	TCTTGTGCAG GOGAAAACTG AAGGCCCAAC AGGGAATTGT CAACCATGTT TAAACTTTTC	120
	CATGIGCATG GAGCICOGIA TGTAGCAATA TATTCTCATA GCIAGAGATC TCACTATATA	180
40	TTACCTTOCC ACATTTATGT CATATOGACG TTOGTTTTTG TACACCTTTG TGTCAGGTAG	240
	CAGGGGCCCC ACATAACTAG TTATAAAAAC GATGCCCCCC GAGAACGAGA TCTACTATCT	300
45	CICIGAGIAG GCACAGITIC CAACGIAITA GIOCTIAATG AGCAAGGGAA TCATICAACT	360
	CATACTICIC TCIGCCTTIG CGCGAGCTAA TTACGIGGAG CCCTTCAAAT CAAATCCATA	420
50	CATTOCTTOC TCAGAGOCAA GCCATTGCCC AAAGGAATGG CCATGCTGCT COCAATATGG	480
	ACAATGOGGG AGTGGGCCGC TATGCATTAG TGGCTGCAAC CCAAAATTCT CGCATAGCCC	540
55	TGAGAGCIGC GIGCCAGTGC COOCGCTACT ACCGCAATTG GAGATAGTGG CCAGCGATGA	600

	TAAAGGAGTA TACCIAGAGA TGTCGGGTCA CCCTGCCTTG GTCACAAAGT TCCAGCGCAA	660
5	GASCITUSSUG CAGITIGITIGG AGGIACATCA CGAGGAACAG CAGIATOGIG TGITUGGCAIT	720
	AGAGCAGGAC	730
10	(2) INFORMATION FOR SEQ ID NO:640:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 719 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG143OUP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:	
	GATOGATTIG GITACCITGT TGTCCAACOC ACGTACTTCA ACACATTCCG ACGCACAGTT	60
35	GTAGACAGOG TACCTATTOC GAGCGACAAA AGTOCCAAAG CTTCCCTTAT CCTCAACTAT	120
	ATTTGTGGCA TCAACAGCAC GGCTAGCCTG TTTTGGAAGC AGGCAAAGAG CATACCTATC	180
40	GOCATCOCTG CTACTTGAGT TCACGAGGAG AGAGTGTTGC GAGGGATTAT AAGAGATGGA	240
	CITICAACACG TTATATIGGCT TTCCAAAGTT TTTTAGAGAA ACAAATIGGCA GAGACGACAC	300
45	CITCITITCA TAGTCAAACA TITGGACCIG CITCICTITIG TIGACAAAGI AAAGCIGGIT	360
	CTOGETICACA GOCACAGGIG GICTICTICACG GTOCAGTITTA AAGACCATGA TACCOGAGTIC	420
50	ATGCGCCGCG CCAAAGAGGT TCACATTAGG GTGCGCCCTA ATCCGACCAGA ATCTGTCCTG	480
	TICICITTIG AACIGITTIA CAGGAGTOCG CITGICTAGA TOCCAGACCC TAATOSTAGA	540
55	ATCCTCCCCC ACAGAGATAA TTACGTTTTC AAATCCCTCA AATATTACAC TGTCCACGTT	600

	GITTOGIATGA COCTOCACTIT GTOCCACCITOC CACOCTITTIGG TGCAGCTICAT ACGOCCACAAC	660
5	TTGACCTGTC TGTCTTCAGA ACCOGAGACA ATCAAGOGCA GAATCOGATG GAACGAAGG	719
	(2) INFORMATION FOR SEQ ID NO:641:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 730 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1431RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:	
30	GATCATGTTA TACAGACCTT CAAAGTTGAT ACCAAAACCC TCAATGGACT COCTGACCAT	60
	ACTIGGIACT TOOTGITTAG AGGCCCTGCG GCACACTTAC TGCCTCTACA AGAAAAAACT	120
35	GUIOCCICIG AATTOCATCA COCTITUTOG GACACTAACC ATTUCCAATA CAATOCTATA	180
	TTGCCTCTAT CAATGGTCTA TTGACCTTGT TGAATCCAAG CTGGAAATCC AGCAATGTGT	240
40	ACAGATACTG CAGCATTTCG GTGAGAAATG GGTTTTTGCC AAGGAGTGTG CGGTGGTCTT	300
	TCAAAATATT GGAAATGCGA TACTAGATAT AAGTCTCTCC CGAGGACAGG TAGAAAACGT	360
45	TGATAAATIG ACTAGGGAGC TATITGGAGC TAGGAATGAA TAGCAAGATA TATIGGAGGA	420
	AAATAACOTA GATATATOCT GGATTGACCT GGCTATCTAA TTTCTGAAAC CATTGAGAAC	480
50	CIGITTAAAC TATTIGGCAG TAATICATAA TGTATIGGIT GTTCCATAGC TGAATIGCTA	540
	TIGOCCCTAT GCAGTICCTT ATCCAATACA COOCITAGIG GGICATIGIC GIGITCTTAT	600
55	ACCCADACTA ACCGADICOS GICTIANICS ACTOCOSTAS ACTITISICAT CONSTANÇÃO	660

	ATGICTTACA COCCCATTA ATGITTGTAA TCTTTAATCG ATGAATGAGA AATGGTATAT	720
5	GIATGIGACT	730
	(2) INFORMATION FOR SEQ ID NO:642:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1431UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:	
30	GATCTCCTGT ACCATCATGA AAGTCTTTTT ATCACGGGAA AACCGGTTTC TCAGGCACAT	60
	CTGACGCAGT GCTTGTCGCA CATCAAAGGT CAAGTTCCGA TCCCTTGTGA GCGCTTCCAA	120
<i>3</i> 5	CICCCAGAAC TOCITCIGCA GATTITITAC TOOCCCCCC ACAACTICIG CCIGOCICIG	180
	GOOCACATAT TICTITAACA CCICCTICGG AATCITAAAG TOCTICACAT TATAGOGACT	240
40	TACCACACT TOGANTANCA ACACCCACTT TATATATACG TITICACATAT CCACTITICAT	300
	CTCGCACCCC CGCACGATCA GGTCCCCGGTA GTCCAAGTGC GCCTTTCTTC TIGAATTCGT	360
45	AGASCICOCC CCCCAGGATG ACCCICOCTG ATCAGAGGTG CCTGTCTTCA GCGAGAGCTG	420
	TESCATACTO SECTETETES CAASCTOCAC CTTCACCTEC TTESCAAAGT TCACATTTAG	480
50	OCCUTOCOCA AACOCOTOCA GTOCACCCAA CATATOCTTC ACCACCTOCA GTOCCATOCC	540
	CATCTTGTTC ACGTCCAGTG ACACGTTCCC TTGGCCTAGC TGGTGCACTA GGGCCGCCCT	600
55	CIGIGIGAGT TGTCGCTGCC ACACAGAGTC CAATTCCACT CGCATCATGC GCATCGCGTG	660

	CITCARCICA COCTCACTIGA TOTOCOCTOS CTCAGOCATO TIGIOGRAGOCT CTTOTOGOCT	720
5	TC	722
	(2) INFORMATION FOR SEQ ID NO:643:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genemic)	
20	(vi) ORIGINAL SOURCE:	
	(A) CRCANISM: PAG1432RP	
25	(vi) SECULARE DECEMBERS ON A STATE OF	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:	
30	GATICCAGGAC TGCCGTGCTT GGTTGCGCTC AAGGGAGACT TAGAAATGAG GTGTTGGGCCC	60
	GCATTCTGCG CTGCAGATAG AAACGAAGAC AAGATGCCAC CGTTACCCAA TTCCTCAGCC	120
35	CCAGAGAAAA AATTCCCCGTA CCGGTGCTTC CCAGTACCAT CCTGGTCAAA GGGTGTCATA	180
	TOOGAAAATT TATOOTOAGT GTOOTOOTTG TATOOTGCAT COGAGGGGT GOTTTGGGCC	240
40	GCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCCCCCCC	300
	ATTIGGCATICC TIGAGOGACIGA OGRAFITIGOTIG TIGGCCCCCCCC TIATIGCCAGCT GCCGCCGTCC	360
45	CCCCCACCCC ACCCCACCCC GACCCACCAC TITICIOCTET TOCCGIAAAC CACCCCTOCC	420
	GACATGAGCC ACCAPTICTICS TOCTGACACC CCCCTCTCCA CATCCGAGCC CTCCCCCGCC	480
50	GCCACCTCGA CATCACCCGC CTCCGGCCCC GTCCGCCGCT CCCCATTCCG CGTCGCTACC	540
	CGICTITIEG CACIGCTCOC CCCCCCTTC CCCCCCCTATG CTTCTTGAAA	600
55	AGTGCCGGGC GCTCTCTCTG AGCGACCGCG ACCGCTTCCGG CTCCTCTGCC ATCCTTGCTA	660

	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	720
5	AACA	724
	(2) INFORMATION FOR SEQ ID NO:644:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 615 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGI432UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:	
30	GATCCCGGIC COCCGCTCCT CCTCGAACAT GICCTGTACC CCGCGCAGCG CCTGGAACAT	60
	CCCCCCCACCCTACT CCCCCCCCAAA GAACTGTGTG TOCACCAGCT GTTCGTGCCG	120
35	COCCIOGRACIC GEOGGECCICA TATTETECCIC CICCIOGRAA GOCTOCROCI GEAGAGACTE	180
	CCCCAACTIC TOGTOGTCGT ACTOCCCCCC CGCCCCCCCG CTTGCAGGCC CACTGCGTGC	240
40	GOCASCOTISC GIGTOGCCSC CGTGCTCGAA GIACAGCGAG AFTGCCGITT CCACGTCGCC	300
	ACCIGCCATA TOCAGGAACT GOCGCGCCAG CICCGGGTCG GOCACACGCC ACATGCTTIG	360
45	GAATACGCCG AGCTGCTTGT CTGAACTCAT GCTCCTACTT TCTGGCGCTG CCGTGCTGTG	420
	TOGCACACTC AGGAGTITIGT CTGACGTTGT COCTGGCTCC AGGCTTTTAT ACCGGCGCGT	480
50	OCCACACATG COCCOCCCC ANACOCTTAT ACATATACAT OCTACTTAGT CCGCCGCTTG	540
	GTCACCCGCC CGTCCTCGAA GCGCGTGTGC GTGCCCTGGA AGTGCACCGG CTCATCGCCG	600
55	COCCOCTOCOG COCCG	615

(2) INFORMATION FOR SEQ ID NO:645:

5	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGIH: 688 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
- <i>-</i>	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1433RP	
	(iv) ordered. Marketsia	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:	
25	GATCGATGCE GACCACCETC COGAGCAGCC CGCAGGTGGA TATGCAGTTT GCGGCGCTGA	60
	GCGCGCCAT TTCCAGAGCT CGCCGCTCCG CTGGCGTGCC CGCTTCGCCC AGCCACGGAA	120
30	CCASCIGACE CCASCIGICI COCCOCCOCI TECCCATITE COCCACACIGE CICECCOCCI	180
	GGTAGTTCTG TAGCCCACGC GGCCCGTTAA TCTCGGCCCAT TACGTAGCCG AGCATCTGCA	240
35	CGAGCAGCGG CGACTCGCGC ATCTTCTGTA THTTGAGCAG CTCGCGCTCG ACCTTCTCGT	300
	CTGGGTGCGC CATGTCCGCC CCCAGCCGGT ACTGTTCCTG CAGTCCAGCG TCTGTCACGT	360
40	ACCGRECTAT TRECCCCICG TREASCACTE CGREATICTE AGCCACCGGE ARTICCCAGGA	420
	OCTIOCATAT TOCCCOCCOT TICIGIAGGA GAACGIGGIA OCCCOGGAIG ACCITACGIG	480
45	CTTTOCATOS TETCATTOCC GOCGIATGIT TCACGOCGCT CTTCCCCGTA ATGCTTCTTC	540
	GCITCCIGGC CAGCAIGIAT GAAAGTTAAA COGCAGTTAC TACIGGIACT AGATATGCCC	600
50	TCGGAATGCC ACCCGATGAC CTGCTGGTGT ACCTTGCTTT TGTCATCACG ATGCTTCGAG	660
	CTGAATCGIT GAAGAATTIC GAGIGAAA	688
55	(2) INFORMATION FOR SEQ ID NO:646:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 712 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1433UP	
15		
20	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:646:	
	GATCACOGAA GAAGOCAAGG TCAAGAAGGT TACATTIGAT ATCGAGCCGT ACAAGCCCAT	60
25	CAACACTAAG CTATACAAGT GTGACAATAA GTTCCCGACG GAGGTGCTCT CCCAGCTGCT	120
	GCACCOTICAC GACAAGITICG GGITICATTIGT GATGCATGGT CAGGGGTGTC TTTTTCGGTAT	180
30	GITGTCCGGT AACACCCGGA CTGTTCTACA AAAGTTCACT GTGGACTTGC CGAACAAGCA	240
	COSTAGAGGI GGTCAATCCG CGGTGCGTTT CGCCCGTTTG AGAGAGGAGA AGAGACACAA	300
35	CTATGIGOGC AAGGICGCIG AGGIGGCAGI GCAGAACTIC ATCACAAAGG ACAAAGITAA	360
	TGITAAGGGG CTAATTTTGG CTGGTTCTGC GGACTTCAAG ACGGACTTGG CCAAGTCTGA	420
40	ACTOTTICAC CTCACCITICG CACCCAACAT TOTCAACATT GTACATGTAT COTACCCTAC	480
	TGAAAATGGT TTCAACCAGG CTATTGAGCT GTCCGCCCAG GCGCTGGCCCA ACGITAAGTT	540
45	CATTCAGGAG AAGAAGITOC TCACOGAGIA CTTTGATGAA ATTTCCCAGG ATTCCCCAA	600
	ATTOTOCIAC GETETTGACE ATACTOTGAA ACCOCTAGAT TEGGTECCGET GGAGAAATTG	660
50	ATTGTGTTTG AAAATCTAGA GATTGTTCCG GTACGTGTT AAGACTTCTG AA	712
	(2) INFORMATION FOR SEQ ID NO:647:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 716 base pairs

	(B) TYPE: mucleic acid	
_	(C) STRANDELNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1434RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:	
20	CATCACATOC TICTOTOGIC CTACACAACA CTOCTATICT TAACCCTTCG TCAACGAATA	60
	TAGOCCEAGGA CGAGTITIGIC GATOCCATAG COCAACCTOC ATCCGCCGTCC GTOCATACTA	120
25	COCCTIATET CACCOCOCC COCCATTATT CCTCOGAAGA CACCOCOCAA CCTTCTCAAC	180
	CTACAATAAC GGAATACAAA ACTGCAATIG AATCACCATC CACCTTTGGC GACGATAACG	240
30	AGAGTGTATT TOTTGTAACT TOTGCGGACC TGCATCCATC GGTGTCCTCT GCGAGTCAAA	300
	CATTAACAAC GCAAGAGCTT CAAGCCGTTG CGAACAGCCA CCAATATAAG ACCGAGGTGC	360
35	AGATTGTAAA ACAAGACGAA GATGAAGTAG AGGATGTTCT AGAATTGGAC TCCCCACCAG	420
	CATCICIGIA TCATCCICAT CITTICAACC ACCCACACAA AAATCATACT ACCAATCITA	480
40	TTCCTGATGA TTCCATAGAT ATCGATGAAT ACCTCGATGA AAACTTCGTT AAAAACTTCA	540
	CATTOCAAAA COCTCTTTCT TTACATCAAA TCTTCCACCA TCATAATGTA GTTTTTCCAC	600
45	AAGAGAAGCT OCTTGTGGAT CCAGACCTAG AATTCCCCGGA ATTAACTGGA ATGGAACAAG	660
	ATATEGAATC TCACTATCIG OCOCTGATTG AAAATGGTAC GCAGGCTGTT CTACAA	716
50	(2) INFORMATION FOR SEQ ID NO:648:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGIH: 715 base pairs (B) TYPE: nucleic acid	

(C) STRANDETINESS: single

	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1434UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:	
	GATCAGGITT TCCCGTACGT GAGAACGIAT CTAAGGCACA AAGGCCITTG GGCGACTGTG	60
20	COGACOCTTG AGTTOCGACA TACAGGACAA AGCTGTTACG COGGCAACTG GTOCAGCACG	120
	homeonia areas and an area and an area and an area and ar	
	AGCAGCCGAG GAGCCATTCT GCGCGAAGCG ACGGTGAAIT CGAGCCAGCT GGTAGCAGGA	180
25	CICCOCCATC GICTATTIAS TICCCACCOG CGICCGAACA CCATGCACGT AAACGTICCC	240
	GTANCACCCC ACTOMOST CACCOCCATA ACTOCCATA	
	GTAACACGCG ACCCTGACGC GACGCCTGCT ACGCCCATAG CACGGCACGC CAAACGACGG	300
30	CAGCCGCTGT CGCCAGAGAT GTCTTCACCA CIGCGCGGTA GCAAGCTGCA GCGGGGGAAG	360
	CACACACTTG ACCCCCCTCC CCCTCCCCCC ACTCCCCACAC ACACCCTCCA CCACCTCCCC	400
	The state of the s	420
35	GOSCAGCTGG AGGGGGCTG CGAGCCAGGGG TGGGAGGGGA AGCGGGGGTA CTGGTATGGG	480
	GTOCTGATCG CCGTTCCGAT CCTACAGTCG CAGGAGGCCA ACCTGACCTG	540
40		340
40	ACCOSTOGAT CTOGTOCTTC TTCCCTTACT ACCOSCIGIG TGACGCGGG TGGCAGAACA	600
	GCATCCGCCA CAACTTIGTCG CTGAACCAAG CGTTTGTCAA GGGCGCCAAA TOCCTCGATG	660
45		
	GCAAGGGCCA CITCTIGGGAG ATCAAGGCAC TGTGAAGGGG CITCTICGGGG ATGGG	715
	(2) INFORMATION FOR SEQ ID NO:649:	
50		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 538 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genamic)	
5		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1435UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:	
15	GATCOGATOC TACCOGTOGC CCTGCCCAACC CGTTCGCCTA GCGTTGACGC CTAGGTCTGA	60
	AACTGAACAA CAGGTGGCAT TGTGGGGGGGG CCAGCAGGCC CTGGGGGGGAC CATGCCGCCA	120
20	TOOOCOGO ATAATACCAC CAGITGIGAA GCCCAGGIGI CIGIAATCIG CACCGAACAT	180
	CITTATCTAC CAAGGAGGAG CCTTGAAAAT TATATATCTA CCCCTCCCCC TAATATATTT	240
25	GACCAATTOG CTCTCCOGAA ACCGAATGAT CGAAGACOCC ATCAGGGCAG CGGACAGCAC	300
30	AGGAAGTGAG GAGTGATCTC GCAGGTACGA TOGAAGCACA GTCTATACAG TCTATTCGGT	360
55	CCAACCAAAG CGTACGGAGC ATCSCGAGCA CGAGCGGAAC CGCAGACGAG TCGCTAATCT	420
<i>35</i>	THEARCOCRE CETTERICAT CETTTECCCC CETERROCRE GCCARACCETT GCAGCCTETE	480
	TOGIGICICC CAGGCAGGGT CTCTGCACGC CGGGGTATCG GCGACTGGGG GCGCGTCT	538
	(2) INFORMATION FOR SEQ ID NO:650:	
40		
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: ENA (genomic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1436RP	
	100, The analysis Frank Andrew	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:	
5	GATCAACCIC GGAAACGIAT TIAAAAGCTT GIACICGACA ICATIAAGIC TICICCICGI	60
	TICCITIGGI AAAGIAIWAG CATCCAGTAA AGTAACAACG AAATGCAATG CTGAAAGATC	120
10	GTATACCCTA GACGACCTAA ATGOOGTATT TTGATCATCC ATACTAGCTT GAAGATCAAT	180
	GAAGTCAATA ATAGTGTTGA CAGACTCAGG GGAGAGTTTG GACTTGATGT ATTCCTCAAA	240
15	GCCAGICCAT CCCACCTICC TAGCACTAGG AGTAATCTTC AGCGATTCTT TAAACGGAAT	300
	ACTICICATA AAATOCICCA GCITTITITIC CICGIAAAGG ATCIGIACAA AATTACCAAG	360
20	CGGGGGGTA TCCTTGTTAA TTATGATTCT TCCAACTTCA ATGACCTTGT GGTTGGGGAT	420
	TITICTICATA ACCICACCAA ATACCATCOG AGATTITTICA AATACTIGGA CCATTAGAGT	480
25	GACCAATAGT TOGTTAATAA TOGCCTTATT TICAACCATA AGACTGAAAT GCTTCGTTTC	540
20	TGAGATCAAA GTCAAGGCCA AATATTCGGG AACAATATTG TAATCATCGA AGAAACAATC	600
30	ATGGAATAAT TOGAACATAG GACTGGAGCC AAACTCCTCT CTTGATAAGA ACAGTTCAAT	660
35	ATCGAGCTIC CATACCGATG TGAGATATAA CAAGGAGTIC TITGAGTITG GGAGTACTIT	720
33	AGACACTT	728
40	(2) INFORMATION FOR SEQ ID NO:651:	
,,,	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs	
45	(B) TYPE: nucleic acid	
43	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
5 0	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1436UP

	(MI) SEQUENCE DESCRIPTION: SEQ ID NO:651:	
5	GATOCAGAAG ATTATOCGAC AATATTAGTG ATATCAAGGC ACAGATOGCT GOCAACACTA	60
	GAGGIATTCA ATTECTTAAC CAACTEGITG ACGITTICEG TCTAGEGACT GITACAAGGI	120
10	ACATOGACOC AATTCAOGAA AATOCAGCTC TTACTGTAAA GAATGTCTTG OGAAAGATTA	180
	CCAACCATTT TGCCAAAACC GICIATTGGG CCCAGGATTA TATGGATGAT GCCICIGITA	240
15	TAAAACTTAG GGTGGAGCTA AATGCTAAGG AAGATAAGTA TATTITTGAT TITTACOGGGA	300
	CITCICCACA GEICCACGET AACCICAATG CACCIGITGC TATTACCAAC TCTGCCATCT	360
?0	TATACIGCTT ACGITGITT GTAGACGAAG AGATTCCGCT CAACCAGGGC TGCCTAAAGC	420
	CCATTACTGT TATTATTCCA GAGAGCTCTA TCCTATGGCC GACCAAGGGT GTCGCGGTAG	480
25	TOGGAGGIAA TGICAIGACG TCTCAGOGTG TAACTGACGT AATTCTCAAA ACTTTTAAAG	540
	TCATGOCCEA CTCCCAAGGA GACTGCAATA ACTITIACTIT TGGCACAGGI GGGAAGGACG	600
30	CHICHACCOG TGAATATACT CAGGSHTTIG GATATTATGA AACCATATGT GGCGGCATG	660
	GIBCAGGIGG AGATCATGGC GIGGICCGGG GIGGCATGCA ACACATGCIG TIC	713
35	(2) INFORMATION FOR SEQ ID NO:652:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 587 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genemic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1437RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

55

	GATCUCUCUC CAUCTATCOC TTCCOCCOGT CAAOCTOCAC TGTAGTATOC TCCCOCACCA	60
5	COCCATCAAG GCCGCCATCA AGGACTACCG CAGCAAGCGC AAGGCGACCG AGCTGCGCTG	120
	AGCGCAGGCC GCCGCAGCCT GTCGGCGGCCC GGCCGGCGCC AGCCGCAGAG GGACGTCCGC	180
10	GOGCCGGCGA GAGCCGCCCG TTTTCTATGT AGCGACTCKA GCATCTAATA GACATGGTAA	240
	TAGCTICTCG TITTCTACGT TTGCACACAG TATACAAAAT TTTCACGCAG CTCATCGCCA	300
15	CITICCACTIC CICAACCOCA GGIACCECAC CAAGACCICG GCIATGICCI CGACTCICIT	360
	TGACCACATC TTCACGATCC AGGAAGIGGA CCAGGGACGG TACAATAAGG TATCGCGGAT	420
20	TGAGGCCATC TCCACGTCGC AGGACACGTG CAAGCTGACG CTGGATGTGA ACACAGAGCT	480
	CTTCCCCCTG CAACCACAAC AGCAGCTAAC GGTGATGCTG GCGACGACAC TCAACCTCGA	540
25	COCAMOGRAE CACACCOACE CETECTICACE COCTICACEC COTICACE	587
	(2) INFORMATION FOR SEQ ID NO:653:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 260 base pairs	
	(B) TYPE: rucleic acid	
	(C) STRANDELNESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1437UP	
4 5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:	
50	GATCCOCCOG GACCOCTACA ATATTCCCAT ATGTATTAYA GOCAACTITA TACCCATCTC	60
	CTAAGTOCAG TACGTACTGT TIGICAGTCT AGOGTCIOOC TCGCGGTGAG CCCCGTGTTG	120
55	000000000 000000000	180

	CONTROLLE CONTROLLE AND TO AND TO THE CONTROLLE CONTROLL	240
5	AACTTCTCCA CGGCCACGTC	260
	(2) INFORMATION FOR SEQ ID NO:654:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1438RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:	
30	CATCTCTTT TAACGSCTGT TACCAATAAC GATACCGCAG CTACATCTGG AGAATAGTCT	60
30	SCATCOCATG CCTCCAAGTT CCTGTGAACA TACTCCTGGG GATGGACCTC GAAGCTGTCC	120
35	AAGGICTCTT COCTAGGACA AAGAAGCGGG AAGATAACAT GTTCCAAAAT GGTTGCATAA	180
	TGTGGGTCAA CTATCGCCCA AGTAGACTTT TGCACCACTG TTTGTTCAAT GAACTCCAAT	240
40	AUGTAATATA GOGACTOOTT GOTTAACCAC AATTOOCCTG CACCOCACCT TTCAATCTOC	300
•	TOGAAATGCA ACTOCAATAG TTGCGGCAGA AACTGCTCCA CATACAGCAT TTTAAATTCA	360
45	GIGIACICAA ACIITITIGCT GAGAGATTCI GAGGCATAAC GITGGAATAA TOGATACATG	420
	TEAGCATATG COCACTETET GOCTCTGACC CATGGATGCG CCCGCCTATC ATGGACCGCC	480
50	AGCGCCATCA CATGCTCCGG CAGCTGGCTT TGTATCACAG AAACATGGAA GTTGGCCCAC	540
	GEANTGAAGT TITCCGACCG TIGGAGAGIG AACGGCAGGT CATTATATGT CACAAACTIG	600
55	TAGATOTICA GCACAAGOTT CAACATATIC COCACGATOT CGITGIGOTT TOCTOGOTGT	660

	ACAAAAGCGC GPTTGCGTAG TGCAGCAAGT CTGGGAAATA TCTCATGATC AGCATCTCCA	720
5	CCTCCTCA	728
	(2) INFORMATION FOR SEQ ID NO:655:	
10	(i) SEQUENCE CHARACTERISTICS:	
,,,	(A) LENGTH: 774 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1438UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:	
	GATICOGICAAA CCTAATOCGT CTGGACGTAA TGTAATCCAA CAGCGACTGT AGAGCTGCCT	60
30	GOOGTTCTCC GACAGAAATC AGCTCATCTG COCGCTTCAA GGOGTTTTCA GGGOGCAAAA	120
	CAGGIGGAGC CATGCTGAAT TAGAGCTATT TGGTGACCTG TTTGAGIAGT GTGGACTTCC	180
35	TITICAATIGIG GICAACTITIG AAGTAGGITIA TICAACTAGA AAATTITITCA CCCAGAAGGA	240
	TOCCCTICTIAT CAGCOCCCCT GTCTGACGAT GATCTCAACC GCGTAAAGGA CGAGAAGTCG	300
40	TAGGICGAGI CTAATCTACT ATTGGTACTG ATGAACGGGA CTGGCCAGCT AACGTGAAGG	360
	CACTIGTOTOC GOGATGAGOC COCAGOGOCA GOGCACGGGC COTGOGATGA GCACAGGTTG	420
45	CCTCCACACG ATTCCCATCG CCTCACCCCA ACCCACGUTT CCACACCCTT CCCCACTCC	480
	CETCETCAGE CTGGAACTET AGAAGGETTG TCTTGAGCTC CGCGCACGCC GCACGCTGCC	540
50	CARGUARCUS GOOGGOCCEUS TUCAUTOGOCC ACAGOGGUGG GCUCOCUGUC ACGUGGCAUC	600
	GAATATGTCA CGTCATTACA COCAGCAGOG CATCGCAGAC AATGCGCAAG CAGCAACAGG	660
55		

	CTGTGCAGC TGGCTCCCCA	720
5	TOTOTOGGIT TACTOGIACO TGTGCGCTTA TATAGGCATT GCCAAAAGGI TTCC	774
	(2) INFORMATION FOR SEQ ID NO:656:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDELNESS: single	
,3	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1439RP	
25		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:	
30	GATCCIGITG GACGICITGC AAAGTCGTCG TCACCCCGAC CAACITCTCC TCTGIAATAC	60
	COCTOTACTT COTTAAGTAG TOCACAATGG CCTCATCTGG CTTGACAAAC TTGTCATAAA	120
<i>35</i>	CTAAGITACA ATCAAAATOG ACGACOCTCA CACOCGICAA CACGIATOCG TITTITIGAAA	180
	GOCACATCTC ACAGTOCATG GCAAACGTGT GAGAACCGTC GTGTTGCAAA CTCACAGTGT	240
40	CCACCCACCC ACTGIACTIC TOCTTATTCT GATACTTTAG CAACAAAGCC TTTTGGTACT	300
	CCTCCCATAA GCCAGGIGIG TITIACATGGA TGGGGIACTC ATTATGCAAT AAGTCATCAA	360
4 5	COGICATTAG CAAATCAAGC AAAGIGATTT CCTTTTIGIT CAATIGTTCC ACCTTIGCGA	420
	TOTTOTOCTT TITTGACAAG COTACATTGA CAAAAGAATT GTATOCAGAA AATAGGGAAT	480
50	TOTTICATION COSCOCIGAT AACOSCAAGA TACACATTIG CTIOCACATO TOTTICATTIT	540
	CACTAATOGA GITTAGATGI GOGICTIGCA ATTICOGGAAT ATTITIATGA AACAATGAAT	600
55	CCTTCGGTAG ACTGAAGICC TCGGGTAAAA GGCCTGGAGT GAATAAGACG ACCACCTTCT	660

	TCAAAGAGGC CTATTTTCTA TCGTAATCCA GTTGGCAAGAG TTGTTGGTAT CGTGGAATAT	720
5	GTACTOGA	728
	(2) INFORMATION FOR SEQ ID NO:657:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 694 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1440RP	
0.5		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:	
30	GATCTATTCT TCATTCAGCA ATCAACAAGA GCTGGTGAAA CTTGGGCAAG AAGCTGAGCA	60
	AAGCGGTAAA TACAACTTGG CATTCAATGC ATACTGGATT GCAGGAGATA TCAACAAGGC	120
35	CACCCACGIG CITTOGAAGA GOGGACGOCA THOOGAGOCT GIGCTICIGG CATCCACATA	180
	CACCTCAGAC AATGACGCCA TCAACGCTGC TGTIAGAAAAA TGGAAGGAAC AACTGAACTC	240
40	AGCIGGAAGA GIATCIATOG CAGAAAGAAT TATACTTTOC GGAGAAGACG ACTTOCCIGC	300
	ACCIOCOCAG ACTITOGICG AAATGGATGA COGATCAGAG TOOGOGICTA AATAAACTAT	360
45	AATTITAAAG ATAACAGCAG GAATAAATTA ATTACCACGA AGGAAATTIG TATGTACATT	420
	CTAACTAGAC CCAATGGTAG AATTICATTG CGLAAACACG GCAACCITAT CAATATCTTT	480
50	COGNITICIOC AGICCCACAA AGIAAAGITC TITICGATTCA GATOGOCATG CTTCCGOCTT	540
	AAAACGCCGC ACTITGGTGA ATACCTTTCG CAGACGCCGT TCTAATAGCT GGTCTTCCTT	600
55	OCCAGIGIAT AACTIOCAAA OCAATGAGOO ACCGGGOOTIC AACAATGCAA TIGCACATAG	660

	CAGTOCTOCG TTCACACAAG TCCATCGACA TGTA	694
5	(2) INFORMATION FOR SEQ ID NO:658:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1440UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:	
	GATOCTIACAG AAATAATOCA GTACAAOGTA OCTOTAATOT ACTGTGTTAA CATOGAAAAC	60
30	ATTTOGOCTT TAGOCTTTTT CTTTTCACCG AAAAGGTAAC GTGTTUGAAA CATATATCAC	120
	GESTIOGAAA CIGACTAAGG TIOCICATOC CTAAACCAGA TAGOCAGCAA TGGCAAGGGG	180
35	CTTGAGGTGG TACCAGAAAA GCTGCCACCT CCTGCTGCGT GCTTACTCTC GCAAACGGTG	240
	TATACTATTA GIGITOGAGI ATTTATTOCT TATTAAATAA OOGAATIGIG GOCCIAGAAG	300
40	TOGOCATTAT CACTGAGCAG CAGCGGCTGG CAGCGCAGAC TOCTCGGGAA GCCGAGCAG	360
	TOCCTTICAG OCACCCITTA CACCTOCACC COTCACCATC AAACCCTCCC COCCCACCAC	420
45	GAGTATGAGG GCTAGCTCGA GCCCCATCAA GAGCTTCTTC GATATOCCGC AGACCTTGCT	480
	CAAATACTOG TOOCAGTOCA COGTICTCTIC CACAATCTTG GTTGAGACAC GTATCAAGOC	540
50	CACTATGAAG CGATGCACAT ACCTCTCGGC GATGGGGCCAG CGGATCTGCA CCGGACCGGT	600
	TTCCGAAGGA GECCATTTTA GCGTGAGGCG GAGTAACAAG CAGCCCGCGG TCTGGTAGAC	660
55	TATOGOGOCA AACATOCATT TOGOGTITGAT GCCGTCTAGG TACTGCGTAT AC	712

(2) INFORMATION FOR SEQ ID NO:659:

5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1441RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:	
	GATCETTAAT TETACCAACC CACCACCACA CATGETCTAC CAAGGCCGTC TACCACACAC	60
25	CACGCAAGCA GTCOGTCCCC AGGAGCAAGC CCCCCAGGAC AGACCACAAG CACACTTCCC	120
	COSTCTICACO AAGOCCOCTICA CTACCOCCATIC CTTAGAGOCA ATOCTTATICC CCAAGITTACG	180
30	GATCIATTIT GCCGACITCC CITATCTACA TIATTCTATC AACTAGAGGC TGTTCACCIT	240
95	GCACACCIGC IGCOGITATC ACTACCACCT GCCATGAAAA CTATICCTIC CIGIGGATTT	300
35	TCAAGGGCCG TCGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	360
10	ACCCCATCTC COGATAAACC AATTCCCCCCC TGATAACCTC TTAAGAAGAA AAGATAACTC	420
40	CTCCCAGGCC TCACGCCGAC GTCTGCACAC TCAGTTAGGT TGCCGTGAAG AATCCATATC	480
45	CAGGITICCGG AATAITAACC GGATTCCCIT TCGATGGTGG CCTGGAAAAT CAGGCCTTTG	540
45	AAACGGACTT CCCCATCTCT TAGGATCCAC TAACCCACGT CCAACTGCTG TTGACGTGGA	600
50	ACCITICCCC ACTICAGICT TCAAAGITCT CATITICAATA TITICCTACTA CCACCAAGAT	660
, u	CTGCACTAGA GGCCGITCGA CCCAGCTITA CAGCCTAGGG CTTCGTCACT GA	712
	(2) INFORMATION FOR SEQ ID NO:660:	
55		

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 718 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original source:	
	(A) ORGANISM: PAG1441UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:	
20	GATCCAACCG AACCTITCCT TCTGGCTAAC CTAGGGTACT TGTACTCTAG GCGAACCAGG	60
25	ACTITIACIT TGAAAAAATI AGAGIGITCA AAGCAGGGC AAGCIGGAAT ATATTAGCAT	120
	GGAATAATGG AATAGGACGI TIGGITCIAT TITGITGGIT TCTAGGACCA TOGIAATCAT	180
20	TAATAGGGAC GGTCGGGGC ATCAGTATTC AATTIGTCAGA GGTCAAATTC TTGGATTTAT	240
3 0	TGAAGACTAA CTACTGCGAA AGCATTTGCC AAGGACGTTT TCATTAATCA AGAACGAAAG	300
	TTAGGGGATC GAAGATGATC AGATACOGTC GTAGTCTTAA CCATAAACTA TOCCGACTAG	360
35	GGATCGGGIG GIGITITICIT ATGACCCACT CGGCACCITA CGAAAAATCA AAGICTITIGG	420
	GITCT00000 GAGTATOGTC OCAAGOCTGA AACTTAAAGG AATTGACGGA AGOOCACCAC	480
40	CAGGAGTOGA GOCTOCOGOT TAATTTGACT CAACACOGOG AAACTCACCA GGTOCAGACA	540
	CAATAAGGAT TGACAGATTG AGAGCTCTTT CITGATTTTG TGGGTGGTGG TGCATGGCCG	600
45	TICTUAGNIG GIOGAGIGAT TIGICIOCUT AATTOCGATA ACGAACGAGA CCITIAACCIA	660
	CTAAATAGTG CTGCTAGCAT TTGCTGGTTG CGCACTTCTT AGAAGGACTA TCGGTTTC	718
50	(2) INFORMATION FOR SEQ ID NO:661:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 722 base pairs	

5	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1442RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:	
	GATCAATTOC GICTTCATCC GATGAGACAT TTTGAAAATT GITGGAATAT TOOGCAACAT	60
20	CASSISTATES TAACACCICC SITICTAAAC TICTAATOSS TASSCICSTC SCOSSISTAA	120
	COCATOGATO ATCAATOGAC OGTOCTOGOG GOGATOTAGA CACOCCCGAA TIGGOGCTTG	180
25	GIGICAGGIT TICGICCOGA CITCICACTI TATCAGGIAT CACIATCACT TGATGAITCA	240
	TTAGATTCCC TGTATCCACA ACATCGACGT GOCTTTGGTG TTCCGAGATA AATAGTAGGT	300
30	CATCAAACGA GEGGETAAAC TIGCACACCC TAAAGGACCC GTTCTGTGCA TGTCTTCGAG	360
	TIGAAGGIAT CICCOCAAGA GOOGIGICCA TITTITCICAT AICGIACACC AGACAGAGGE	420
35	OSTITIOGAA TATOGIAGOC ATGIOCACOT OSTITIOOCT ATACCTIGIG TAAAAGCCGT	480
	TATUACCACO AGGOGAATOG TAAATACGAT CTAGGACTTC GGATCTATOG ACCGOGGCAT	540
40	ACCTIGGAAC GCACTITIGIG COCGACCATT TIGAACCCCA CTCAGGAGCG GCGTCATATT	600
45	GTAATGAAAA ACAACCGCTT AGFTCATCTG TCTATAGACC GCAAACTTGC TGGAATCTCC	660
45	CGAAACCACC ATCGTCTTCC CATCGTGTGA TATTGCCGAG CAGTTTAAAG CAAATTTTAA	720
50	GT	722
30	(2) INFORMATION FOR SEQ ID NO:662:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

55

(B) TYPE: nucleic acid

	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1442UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:	
20	CATCAACCCT COCCAACTICS COTTCACTCC CITCCCCTCC CCACCCTCTC TGTTCCCCCCT	60
	CHICCOCCT CIGHICCOCC CCHICCOCC ICHTHICHIC TCICICIOGI COCCACACIT	120
25	AGGAGCAAAG GACTOGGTGC CATCAAACTC TAGGAACTGC TTGGCCTTCA AGTGCTTCGT	180
	CITICACGITIC TICACCITICG TACOCITCCAT CAACACCITOC TOCTTCTTAA CCAACAACTC	240
<i>30</i>	ACCETOGICE AACTICIOCA COTTICIOSC GACAGOGOCC TIGITICAGGI COCAGITICIG	300
	CTOCTOCAME TACOCCTCCA AGGIGACGOC MOCTOCAGTIG GOCTOCTOCT CCTOGGCAGC	360
<i>35</i>	GTCGOCCGCC AACTCCGCCT CGGCAACAGC GGCACCAGCC TCCTCATCGG CCTGCTCCTT	420
	CTOSTIGIOS CCCCACOCCI OCTIGATOTI CITOSCAGAS TOASTOTICO COGNICIOGA	480
40	GTGGCGCTCA AAGGICTITIC TGCTGTCCTT GGCTGGCCTTG CCTGGCGCAA GAGGGTCCTT	540
	GCACTIGITC TOCCAACOOC COOCCIGCTT GICTCICAAC GCACCCIGGT TOCCGGTTGG	600
4 5	CTTTGGTCTG TTGTTCTTGG CACGCCATGG GTCGGCACAT GGAGCACGCA CGTCCGCCTT	660
	CITIGGAAGAG GTOGTCITICT TCACAAGCTC CTTTOGAGGA GACACAACAA COGTGOCGTC	720
50	(2) INFORMATION FOR SEQ ID NO:663:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGIH: 716 base pairs (B) TYPE: mucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1443RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:	
	CATCTATGCG GTGCTGTGCG CGTGCATGCA CCAGCACAAG AGCTTGGAAT TOGATAGCGG	60
20	CASCITICITO TITICAGIAGG TOCAAGGCAT CITACTOGIAC AGGACTGOGA GOCITICITIGO	120
	COCCUATICUE COCACCCACU COCTICCOCAC COCCACCCAG TACCCCAAGG TCTTOCTAGA	180
25	CCCCCCCCCCC TCCCCCACGIC ACCCCCCACGI CCTCCTCCTC CCCATACTIC CCCCATCCCCA	240
	COCCATOCAG COOCTAGTICC ACCAGTICCAA AACCAGTICGA CCCCTCACAT CTCCCAACCTT	300
30	CICOCTICIC ACAGAGIGOC TOGACATATA CCIGIOGIAT GIGAAOGATA COGITITOCT	360
	GGGGCCCAAG AGCAACTTCC COCTTGAAGA TCTCGTGGTG TTTTGCAACT TGGTGCGTGA	420
35	COCCATATOT CASSOTTIOC GIOCIGASCA TGATIATGAS GIGAACAAGA TGCGCCGCCC	480
	GCTCTCCTTA CTCCAAAAGC TGTATATTAG GCATAGAAGG ACCAATTTCC TCTCCGCGCC	540
40	CAACCOCCAC GACTICIOGG TCATTCCCGA TACCACGGIG AAAAACIGCG ACATTACATC	600
	TOTOCTTOTT TACTITICATE AGITOTACAS AGAACASITE CATTIGITOC TOCCOCASSE	660
45	COGRECTORS CACGARGETOC CARCERCORT CTOSTAGOST GREADAACGA TATAAA	71
	(2) INFORMATION FOR SEQ ID NO:664:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 711 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1443UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:	
	GATCCCCCAT TEACATCTCA CATCHAACCG CCTCCTTCTC TACCTACCCT CTTCAATGTA	
15	THE	60
	AACTOGTOOC AGTTOGAAGT TOGOGTAGTA CTAAATTOGA ACCOCOGTOG COGTOGTAGA	120
		120
20	AGATGGCCAT CGIGAAGGIG TICCACAAAA CIATICGIIT CACCCIGGGA TACIICAICT	180
20		
	TCATAACTGC TTTCTAACAA TACATCTCGG TCATAGTCTT CGTAGGCTGG TGGAGGCAGC	240
	TICATOCCOT TCAGCITTOC ATATCCCCAT TICTTTACGI TTGCTTCAAT GIAGACGAAT	
25	THE PROPERTY OF THE PROPERTY O	300
	CCGTAGGTCC CCAAATTAAC GTGTATCTTG CATGGGACAT TCGCACCAAC AATCGGGTAA	360
		300
<i>30</i>	AGATACTTAA TITTOCAGOC CITTATGTGG CCAOCAATGC GITTCTCATT TAACTTCTTG	420
	COMMITTEE MARKET	
	CCATTOCOCC TCAACAAAAC TGTOCCOCTC CCAGTTCTGT ACCCAATCCC GATGACGTCG	480
35	CCCTTTTCGC AGCCCCGAA TAGTCAAGAG AGTTCCTGCG GGAGCTTAAA CGAGTTGTTT	E 40
35	The state of the s	540
	AACCTACGIG CICCATTAGA GICATATOCA ACTGAGTGAT GGTGTCTGCC GGGAAGCCTA	600
40	AAATAGGGAT ACGGCCGATGT AGCAAGACCA AAGGAAACTA TITIGGITITIC TGAGAGATGG	660
	CTGACCGGGC GGCCAAGCCT GTCACAGAGT CGAAGATCIT GCACTCGAAG T	
	TOTAL STATE OF STATE	711
45	(2) INFORMATION FOR SEQ ID NO: 665:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 736 base pairs	
50	(B) TYPE: rucleic acid	
	(C) STRANDELNESS: single (D) TOPOLOGY: linear	
	12, 100 Secola . ALBREAL	
55	(ii) MOLECULE TYPE: DNA (genamic)	

(vi)	ORIGINAL	SOURCE:
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(A) ORGANISM: PAG1444RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

10 GATCTGGTTT TATAGGTTCA CGAAGGGACT CTGGACGCGG ACCCTGCTGA AGTGTGCCAA 60 CATCCTGTAC TTCGTGGCCG TGATGCATTT CTACGACGAC TACGAGCACG CGCCGGTACT 120 15 CAACAACAIT COCTACTOCA TOTTIATIOT CASCATTOSS ATGAATCAGG CACTGCATCA 180 CCCCCCCCCC CTATTCACCC CCCCACCCC CCCCCCCTCC TCCTCCCICCC CCTCCCACAC 240 20 ATTIGUEGE CAGCCOGCAC TATATATCAG CCAGTICUAC CUGCUGCUAC TGAATGUACA 300 GAACCCGAGC TITCATTCGA CGCCGAACCT TGACATAATT AATCGCACGG TGCTGGTGGC 360 25 CTACGIGCCC CTGCCGCTTC AGTGCTTTCG TCGGCAGCTG ACGAGCTAAG TCACTCGGGC 420 AGRAGOTIGOT COGTIGAGOTO GTIGTIGOTIATIG CIGTIGOGGOGT ATTOGTICAGO GGCATIGAACA 480 30 TETETTATET CTAAATAGEG TICTETAGET TGCTTAATCC TGGTTACCAC ACTGTCGAGC 540 GETATATICTIC OCTOCAAGGG ATOCAGCTICT GOGAAGGCTIC CAGCGGTOGA COCGTGCATA 600 35 COCACCATAC COTCOCTICCA GOCCATGGAT ATCCASCACC TCGCCCACAC TTCCCCCCCC 660 TECTGITCCC CCACCICGIT TETECCOCCC TCGCGCCATC TGAGAAGCGC ACGTCGTGCA 720 CITCGAGGC ACCCTC 736

(2) INFORMATION FOR SEQ ID NO:666:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55

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(ii) MOLECULE TYPE: DNA (genomic)

5	(A) ORGANISM: PAG1444UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:	
	CATCCAAATA CATCCGGTAT ATATGCTACT TGTGCCAGAA GACATGAAAA GCAAGCATCA	60
15	AGGGAGCTAA TGAGCATTCT ACAGGAAAAG GCGGAAGAAT ACTACGTTGA TGAACTCAAA	120
	CCTATCOCAG AGACTGAACT CTTGAGOGAC AAAGAAGATG AAGAAGAACT ATCTGTGGAA	180
20	GAGCAGGTOC AGAAAGAGCT AGAGCAATTG AAGAAAGGCA GTGGTCCTGT GGATACCAAA	240
	AAGAAACCGG TCCTGCAAGA GATTCAGTTG GCATGTGAAT GTATGGTCTT CATCAAGACT	300
25	AGNAGACCAN TCANGCCGGN ATOCTTTGTC NANCGCCTNG TACAGGNACT TOCNTCGTCN	360
	CAAAATACTA CCAAGGITTC GCGGTACGTC CAGAGATTGA CACCCATCAC TGATTCCTGC	420
30	AATOCTAGIC TAACAGAATT GGAAAAACTC TGCAGAAGGG TGCTTGCTCC TCATTTCCAT	480
	ACTGACAAAG AGATAAAGTA CAAGTTOGCG GIUGAGGTGG TAAAAAGGTAA CTTCAACAGG	54 0
35	ATAGACAAAA TOGATATCAT TAAACTTGTG GOGAAGGAGG TOGGTAAGAG TGGGGATTGG	600
	GOOCACTICTIC TOGACCITADA GEACTACGAC AAGCTGGTICA TOGTGCAGTIC CTATAAGAAC	660
40	AATATOGGCA TGTCTGTGGT GGACAAGGAT TACTCTGTGG CTCTTAAAA	709
	(2) INFORMATION FOR SEQ ID NO:667:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1445RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:	
10	GATCATCITC CGAACATACT CGAGGGASTT CGCGTTCGGG AAGTTCTTGT ATCGTTGCAT	60
	GIAGIGGAAT TOCTOGIAAT CGICIGIAAA TAGAAAATIG GOGICAATCA TGITGICCCC	120
15	GITGGACGCG CCCGAAATGA ACATGAACGG TGGCAGCCCG TAGCGCACCT TCTGGCCCCG	180
	GCACGCGCG AGAATCGCAT CGTTGGTGCG CAAAATATCG CTGTACGCGA CCGGCATCTT	240
20	CTCTTCTTCG ATGGGCTCCA ACACCGCCAT CTTCAACAAC TOGGGCCCAT AGCTCATCTC	300
	CATCTCCCGC GAGAGGAGAT TGTAGTGCGC CTGCGGGGGCC CGACTGGTGC CCGACTGCTC	360
25	CGAACGCAGC AACGTCGACG TGCTATTCAA GCTAGTGTTT GAAAAGTGCA CATGCTCGTC	420
	ATACCAGGAA CAGCIGAGCG CCATCICOGT CACGCTGAGA AGGTACTGTT CTTCCCGCGT	480
30	GTACAAAGAC CCCCCCTTGT ATGTCGAGCC TCTGGTGCAT TCCATTGGTG TCCCCATTGC	540
	TOTOGOGOGAS COTGATACAC TOGOCGTOGA AATACTACOG CACCACOGCA OGAACGACOT	600
35	TICCGCCATT CITTIGGITT ATAAAACCCC ACTACGCATA TATTICATCC TGCTCTGGCA	660
	TGTCCCGATG CCGTCCTCCG TGTGACATAG CTGCTTATTC ATCCTGGGCG TTCATTT	717
40	(2) INFORMATION FOR SEQ ID NO:668:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	

50

(ii) MOLECULE TYPE: DNA (genomic)

(C) STRANDEINESS: single (D) TOPOLOGY: linear

- (vi) ORIGINAL SOURCE:
- 55 (A) ORGANISM: PAG1445UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:	
5	GATCCTTACT GACGAGGAAG AATCGAGCAA TAAAGTTGAC GCCGCTTCGA GCTCTAATAG	60
	COSTAAGAGC ACCOCTAGTA AACGTCCAGC CAAAACTAGG AAGCCTAAGG CTGACACTGC	120
10	GOCTACGAAA AKCGGAACCA CCTCCCOGCAT GCCCAAGACT GCTGCTTTGC AGGCGCTGCT	180
15	GAACAAGAAA AGGGGGCTT CGGCAGAATA GACTACTGGT AAACGTAAGT AATAGTATAA	240
15	ACTIGGITT TRATCCCIC GCTATCTCAG ACTGCTAAAG CATGGCGTT TAGGIGIGGC	300
20	CICCICGGIA GAIGGITIGC ACCACGCAAG GIGAAAAAAA GAICACCAAC CCIGAAAAAAC	360
	GITTAACACT TGTCAATCTC TAAAGGCGCT GCAATCAAGG CATATTACCA TTGTGGAGCC	420
25	ATGAATCITG CCAATGAACC CAAGITICCAA ATACAAGITG ATGAAACAGA GGATACAGAG	480
	TOGAACGATA TITTIGAGGCA GCATGGTGTC ATCCCAGAAC GGCCACCTTC ACCCACGCA	540
30	CARCITOGAGG AAGOOCITOGA GGAAGITOCTA CNCAGACCAC ACGAGAATAG ATTAGAGAAC	600
	ANAGNOTOR TGANCTOCAG CACTOCANGA TGANGANGAT CATGANTTIT TGGAGTTITA	660
35	CCAACGIAAG AGAAIGECAG AAAIGCAGAA GCAACAAAGA AGCGCAAGIA IGGGGAC	717
	(2) INFORMATION FOR SEQ ID NO:669:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 775 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1446RP	

(xci)	SECUENCE	DESCRIPTION:	SEO	\mathbf{m}	NO:669:
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GATCTGCAGG	CTGCTACGGA	GGAACTCGTT	TOOGAGGITG	CTCGCCTGAG	TAAAGACCCA	60
AACTITCCTA	GCATTTTCGC	GCAGGAGCTA	CAGAACCTTA	CTGCTCAGCC	CCATATAGGC	120
GGCAAGGTGG	ATGATATAAC	OCTACTCATC	GIGAACETAG	ACTAGTAGAT	TGCACATATG	180
TAGAATTACT	AATATCATTC	GAATTTCTGG	CTTAAGACAA	TGTTCTTAAT	CCCCTCTCTC	240
TOGCTCTTCA	ATCICICCIC	CCCTTCTAGT	ACGTCATGAA	CAAACTTGAC	GLGGGLGGGC	300
AGGCATATOG	GGCGGAGTTG	AGTOCOCTTT	CCTGATTTGC	TGAGAAACGT	AAAGGGCACC	360
TTACCCGCTT	CGACTITITGA	TGACAGATTG	CTGTTGACCT	GIGIGCIGGI	CCCAGATCCA	420
ACGATAGGAA	TGITGITCAT	GGGGATTITC	TCATTCTTGC	GGCATTCTAA	AGATTGTTGC	480
ATCACAGCTT	GGTACATCTT	TTCCATTICA	TCTTCTGCTC	TCCGCTCCTC	CTCCGACTTT	540
ASCITICITY	OGTATTCTTC	GITTATCITT	TIGOGCICTA	GATCICIGIC	AATAGTAAAC	600
ACCICICICI	CGTCGTCAGT	ATCTTCTTCA	CITTCACIGC	TTGACGGGGA	ATCACTATCG	660
TOGICATOOT	CATOGITATO	TTCCTCTCAT	AAGTGCTATT	AACGICTICT	TOTTOTACCT	720
CCCTCGAGTC	GGCACTGTCT	CCACTACTAG	ACTOGTAGOC	ACTATOTTOG	TECTE	775
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(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genamic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1446UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

5	GATCAATTAC ACTACTAGCA ATCTACTTTT CAACAATCTG ACTGTCCCCG AGGTTAAACT	60
	CTACCGIGAA CAGCIGATGG TACICAAAGA GCAGAGGITT ATAGIGGAGG GCATGCIGCA	120
10	GAACGCCAAG AAACAGCGC GITTTGAAGA GGTTAATACG TTAAAGGAAA ATACCAAAGA	180
	OCTAGACAAT CAGATAGOOC AGCTOGAAGA AACOCTAGOC GACCAGOGIT TIGITIAGTA	240
15	TCTAGCATGG AGITTTTTGC TIAACIATAA TIACTGTGIA GATGCCGCAG ATAGCATGTC	300
	GTAGCATAAT TOCGAATTIT CACCAACATG AAAAAGTGTA TGTGTATAAG GCATCCAGTG	360
20	AACTOCTAAC ATGCTGATGA GGTTTTAAGT AAAGATATCA CTAGCAATGA ACGTAAGTGC	420
	AGTTTTIGAG CTTTATGTCC TCTGTAGAAC ATAATATTAA CGACAGGGG ATAGGATGAA	480
?5	AGAAGACAGO AGITATITGA OCTGAACAGT GAAGOCTOGT CTOGAATIGA TOCGTTCCCG	540
	AATAAAACCA GCAAGCTTCA CTCAAGCATC AAGAGAAACA CAGGGTTTAT CAAAAAAGCTG	600
3 <i>0</i>	AAACAGGGIA TCACGAAAGA CTCGAAAGAT C	631
	(2) INFORMATION FOR SEQ ID NO:671:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 703 base pairs (B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1447RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:	
5.5	CATOCAGGAT CATGAATTIG ACCAGGAGGAGG COGTOCAGAA GAGAATGACG ACTACTCACG	60

	GTTTAAAAGA TCCTGCATGT CCTCCCACGT CCCCGCGTTG TAGTAGGCAT AGCGCTCGTG	120
5	GUACOCCCG TOCGCCATGG CCCGCCCAT GOGCGCGGGC CCATGCGGCCC ACCCCGUGGC	180
	GTACATGTCG TACATCCGGC GCCGCGACGC GTCCGAAAGC AGCGCGTAGG CCTCGTTAAC	240
10	CASCITIGAAG COCCOCAGGC GITICGTOCTC ACCCAGGCCCC TGTTGGGCAG CCCCCGCCCT	300
	GICCOGGIGG TACASCITCG CCASCITCGIG GIACCGCITC TITASCIGCC GIGCATCGAC	360
15	OCCGGICTIC ACCAGICCCA GTACCTCGTA GGGCGTCGGC TGCTTGCCCT GGGGCCACGA	420
	TAGCCCCCCC TGCCACCOGG CGACGGTOCT AGOGCACGGC ACCGTACTCC GACCTGACGC	480
2 0	TGTAAGCGAG ACCGCCAACG TGCGCCAGTC CTGAGCAGTG CAGTCGGACG CGACAACATA	540
	ACACTTAAGC TOCTAGTTAA COCTTTOOCG ATOGAGATCT TGTCGGTOCA TOCACATATC	600
25	CARGACOCCE CTCCGCCTCC GCTCGACTGC TEGCCGTCCA GGCTCCAGTT GGCGCGCTTA	660
	OCCATATOGG CGAAAAAATA AAGICCIGCT CGAGGCGCGA TGA	703
30	(2) INFORMATION FOR SEQ ID NO:672:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGIH: 684 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1447UP	
45	(ii) Statistical Practical	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:	
	CATCCASCAG ACGCTCCCSC TGCCTGTTGG ACATGCACTG GCTCTTCGCG GCCCAGTGGC	60
55	GBCAACGCGC CCGCCGGCGC AGACGCGCCC GCCGCCGGCC CGTGCGGGTTA CATCCGGCACC	120

	ADDITIONAL GUICAMACIC CAMBOCCASC TIGHTICIGI TOTICHICOG CHTCGGCTIG	180
5	TACTIGIAGE COGGETACIT CITICGOSTICE TECTICCINCT CEAGTICOGE CITIGICGIGE	240
	CACTOCTTCT TCTCCTCCCC CGTCAGTTTT TTCCACTCCT AGCTGATGAT CTTGCTCACC	300
10	TOGOAGITOT OCCUCATORO CTOGOCOGAC TOCTTOCAGT AGICTOTOAG CAGCITOTOC	360
	TOSTOCCACC CCAACACCAT GAACCCCTTG CCCCCCCCCC CCATCTCCCT CTTCTCCCTTG	420
15	TAACCAGOOC GOOGGOCCG GOCTIOGCCGC CCTICGCCCTC CTICGTCCGCC ATCCTICGTICC	480
	OCTOUCACTC CTCGCCGCCG GGGGGCTGGT GCCAGAAAAA CTTCTGTGCCC AGAGGCCGCTG	540
20	CORCOCIONO OCTORCIOCO CORCIOCATO GONOCIC CORCUTORIO CORTIGUICA	600
	ANDSCAACAA TTGCCCCCCAT CTCCCCCCCCC TGCTGCCCCT GGTGTACGAT CCGTGTGATG	660
25	GTCAGCTTCT GCTCCAATCA CAGA	684
	(2) INFORMATION FOR SEQ ID NO: 673:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) Original source:	
	(A) ORGANISM: PAG1448RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:	
50	GATCCOCUAC GTATACAACG ACATATTOCT ACGTATCGAA TGTGATGTGA CAACATGCAA	60
	GATTCTCAAC AACAAGCOCA AGTOGTTTAG TOGTAAAATC CATOGTTOCC ATOGATOGOC	120
55	CCCCGGTTCG ATTCCGGGCT TOCGCATATT TTTCACAACA TOCACACACT GIGIOGCTAT	180

	CAGACCACACTACCA CONTROL TROTTED TACACCAC CATACTURA CAGACACACACACACACACACACACACACACACACACA	240
5	CTATTGTGTC ATTGATCTAA ATGTCGAGTC GATAGAATCC TTCAGCTCCT TGTAGCTAAT	300
	GATAATICCAG TICATCICGI COOGIGICAC CAAGATTATC TITICAGATA COCCEGIGIC	360
10	CAGTITIGITIC AGSCACCOGA GTACGTOGGT GAGGTCCATC ACOGATITIOC CGTTCTOGTC	420
	CACCTOGTOG AACACGTAAT CGTAGAACAG AATGATOGGG AACTTIGTCCC CCGCCTCAGA	480
15	CCAGTOGATG TOCATGCTGG ATTOCATCCT ACCAAAGATG AAATTTAGCT TOCACATGAG	540
	CCTGAAGAGC CTGCCATTCT CTAACTCCCG CGACAAGTGC TGCTCGATGT TCTCCCGAGTA	600
20	GCTCTGCGAC GAACTGATTA TGTCTAACAT CTTGTGGCTG AACAGGCCGG TGAACTCCGC	660
	AATCGICTIC TICTOGTOOG ACAAAAGGTA CGCCAGCACC CGCTTGAACA GCGGGTOG	718
25	(2) INFORMATION FOR SEQ ID NO:674:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1448UP	
40		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:	
	CATUTOGUCA GUGUTOUCAT CUGUAGAGUO DUAGGOGUCO GUGUGUCAG GUGUCOGUCAG	60
50	GCCACTGCCC CACAATGCTG TCCCATAGCC CTCAACATCC CAACTAGCTA GTCACCTTGT	120
	GUAATOGGIC TACCGATGGT GIGIGCGGCG GGGACAAAGC CGIGGTGAAA CGCACACITT	180
55	TCAAAATGGG CTGATCTGCA GCAGTIACACG ACCGATGAGC TGCGCGCACG GCGACAGCAG	240

	TOGOGGITOG GOGOCIGGOT GOGCATAGEG AACTTAGGTA TAGTATAGAA GOGOCGICTA	300
5	CTIGGOGIAG GCAGOGAGGA TGTCGTCGTT GTAGOGGAGG TATTIGCCGT TCGCGCAGTC	360
	COOGRATISCOT CTCAGCOCCA COTTIGGCCAA GATGGTGGCC GGGATICTGCG GGTCCAGCAG	420
10	CTCGCTGTTC TTCTTGAGCT CCGTGAAGCG GCGCAGTGCC TCCGGCGCCA TGCGATGCCC	480
	GAACTTIGTCG COGATIGTCGT TCTGCATCTG CGTGTCCACC ACCCCCGCCG CCACCGCCAC	540
15	CGCGCGCACC GCACGCTCTT CCGCGGCCAG CGTCATCGGCA AAGTGGTTCA GCGCGGGCTT	600
	CCACCACCC TACCCCCCC ACCCCCACTG TCTCCCAGTT AGIACCTCCC CCTCCCCTCC	660
20	TOTOCGTOGT ACATACATAT GOOTTOGTOC TOGOGOCOGA GOTCACGAAC ACCACACTGC	720
	cacc	724
25	(2) INFORMATION FOR SEQ ID NO:675:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 697 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
3 5	(ii) MOLPCULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1449RP	
40	(A) General Pagistre	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:	
45	GATOCAAAGA COGOGTECTO GCACTTOCAC ATGTOTOCAA GOTGGACGOG AACAAGGATA	60
	TOTTACTOCC COTCAAAGAA ACCCCGAATC ACAAATCCCC ACGATGCTGG AAGCACGCAT	120
50	CTCCCGAGGC CGACGCTCTA TGTAATCGCT GCGCCAGAGT CCTCCAGTAA GCCAAACCTG	180
	AATTITICAA AAATTGAAAA CITCACCATG GCTCACATGC TGACTGCTTT AATATCCTGT	240
55		

	AAATACAAOC GCACTCTGCA GGTCGATGCT CCCTCACCTG GGCCCCCAAC TCTCCCTTGT	300
5	ACCESSIONE GOOGICOCIG COTCATIONS COTCCATOR GOITCAGAG GOSSOSCITO	360
	TOGOGTTOCOC GCGCCCCCTCC CCGCATTICAT CGCCCCCCCC TACCGCCAGCC CACCGGGCCA	420
10	COCCACCAG ACCCCCCCCT CCACCTACCT CCCCCCCTCC CCCCTCTTCC ACCCCTTTA	480
	CGCCCCCCCT TCGTTCCCCCC CCTACATCCA CCGTCTCCTG GCCAACGGCC CGGTGCCCAAC	540
15	ACTOSCOSCO TROCTOCTOC TOCATIGAGOS CACOGOCATO GOTOCTICTOG OSCIGOTIGIO	600
	GIGGGGGTC TACAGCTGCG ACGTGGTGGC GCTGTTGCCG CAGGGGCTGC TTGACTACCT	660
2 0	GOCCGAAGCA COCATCCTOC CGTCRAGAGG TTCGTOG	697
	(2) INFORMATION FOR SEQ ID NO:676:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1449UP	
40		
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:	
45	GATOGOCTICA ATGOGTTGCT GAAGCCGTGT CTTTCGTAAG ATGACCTCAA CTTAAAGGCA	60
	GOCTOTOGAT ATCTOGTTTC TTTTTTTAAC AGGIGAGOTT TOGAAAATTT TTOGTTCTCA	120
50	GCTCATCTCA TCTACAATAG TATGTCTAGC ACCCCAGCAA AGCTTGCGTA ACCGCTCTAT	180
	TCAATATGAG TAAGCAGGTA AATGATACTA GCAAGAATGG TCTTGACCTA AAGACGCTGT	240
55	TTGTCCCGAA TATTCCCTTT GATCCTACCG ATGCAGAGT GACAGACTTC TTCTCCCAGT	300

	TIGCACCIAI TAAGCATGCT GIGATCGTAA AAGATAATGC GGGCTCGAGC AGAGGGTTTG	360
5	GETTIGTIGTIC GITTOCTIGTIG GAAAGTIGATA CACAGGCTIGC ATTIGGACAAG GGACGGAAAA	420
	CACAGITCAA GOGCOGTCTT CTGAGGGTOG ATGTTGCCAA AAGAAGAGAA CGTTCGAAAA	480
10	AMBRICATICA COCCEMBREA CAGACCTICCE CREAGRACRE RECAGARRORE ACTRICITECTIC	540
	CCCACOCTCA CCACOCCTC ATGCCGGGCA ACCCCAAGCT CATCATTAGG AACATCCCGT	600
15	GGTCCTGCCG CGACCCGACC AAGCTGAAAA AGATCTTCCGG TAAGTTCCGGA GTCGTTGCCGG	660
	AGGCTOCATC COGCGCAAAG COGATGGAAA GCTGTGTGGG TTGCATTTGT CACGA	715
20	(2) INFORMATION FOR SEQ ID NO:677:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 705 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
	107 101 00001. III MAL	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1450RP	
35	113) CALFULLY, FREALY-OURF	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:	
	CATCAATTCT GICTIGAAGT AGGIATTAAT CAATGGGICA GGCTGGGIGG AATTGCTTAC	60
15	AAAAATACCA ACCCAATCAT CTTGTAAGTT GGTGAGCGAT ACGTAGACAA TTTGCCTCAC	120
	ATCAATCITA TAATCGACAG CATAGGIGAG TIGATTATTA ACCAGIGICT TICCGATAAT	180
50	GIAGAAATGG GATGGCGIAA GIATAAAGGT TITIGGGIAGC CTTTGGGCCCG ACCIACCAAA	240
	TITTGAATGT ACCOCTICCC CATTGATAGA GAATACGACA TGATCATTAA TTCCACCTTT	300
5	CCITTICACA AACOCACCCT TOGATTICAG CICATTACAA GAAACCIAGT CICCCACGAA	360

	TOCCCTOTAL CCDALAMAS ALATTICACS CCTCTCCTTT CTGCCACCA ACAACTIGIT	420
5	ACCGTAATCC COGAGTTGTT CGAATTGGTT CCCATGTTTC ATCTCACGGA TAGCACGCTG	480
	CATACGAATC GCAGAATCGA TACGCCGTTG TAAAAAACCGC CGCCAGGCTC TCTGAATGCG	540
10	AGATGCCATA TTATGCCAAT ACTIATCCCT CATGITTICC AAAGCAAACA AGGICTCAGG	600
	TGTTTAATA AATACCTTCG TTACACCCAA CTGATATTCA GTCACAGGAA TTGAAGTATC	660
15	TCTCAAAATT AAATTGACAG CATCTAAGGT ATTACCTTGC CATGT	705
	(2) INFORMATION FOR SEQ ID NO:678:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) OFGANISM: PAG1450UP	
35		
33	(xí) SEQUENCE DESCRIPTION: SEQ ID NO:678:	
	GATCOCAAGT TOGAAGACCC ACTIATOCATIA TGATTACTOG COCCAGAGACCC CCCOCTOCCG	60
40	CATCAAGCCT CAGACAGTTA TCACTCGGCT CTCCGAAATC GCAAAGGCCA CCGGAAAGGA	120
45	GETCATOGTIC ACCACCEGTIC TAGGTCAGCA CCAAATGTGG GCCGCCCAGC ATTIGGACGTG	180
	GAAGAAACCA COCACATTTA TCACATCAGG COOCCTCOGT ACCATGOOCT TTGGTCTACC	240
50	GOCGOCCATT GETGCCCAGE TAGCCAAACC CGATGCGATT GTCATCGACA TCGATGGCGA	300
	COCCICCOCIC AACATGACCT TGATGGAGAT GTCCAGCGCG GTGCAGGCGG GCGCCCAGT	360
55	AAAGATATIG TIGITGAACA ACGAAGAGCA GGGAATGGIC ACTCAATGGC AGTCTCTATT	420

	CIACOASCAI COITATICIC ACACCCATCA GCTAAATCCG GACTTCGTCA AGTTGSCTGA	480
5	TOCAATOGOG TICAAAGCAA TOCGCCTAGA GGCGCAGTCG GACATOGAGC CCATGCTGCA	540
	OGAGITIATT AATTOCAAGG AGCCCGTGIT ACTCGAAGTG OCCGTCGAGA AGAAGGTTCC	600
10	CGTCCTCCCG ATGGTCCCTG CCGGTAAGGC CTGCATGAGT TTATCTACTT CGACCCAGAG	660
	GTCAGCCACA GCAAGCGCAG CTTCGCAGCA GCCGTACGG	699
15	(2) INFORMATION FOR SEQ ID NO:679:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 708 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAGI451RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:	
	GATCTIGGIG GTAGTAGCAA ATATTCAAAT GAGAACTTIG AAGACTGAAG TGGGGAAAGG	60
40	TTOCACGICA ACACCAGTIG GACGIGGGIT AGIOGATCCT AAGAGATGGG GAAGCICCGT	120
	TTCAAAGGCC TGATTTTCCA GGCCACCATC GAAAGGGAAT CCGGTTAATA TTCCGGAACC	180
45	TECATATECA TICTICACES CAACETAACT GASTETEGAG ACGTOSECCT GASCOCTEGG	240
	AGGAGITATO TETECTECTE AACAGOTTAT CACCOGGAA TEGGETTATO COGAGATOGG	300
50	GRETTATOGE TOGAAGAGCE CACCATCTAT OCTOGGTCCG GTGCGCTTAC GACGGCCCTT	360
	GAAAATOCAC AGGAAGGAAT AGITITICATIG CCAGGTOGTA CTIGATAACOG CAGCAGGTCT	420
55	CCAAGGTGAA CAGCCTCTAG TIGATAGAAT AATGTAGATA AGGGAAGTCG GCAAAATAGA	480

	TCCGTAACTT CGGGATAAGG ATTGGCTCTA AGGATCGGGT AGTGAGGGCC TTGGTCAGAC	540
5	OCCOCANCIE TECTTETEST CIGICCICOS GEOCTICCIC CIGOCEACOS ACIOCITOCO	600
	TOCTICTOTOS TAGACOSCOT TOGTAGACCA TOTOTOGTOG TOSCITOCTA CAATTAACGA	6 6 0
10	TCAACTTAGA ACTOGTACOG ACAAGOOGAA TCTGACTGTC TAATTAAA	708
	(2) INFORMATION FOR SEQ ID NO:680:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1451UP	
30		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:680:	
	GATCCCTTIAG CGACTICTICTIC CACCCCTTCGA CGAGGCCCATT GAGCTCTTIAC GAACTGCACA	60
35	AACCIACIOG AACICIGITT CCAGACIICT TICIGITIGI CIICAACIGC TITOGCAIGA	120
	AGTACCCCCC AGGCTATTTT TCTTACCCCC CTGGTGTTTG TCTXTATACC CGGTTGTATT	180
40	TITUATAAAA AACTCAGCIC TTCCICTACG GCAGAAATAT ATATCCAGIC CITAGCGCCA	240
	TOCCAAAATC TOCCTTTTTA COOCTGTTTC TOCCAGTCTT AGCACTGGCA GAAAAAAGAT	300
45	GTATGGCGTA TAGGCCCTCG CCCCCCCGGAA AAAAAAAAA AATAGAAAAA TAGAAAAATA	360
	AAAAGACTIC GGCCGCCCCC CGCCCAGAGA AAGAAAAAAT AGGCGCCAC CCCTCCAAAG	420
50	AGADGACAGG CGAGACATAA TAAAATOOCA CACCAAGOGA AGAAAGTCTT GTGCACGCTC	480
	CCGCCCICNT ACCCTGCCAT TCTGTTCCAT CCGGCTTGCA AACCCAGTAG TGCCATGTCA	540
55		

	AALCATIGUT COLACGUICO GCIGOCUTGO AGIOGACATO CUCTUOCIAA COCCAGOCAG	600
5	ACTICCCATA CITTOCACIT CACATAGCAT ATCACTITIC AGATCACTAC GIGACATICG	660
	GTACOGAATG GCACTOCAAT GCCGACAAAC CTCTTCCTAC CCCGTGACTT ACCCCGATGT	720
10	GC C	722
	(2) INFORMATION FOR SEQ ID NO:681:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 719 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1452RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:	
35	GATCARATGI GOCTCIACAA GGGCGCAAGT GCCACAGAAT ATTAATCAAT CAGTTCCGCT	60
	GACATATTIC TATTCICACC GIATTCCACA TICCTITICAG TACGIATGIC CGICIAGCAA	120
40	TOOCTOCCTT AGTAACOCTT AATATTAACT GAAAAGCOCA GCAGTGTAAT CCATCTAGTA	180
	ACTAACACAT ATCCATTAGC ACATGITTCG TTCAGTACTA CGICATTCTT ACGCCGTCCC	240
45	TACTIGIGAAT TACACATIGGT CCTCGAGAAG CCTCATIAAGA TICTTCACTA GCGATGAGAA	300
	GOCAGCTCCT CCATCGCTTC CGAGAGAGA GCAGAAAGAG TTCGAACGGC TTCAGAAGAT	360
50	TOCACAGTCA CAAGCTOCCA TOCACGAGTA CAACAGACAG TTOCACAATG ACCATACGAA	420
	GGAGTICAGGG AACTICTCCCA TCCTCAAGAC AGAAATAGGC TCGTTCTCAC CGGAATTCAG	480
55	CAAGACGTTG CCAGAGTTCG ACCCCGACAA GAATCCCCGAG ACACCCGAGA TTCCCCGGCCC	540

	GCGCCAAGAC CCACTGCGGT ACGGGGACTA CTCATACAAC GGCCGCGTGA CGGACTTCTG	600
5	AGGTATAACT TGTGTTTATA TGTTTGCAGG TTGGTTAAAT ACATAGCTTG CGCTCCAACT	660
	CTCTCCCAGC TCCAGACAGG TTGTCCGTICC ACTCCGTGAT GAATTTCCAG TCCAGCTTT	719
10	(2) INFORMATION FOR SEQ ID NO:682:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1452UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:	
30	GATCACCAAC TCTACAGCAA GAAATCCTAC GCCCAGCAAA AGCTGTCCTC GATGTTCTTC	60
35	TATTOTOTA ACASTITIST ACTICISSIC SCTISTATCT SCAISCISCTA TOATCTTTTC	120
	ATCHOGAGOG TTTTCAGCCC GAAGTIGTOC TACCTTCTOG GCTGGAACAT CCTCATCCAC	180
40	TITICICACIG ACACOGIGCT TGAACCITTIC TIGCICATIGG TGGCGGGCTG ACTGTCTCTA	240
	GUICCACUTG TATAATATUC CUICATCAGT GAGAATCICA TAGUATIGIC ATATATUAGA	300
4 5	TATUATCIAG GICATGUUT AGAGAATAGG TCTCTTCCCA AAAAATTGGC TACCACTGCC	360
	AATCATTACA TGICAGAACC GACCATCTCC AAGTGTCGAA CCGTCCCCAC TGCAAATGCT	420
50	CICACTIAGA TOCASCITICA GACGOTTATT TICTGITTICO TOCAGGGITI ATGACCAGCA	480
	GOOGCAGAAG GOOGTGTCTT CCTGCCCCGC TGGCACACCG CTGAATCTGC TTATAAAGAA	540
55	GGGGGGAAG GAGCCGTTGG CTCTCGAAGA TCCGACTACC CGAGTGGTTA TGGAAGGTGC	600

	TTGACCTGAG GCGCAAGCCG CAAAGCTGGC AGAGGACCCA TTAAAGCGCG GAAGAAGGCT	660
5	CTOCOGCOGA TGAACAGAGA ACACATOCAG CAGCAGAACT TOCTOGCGAA GATGTGAA	718
	(2) INFORMATION FOR SEQ ID NO:683:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1453RP	
25		
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:	
30	CATCITAATT TAAAATITTA ATTAACTATT TATAATITAG AAATATATAA TCTAGAGATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
35	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATTIG TGGCATCTTA	180
35		
	ATTITUATIA TITAATIGAT TATTATCITAT TITAACATAAA ACATTITAAA AIGITATAAA	240
40	ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGIA TTTAATTTAA TTTTAATATT	300
	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TIAATATTAA GIGATATATA	360
		400
45	ATTTAATITA TATAAATTAT TIAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TITCATAATA TITATTITTA TIAGTOTAGI AATATTICTA TITAATAGIC TACCCTTTAA	480
	THORISMIN THATTIM TRANCING MAINTICE HIMMING TACCITIM	400
50	TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC	540
		3.0
	TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTTATTAT TATTTAAATT	600
5 5	TATAATAATA OTTITITAAT ACAATTATIT TATITATITA TATITAAATAA TAATTATTA	660

	ATCATAATTA AATOGTAATT TATTAATAAT TATCTTTAAT GAATTTAATG ATAAACCATT	720
5	ATTA	724
	(2) INFORMATION FOR SEQ ID NO:684:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 732 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1453UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:	
30	CATCAAAATT TCAACAATTT CCATTICATT TAGTACTACC ATCACCATCG ACCAATTGIT	60
	ACATCATTA GITTATTAGG TITACTATTA ACTTIAGCTI TITACTATACA TOGIATTATI	120
35	GGFAATATIT ATCCTTTATT ATTATCTTA TTAGFAGTIT TATTACTAAT AACTTTATGA	180
	TTTAGAGATA TIGIACCIGA ACTIACTIAT TTAGGIGATC ATACTITAGC IGIAAGAAAA	240
40	GGIATTAACT TAGGIFFCCT AFFATFITGIT GFATCIGAAG TAFFAATFIFF TGCFFCTFFTA	300
	TTTTCACCTT ACTICCATTC AGCTATAAGT CCTCATATTC TATTAGGTAA TGTTTCACCA	360
45	CCAGIAGGIA TIGAAGCAGI TCAACCAACA GAATIACCAI TATIAAATAC TATIATITIIA	420
	TIACCATCAG GICTAACTAT TACATATAGT CATCATGGTT TAATTGAAGG TAATAGAAAA	480
50	CATGCTTTAT CAGGTTTACT TATTACTTTC TGATTAATTG TTACATTTGT ATTATGTCAA	540
	TATATTGAAT ATAGTAATAC ATCATTTACA ATTACAGATG GTATTTATGG TTCAGTATTT	600
5.6	THICCICGIA CICGIPTACA THICTTACAT ATCGITATGT TACTAATTAT GITAGGTATT	660

	TATGAGACTA	720
5	CEACIATITA IT	732
	(2) INFORMATION FOR SEQ ID NO:685:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 714 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1454RP	
25		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:	
	(AI) SEQUENCE DESCRIPTION: SEQ ID NO: 685:	
30	CATCATGCCT CACCOGCGIG CAACATGCAG GICAGGGGTA TGTACCCCAT GTTGCCTTAT	60
	TITTICACCI GAAGOGGATT GOCTCITGIT TATACAGACT TITICIGCATC CCTTGGGGCC	120
35	CAGAGCTAGG GCCTAGAATC CGTGTCGTAA GCGTTGGGCA CTGATTCAAC ACGAGCACAA	180
	TTCCAGTGCT GCTCGTAGAA ACGAGGCCCC TGAAGTATAT GGTGATATCC ACATTGCCGG	240
40	AGRATAGITC TCTGTGGGGG CGACTTCATG CCATGTGCAT CTCCGGCTTA CTCCACAGCC	300
10		
	GCACACGCIG CATIGITITIG GGAACATCAT GIGAAATACT GGTATAGAGC GCATTICATA	360
45	GOOGTGCCAG CACCTGTAAT AGGGCCCCAT ACCCCCCTCT ATTTCATGTG TICATGTGCT	420
	AGTITAÇÃOS TATTITITGAS GIOCATOSSI TATOSCITAC TITIOCATAIG GAGATOTOAT	480
50	TOGCIOGIAA CGTATATAAC TGAGGTAGCC GTAAACTTGC ACTGGTTCCC ATTGCCAGAG	540
	CGAAGCTACA ATAGCACCAT CIGGCIGCAA GITGIGAACA ATGCATIGGA ATCGCATACT	600
55	CTTTTGGGGC TGTGCGCTTT TGCTGCAACA ATTAACAAAT GCCTTTGATG AAGGAGTGCT	660

	AAGGAAAIGI TAIGAATCIG GIGTATGCCA CCGGAACAGG CATTACGGAG AGAA	714
5	(2) INFORMATION FOR SEQ ID NO:686:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1454UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:	
	GATCAAGOOC TETATOGITC COOCAGOOCC AGTAACAGOO GTOCTGTAGG ATTTCAAGGA	60
30	TTCCAACATG GACGATGATG GCTCCAAAGT TATGTTCCCG ACCACGCTTG AACTCAAAAA	120
	CETTITICAS OCTATICATI TICASCOCAT CAAACCCCG CIOCAAGIGI TICCCATIAG	180
35	GAATATTOCT CCTATCTTCC GACAGGTOGG ATTCAAGAAC GTAAAATATA CCGTTCTGAC	240
	ATTCAACCC CCCCATTICG TCAATGAAAT CCCCTTCGTG AACCACCTAC TICCAACGTT	300
40	TCACTACGAT TITICTAGIGC GAACCITITT AACIGATOGI AGIAAGIATC CAGTIGGAAC	360
	TGACCCACAG ACACTGCOGA GGAGGTACAT TGATGAGCAC ATGGGCCAAA TAGATGACAA	420
45	TGCAGGATGC TTGCGTCTTA TTGCAATCAC GGCGGAAAAA CCAGAGTAGG TTTCCACCGT	480
	TECTATIECT ACCESSESCA ATTOICCOSE TOATTATATA TETTASCASE TETCAATACO	540
50	TCCTTACAAC CTAATATTTC AAAACCTAAT ATCTTCTGCT CCTTAGAAAG AGCCACTTCC	600
	TTATAIGITA ATATCTACCG CTAGTICTAT CTAATAATTT TATAATTTG ATAAATCTTG	660
55	ACGIACATOT TATCACTAAG GAAGATOTOA TOACAAACTO OGCAAAGTGT TTCATATATA	720

	(2) INFORMATION FOR SEQ ID NO:687:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 712 base pairs(B) TYPE: nucleic acid	
10	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1455RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:	
25	CATCHOTTOG ACATAGIGTO TTAAHAGGOO TGCTGAGGAC TTCACTGAGA AAGCHICAAT	60
	AGCGGGCAAT GGCCCATCTC ATCAACACTT AAAATTTTTC GTGGCAAAAG AAACAACACT	120
30	GGAATCACGI GACCACACAA AACTCACGAT TTACTGITGA ACCOGACCAG GCTACGACGA	180
	CTCTTCTTCG CATGGTAACT CGCTGCTGTC CACTTGCCGC TTGCCGAGCCT TCTTTGCTGA	240
35	COCTOCCTET TICTCCTCTT CTAACAGOCT CTCCCGGTTA GCTGTGATGT AGTGGATGAA	300
	GAAGTOOCCA TOOTTOCTOC GITTCOCATO ACOCAGEAGO GICTOGACAT CGTOGTATAT	360
40	ATCAATGCGT COCTTTCGCA GITGGITTAG CAGCTTGTTA TCACGCCCTG CACATTGCAA	420
	CTTCGCCATG OCTTTGGTCG ACTTGAACCA CACCTCGCCC GGTTTCATAT ATCCACATTT	480
45	COCCAGGITG TOCCAGGOOG TOCTCACAAT OCTACATTGT COCTGGTTGT TOCCTTGTAC	540
	AGACTOTGAC TTOCACAACT GCAGGCAGGC ATGCAGCACA TCCCGCGGCA CGTCGCTGGA	600
50	CCTCTCCTCC TTTCCATGTA ACTTCAGATA GACATGTCCC CTCCCATACT TGTCTACGTT	660
	GCAACCAGAA GIAGIITAAT CCCGGIACCC GIGCTIGAAC AAAAGGICGI TC	712
55	(2) INFORMATION FOR SEQ ID NO:688:	

	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 720 base pairs	
3	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10		
	(ii) MOLFCULE TYPE: DNA (genomic)	
	() ODIOTRIA OCTUBER	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1455UP	
15	(n) Otoratell Indianous	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:	
	GATCCCATCA CATGAAATGT CTAGAACTCC CTGCATGACG CGAATGAGGC CAAGAATGTC	60
25	TOGTOSOCTT GOCTAACOGA TGTTOGCAAC TGCAACAAGG GGTACCTGGT GTTTATAGCC	120
23	TOSTOSSETT GOCIMACCON TOTTCOCNAC TOCAMENTOS GOTALCIGGI GITTATAGEC	120
	GTATGTOGTO ATCCCCCATT CGTGCAACAG GAGAGAAGAA CGGGACCACA AGGAAACCCG	180
30	GTAAACCATC TAGAATCAGC AACCCTAGAG AACGTTTGTT OGTOGTTGGC GCAAGAGCAC	240
	GGAGCGTAGG GGCTGGGAGT TGCGGTGGCT ATTCATGCGT GGGCACGCCG GGTATATAAG	300
35	TAGGGTATOC GTCCGTTGAA CAGAATGGAT CCGTCTCAGA ACAATACCAA AATCCCATTT	360
	GGAAAAACAA CCACTAATAT GAAGTACACC TCCGCTATTC TACTCGCTCA AGTCGCTTTT	420
40		
40	GITGCAGCAC AGTCATCCTC 93931CTGTT ACCGGCAGOG CTGCCCCCGC TCCGGGGTGCG	480
	CONTROLOGIC CARCUATUM MACCACCACC ACACTICACCA CONTRACOMINA MACCACCAC	E 40
	GOGTICGOGCE CAAGCATTIC TAGCACCACG ACAGTCACCG CCICAGGTTC TGGACCAGGC	540
45	OCCACCTICCC CTCCTACCTC COCTCCACCA CCCCCCCCCC CTCCCCCCCCC CCCACCTICCC	600
	OCCOCATGIG OCOCCCAGG TOOCCCCCC GGITCTAACT CCCCCAACTC TOGCTCCAAT	660
50		
	GGNICIGGCT CCCGGCCAGA ACACTCTGGA ACAGAACACT CCGGCCCAGA ACACTCTGGA	720
	(2) INFORMATION FOR SEQ ID NO:689:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENCTH: 696 base pairs	
_	(B) TYPE: mucleic acid	
5	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1456RP	
	(ii) Violetties. II=14=50(C	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:	
20		
20	GATTCACOCC COCCTOCTGA CCAACGTCGT CATCATOOGC GOGACCTCCC TOCTCCAGOG	60
	CCTGGAGCAG CGCCTCGTCA ACGACCTCAG CCTGCAGTTC CCGCAGTACA AGCTCTCTAC	120
25	CTACCCCACG CCCCCCACG TCGACCCCCA GCTGCAGAGC TGGCAGGGGG GCGTCAACAT	180
	GLECCYCCLC CCCCACLOCY VGCLCCCCLC CLEGGLCYCC VYGCYGCYCL VCCLCCACLC	240
30	CCTCGACAAG TAGCTGTGTA GTATGTAACC GTATGCCGGG ACCCTGCGGT TTCTTTCCCG	300
	CTCCCCCACC CCCATGACGC CCCCCGCCCC CTCCCCACC TCCCAACGCCC TCGCCACCC	360
35	COCCCCCCC COCCACACCC TOCCACCTCTA CCTGCACTAC TGCTGCCCCT TCTGCCCCCG	420
	CCTCTTCCTC GCCTGGCACG ACGCCCTTTT CCCCCGCGCG CGCGCCGACT CGCGCTTCCA	480
40	GATOGICTIC AACCACGICA TOCAGCCCTG GCACCCCGCC TOCCAGTACA TGCACGAGGC	540
	COCCTORCO GIORNOCOCO TOCACCOCOC COCCTICUTO CCCTICITOC CCCARCICIT	600
45	CCTCCACCAG GACCGCTGGT TCGACACGCG CACCGCGGAC AAGTCGGGCC ACGCCGTGTA	660
	CCGCAAGCTC CGGACTTCGC GCCGACGCC GCCGGC	696
50	(2) INFORMATION FOR SEQ ID NO:690:	
	(i) SEQUENCE CHARACTERISTICS:	
5.5	(A) LENGTH: 739 base pairs	

(B)	TYPE: nucleic	acid
(C)	STRANDELNESS:	single
(D)	TOPOLOGY: line	-ar

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1456UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GATCTGGAAT ATTACCGGCA CAAACTTGGC GCTGTGCTTC CACACCAGCC TCCCGTACCG 60 CTTCACOOCC ACCACCTCCT OCAGCAAGOG AATGCACAGG TATGCCAGCT CCATGCOCTC 120 CAGATTAGIC AGAACCOCCA GGIAGITGGG GITICGACACC AGCOCCTCCA CCAGCTCCTC 180 CCTCTCCACC CCCTCCTCCA TCACCACCCA GACAACGTTG AAGCACGACA GCACCACGAA CTOGTOGTOC GCCCCGCTGT CCGTCAGTGT CGACTCGTAC AGCTTGCGCA CAAGCTCCGG 300 GCCCTICITG AASTACCGCA GCACCTCGTG CACGTACTIG TCGCTCGTGA ACAGCTCCCA 360 CAGCAGGITC ACCACCGCCC GCITCGCATC CAGGITGITC GACGICGCCA GCAGGIGCAC 420 CAGCCCCTCC ACCCCCTGTT CCACCCCCAG ATCCACCCCG CCGCCCCCC CCTGTTTCAA 480 540 CAACGTCGAC TOGAGCTTCT TGGCAATCCC CGCGTCAAAC TCGCTCACCT CGGGCGAACG CACCACGCG TCCCACGCCA CATGCCTCGA GCTGATGTTA TTGCGGATAT CGTTGAAGTG 600 CGTGCTATCA AGCAGAATCT TTTGAACCCC CTGAGCCACG GGCATCGTCA CAGCTAAGAT 660 720 CTACGCTTCC ACCCCACCGT ACTGCCCACT TTGAAACCCG TGGGACTAGT CAATATCTGG 739 CGREGACTICCC

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(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

55

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic)	
•	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: PAG1457RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691;	
GATCAATATC GGGACGAAAAT CTGTTGTATC TACTACCGGC ACGGCGACTG CGCCCAGCGC	60
20 ACCAGGATCT CAGGCTTOGT CAGGGAGTOC GGATTOGTCA GCTAAACAAA AGAAAGATTC	120
ATCICCACIA CCTCTTGACT TACCTCCACC GAAGGATTTT AGCAAAGAAA TCGAGGAGAT	180
25 TATAGAACAC GATTIGACTA AATTGGCCTT TCAGAATCCT CTTTTTAAAG ATGAACTITCC	240
ATATTOGITA CAGOCCAAGA GOCCATTGAT CCAACCGTAC AGCACTATGT CTGAAAGAAT	300
30 GFIGAAACAG CIGGAATOCT CATTACTTAA CIGCOCAGAT TOGCTTGACG CTGACACACC	360
	0.00
ACATCTCIAT CAACACCOSC TCTCTTTACC GCATCCCACC TCCATTTTCT TCCCTAGTCA	420
35 ACCGATCACG TICGICOCTG CTGGCTGGAA TAACCATAAT ACGTCCACTA AAGATATCTA	480
	400
TOGAAAAACT TCTATOGTTC AGATAATGAC CAAGTTOGAT TTOGATACCC TGTTTTTTAT	540
40 CTTTTATCAT TATCAGOGAA CGTACGAGCA ATTOCTAGCT GCCAGOGGAA CTAATCATCC	600
	000
GTGGGTGGAT ATTTAATAGA GTCAATCGGT GCTGGTTTTA CAAAGAAGTT GAAAAGCTGC	660
45 CCCCTGGAAT GGATCAAAAA GAAGAGGT	688
	000
(2) INFORMATION FOR SEQ ID NO:692:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 711 base pairs	
(B) TYPE: mucleic acid	
55 (C) STRANDEINESS: single	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1457UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:	
	CATCCACCAC TICAACCACT ICCCCCACCT CCCCTCCAAC ACCCCTCCCC ACCCTCCACTA	60
20	CCACCITICCC GCCGTCCACC TCACCACCGC CCCTCTACGC CACCGTATCT CCAACGCCGT	120
20	TOOCTTOOCG ATCOCCACG CCAACTTOOC TOCCACTTAC AACAAGCCGG GTTACGAGTT	180
2 5	GTCGCACAAC TATACGTACG TGTTCTTGGG CCACGGCTGT TTACAGGAGG GTGTGTCCTC	240
	CCACCCTTCC TOSCTTCCAC CCCATCTAAA GITCCCCAAT TTCATTCCCT TCTATCACCA	300
30	CAACAAGAIC ACCAICGAIG GCCACACIGA GGIGICCIIC GACGAGGAIG TCIIGAAGAG	360
	ATACGAACCA TACCOCTOCC ACGTGTTCAA CCTTGCCAAC GCTGACGACA ACTACAACAC	420
35	ATTROCCAGTG CCTTGGAGCA GGCCAAGAAG AACAAGGACA AGCCAACTIT GATCAAGTTG	480
	ACCACCACTA TIGOGITTOG CICCITGAAT GOGGCCTOCC ACACTGTOCA CGGCGCCCA	540
40	TIGAAGCOGA IGAIGICAAA CAGITGAAGA GGAAGITGGG CITTAACCCA GAIGAGICCI	600
	TOATTGTGCC TOAGGAGGIT TATGACCTOT ACCACAACAG CACTATOCAG CCAGGTGCCG	66
45	ACTOCCAAAA CCACTOCAAC CCTCTACTOC ACAACTATOC COCTCACTAC C	71
	(2) INFORMATION FOR SEQ ID NO:693:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LEWITH: 688 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
55	(D) SODOLOGY: linear	

(ii) MOLECULE TYPE: INA (genamic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1458RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:	
15	CATCCOCAGT ACCTGATTGT TCGGGTGGCC ACCCGAATAT TGCTGGAAGC GGTTCAGGCG	60
	CGIATATTIG CTCTGCCCAC COCCAAAGIA CCCCCCACG TIACICITGC IGGICGIACT	120
20	AGAGAAGITG CGCACTGCCC TAGCAAGTGC GGTGCTAGGT ACGGGATTTA GCTTCGCCAG	180
	TAATIGGTGTG AAGACGTTGC GAAATGGCAC AGACGCCTGT ACTGGTCGCA CTTGCAAGTG	240
25	CATACCETTE CTAAGAAAGA AACACCECCC ATACCAGCEC GTGAACGTAG ATAACCTCAT	300
	GGTCAGCAAT CAACAAGCCT AATGATGATC TICCITACAA AATGAGGTTC TAAAGCCACG	360
30	TTAAAAAAGG ATGCCCAACG CTATGTTCGA CACCTATCGA ATATCCGTAT GAATGACTGT	420
	GTATCATTAA CGACGGTACT TCCTTACAGG GCAATGGCAG GATGGTAACG CCCAGTAATG	480
35	TCCAATAATC ATCATATATA CICIAGITAT ACCCTATGAG COGICATTIG ATGTATTGIT	540
	CGITCOCCTA TOGOCTATOC TICAAATTOG ATGAOGITOG GCAOCTOOCC ATTOGTACCT	600
40	GCGGGTGGCA TGTTCACTTT CTCTAGTCTC TTTTTGTGGGC GGTTGTCTTC GTCTTGGTCC	660
	ATGICAAGGT CCAAGAGATC ACAGAAAA	688
45	(2) INFORMATION FOR SEQ ID NO:694:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 724 base pairs	
50	(B) TYPE: nucleic acid (C) STRANDENESS: single	
	(D) TOPOLOGY: linear	
5 5	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL	SOURCE:
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(A) ORGANISM: PAG1458UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GATCTUTTOC ACCTOCTATT TCAGGCAGAT TTGTCGCTGC AGCAGCGCAT GGCCATACTA

TCTGCTTTGG CGCTCGCTGC GCGCGAGTTG CGGGGGCTGG AAGACAAATA CGTGCTCAAA

CCCGTCTTIG ATTICCCCAC ACGCCGCCTG CCCAGAAATG ACGCACCATC AAGAGCCCTT

GAAAGCCCC AATCCCGTAC AACCTCCGAG GCGACCATCT CTGCACACCA CACCGTCTGG

COGTOGCICA AACTTGACTC AGOOCCAGCA CCAGAAOGTC CGAAOGCCTT TOGGAAGCAT

GCACCIGOGT TITTCTTCCC GCTGGGGCAC GCGTGGCTGA ATGGCATCGA CCTGGGCACT

TTTGACGCCC TGTTCAAAAA GCACTACCTA AGCACCCTGC GCCTTATTCT TGCAGCCGCC

AACCCGCATG CAGAATTTGA CCGGATGTCC GAACTCATGA GCTACGTTTT GCAGGACGCT

CAGGOCIACG ATATCAGCAT TGAGTAGOOC GTOGOGCATG TGTCAGCGCA TCTGTGGACA

ACTOCTIGCTT GCAAACTGTA TOCOGACCAC TACCATGCAT TAGTATCAGA TOTATAGAGC

SCCAATIGCA COCTAGAGA GATGTGAACC TCGCAATGCA TCTCTTGGGA GTCTCTGTGG

COGCCAGTAT CTGCTAGTAC ATACTCTTTG TAACTCTACA GAGATGTGAA GTCTTGTTAC

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(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGIH: 569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: PAG1459RP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:	
10		
	GATCATOCTG GOGCATATCT GAATOCTCTT GAACAACGGA CTAGATTAAT GCAGCCTTGC	60
	ACTICACACTA INTOCCACA MOCACCIONI I	
15	ACTCAGAGGC TTGGGCAGGA TGCAGCTTAT GCGGGAGCGG CIGITGGAGC TTTACAATAC	120
	CAAGCAATAT GTGGTGCTGC CCCCAGATGA GACAGTAAAA CTGCAGOGAG AGGTGACGGC	180
20	CACCTIGAAC TCACCAGATC CAGGACTCAA CGACGTTGAC CGCATGGCCC TAATGGAGAT	240
	GAACTICIAT TIGITIGGIGI ACATTOSOGA AGAAATAGAA GCAGACGIGC TCTACCGCAC	300
		300
25	ACTIGITICA CGINTAGGIG AGAACTOGCC CCGGATGCAC CICATGAAGG CIACGTTACT	360
20	GCAGGITACA GAAGGIGATC CCCCTGCCGC GAAGTACCTG AAGAACCTGC TTGAAAAACA	470
	THE PROPERTY OF THE PROPERTY O	420
30	GCTTGAATAC GATACAGATT CCGTGGATTA CCTGCAGGTG GGCAAGAAGC TAATTGCGCT	480
30	GCAACGCCC CCCTTGTCCA CCCAGCTGTG CATGAAAAAG CTGCTGTCGC CTGCTAGAGA	
	CIGCIGIOS CIGCIASCA	540
25	AGITTOCACT GGACGCCGAA CTATGGTGG	569
35		
	(2) INFORMATION FOR SEQ ID NO:696:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 572 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
45	(5) Idiologi. Illedi	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(A.S.) CONTRACTOR CONTRACTOR	
50	(VI) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1459UP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

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GATCACGTOC CIGCGACATG GOGACTTCAT CCACTGOOOC CCAGCTACGT GGTATATGAC

5	ATTATOSCOG AGAGGITAAG GOGTGAGACT OGAACTAAAT TGAGGGATOT CITOGGCTOT	120
	GCCCGCCCAG GTTCCGAATCC TGCTGATGTC GTTATTTTTT GCTTGCGCCG CCTACGGCCC	180
10	OCTIGUATUTT OCTUGUTOCT AUTUAGAUAA ACGAGAUAGC TAAACUATOG GUAGAACTOG	240
	COGTACTICC CGTAGTACTA COCTCTCCCC AACCCCCCCA CCCCCGTCAG CACCACCCC	300
15	ACCOCTITICG CCAAACCCCCA TGGCACCCCT CTGATGAGCC CCGTCAACAG CATCACCGGAG	360
	CTOCCOCCAA GOOCGACCTC GAGGCCCCCC TCTGCGTTCT TCCCCCAGCAA GTACCCTGCT	420
20	ACAGOSTAGG TOCTACCAAA AACGAGAOCT GCAGOCAGOG AGGGCACAGA CCCTTTAGGC	480
	CACTACCCCA TOCACCCACC GATGACCCTC ACCCCCCCCA GACTGAAACA GOCATGTTOC	540
25	CTTOCOGTICG TOCTICGOGG AA	572
	(2) INFORMATION FOR SEQ ID NO:697:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1460RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:	
50	CATCCOORTIC CACACACCAA ACTACACACA CACOGACOGC TGTTGGGTGG AAGGAACTAC	60
	CTOGTGGATA CATTICCAGCT GOCOCAAAAG ACACATAATT TCTATGTGCT TGTCGACGAG	120
55	CIGATAGAGA TITTIGCATITI CCAGGGGAGC GGCTCTGACT TITTIGCACCT GCATAATCAG	180

	CTGTACCCOC TGGACCTCAA AGACAACGAG CGGGCCTTGC TTGCAGACGC TGGGTTGATC	240
5	AAAGGCGAGC TGCGCTCCCC ATACTACGIT ACTGCACTCT CITCATACAT CATTTTTGGT	300
	OCTOCTATTG TGGCGAGCGG CTGTAGGATA ATAGATGACT ACTGGGAGCA GCCCTTAAAG	360
10	GASCAGGGAT TCACCATGCA CCACCGIGIA TICTCTCTGA ACGGCACGCA ACTITICATTG	420
	CTACGCCTGC TGAAACCCCC GCGTCCAGAA TCGCATCAGC AGGGTGAGAA GCTGGATACC	480
15	AACTOOCTAC AGAAGTOOGA GGATCCATAC CCAACGATCC AGGAACAACC AAATOCTGAA	540
	GCACGGGGG AATACGCTAG AGAACACGCC AGAGGTGAGC ACATAACGAT GATTGTTCCA	600
20	GGICAAAGTA TTAGCGGCAG TATAGAACTG AGCCTAAATT ATAAACTTCC TAAGTACCAC	660
	TACAAAAACT CATTTOCTAA TOOGTTGA	688
25	(2) INFORMATION FOR SEQ ID NO:698:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 649 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(2)	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1460UP	
40		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:	
	GATICUAACAA TITOCOOCAGO GOOGOTOCAG COGTOGTOTO COTOGCATICA AATIGAGTOCA	60
50	COCCIGICIC ANICCCOCAC AGCIGCOGIC CATGOCOCAC CICGAACTGC AICCCCCAAC	120
	CAAACAGCTG GATAAACAGC COGTTCTGCT OGCACCOCCG CCGCAGCTGT CCAAAGAGCG	180
55	CCTCCGCACC AGCTGCTATA TCATCGCCCC AGAAACTCTC TAGGAATGCC CCCATCGCCG	240

	TGTACCTOGT CGTAGTTGTG CATGTCGCTG CCTCTTCCGG CTGAATTTTG ACAGTCTGGC	300
5	CCCCCACCCC AGCTCCGGAA COCTACGTAA TACAACACAC AACCAAATGC CCTACCCGAA	360
	GETCOCAATC GTCTTCTGCA CCGGCTGCCG CTGGGGCTTG CGCGCAAGCT GGTATGCTCA	420
10	AGAGITOCTA CAGACTITICG GCGACTCCCT AGCCGAGATT GCCCTOGTAC CGGGTCCGTC	480
	COGTICAATTIC CAAGTICCTCT GTTACGCAAG CCAAGAACAA GAGGCCACGG GACAGCGGCA	540
15	ACACCATCIG GGATOGGCGC CGCGACAAIG GITTIOCIGA TAGIAAATAT CTGAAGCAGG	600
	CIGICAAGOC ACICITITIG CAGACAGOGG AACOGCCIGG GOGCCACAT	649
20	(2) INFORMATION FOR SEQ ID NO:699:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(b) 100 value 1. Linkell	
3 0	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1461RP	
35	,,,	
40	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:699:	
	GATCAAACCA CCACGOCACA TCATCATAGT TGATTAAATC AATTAGGTAA GGCAACCATA	60
45	GITGCAGACT TIGTTICTGI ACCATTITICT TGGGATTAAA GAAGIAGGGA GICACGAGGA	120
	AATGCACCGC ACATGCTTTG AGATTGGTGT TITGGCATTT TAGAAGGCCA GIAACGAAGA	180
50	COGICAACCA OCTOTOCAGO CATAGATTAT TTTTAACTOG ATGAACCTTG TAGCACTCGA	240
	TGTATAGGAC AATCGCCAAC CAGAGCAATG TCTCGTGCAA CGGGTTCTGG ATGACAAGCG	300
55	CACGCGGGGT GCTCGTGAAT GGTAGGAGTT GGTTGCTTCC TATCCCACGG TTGCTAAATG	360

	CCATGIACIC TIGGICCITG GGGITCGGGG CCACGCIGAC CTITAAAATG TATTTGAGGT	420
5	CCAACTOGTG ACCATAGOOG TOCACTAGTG ATAGCATGAG TGCCTCTAAC GGCAGAAGAA	480
	GCCCTTGCGG AAGCGAAACC ACCTCCCGGC ATTTGAGCAC CGCAGACATT AACTCCAAAA	540
10	COGIGTICOC CCACCACATO TOTOCTOCOGA ACTOATOIGO TICTOATTOA TOCCOCACCA	600
	AGTGTATCAA AAGCCCGGGC AAACCCACGG GCACAGCCCG CCGCACATCC GCGTCCCCAT	660
15	TACAGTAGIC TATCCCACAG TIGITICAA	688
	(2) INFORMATION FOR SEQ ID NO:700:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1461UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:	
	GATCOCCAG TITAAACITA AAGITGATAG AGITCOCCTC GTOCTCTCTG GATACAATAG	60
40	AGRICACIGA GIOGACGIOG COCIGOACGI AGIOCOCOCO GIAGOCOCCIG TOGICOCAGA	120
		120
45	TOOCCCTTTC TAGGTTGATC TTOGAGCCAG CTTTCCAGCT GCTCACTTCC GTCCCATAAA	180
	CTETTTCTGG TGCGATCCCG ACCTTGAAGC TATCGGCCGT GAACTCCGTC ACCGTCAGGC	240
50	AGATACCATT CCATGCAATC GAGTCACCGA TGTGGCAATC CGCCAGTATC GGAGCCGCAT	300
	CCTIGATAAG GACTGACACA CCGTTGCCGC CTGCCTCGCT GGCATCGTTC TCCAAGTACT	360
55	CASCAACAST GCCAATGTGT TCCACTATAC COSTAAACAT CCTATCAACT TCTATGGGGG	420

	ATATAGOCTT COGTATOCCA TCTATOCATC TTCTTTTCTG CTACCOCGAG CTTTTTTAAAC	480
5	TOGTAAGACA TOCATAAGGA AATOGCOGTT COCCATGTAG CTGACTAATA AAACTAGAAG	540
	ATACGACIAA CIATCIGATT ATACTITIAGG ACIATCICIC CITGOGCIGG TCACAGAAAC	600
10	ATCGFTGAGC AAGTCGCGTC TATCGGGAAA ATCACTTGGT TCCTTTGTCG TAGACCTAAC	660
	TOCCIGAÇÃA OCTOGRARACO OCTICTITITAA AGRICIACTIC GARTOGIOGI GIACOTOGO	720
15	GIGCIGGC	728
	(2) INFORMATION FOR SEQ ID NO:701:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 701 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1462RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:	
40	CATCTTAATT TAAAATTITA ATTAACTATT TATAATTIAG AAATATATAA TCTAGAGATA	60
	TATAATCITA AAATCATAGG TAAAAATACA TAAGATAGIA AGAATAAAAT TAGTAAAATA	120
4 5	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAAIG GAATIATITIG TOOCATCITA	180
	AUTTITATIA TITAAUTGAT TATTATCITAT TITAACATAAA ACATTITAAA ATGITATAAA	240
50	ATAAATAAGA AATTACTTAT AGAATATITA TTAAATAGTA TITAATTTAA TTITAATATT	300
	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TTAATATTAA GIGATATATA	360
55	ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420

	PRICATAATA TITATTITTA TTAGICTAGI AATATTICTA TITAATAGIC TACCCTITAA	480
5	TICCATATTA CIACCTACTA AATAITTACC TAATAATATA TIATTAAGAA TACTTAAAIC	540
	TAATAATTTA TTATCTAAAG TATATAAATT ATTTAAACTT TTTTATTATT ATTTAAATTA	600
10	TTATTAATTA GIAAATTATA TTTATTTATT TTATTAACAT AATTITTTGG ATAATAATAT	660
	ATCATTATTA AATGSTAATT TATTAATAAT TATCTTAAIG A	701
15	(2) INFORMATION FOR SEQ ID NO:702:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1462UP	
30	T. ELIZACEOF	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:	
	GATCAATTAA TAAATOOFTI AACTAATAAA GITAATAATA AATCTATTAA TIATATAAAA	60
40	CTACCIGATT TTATTGAATC AAATAATATT TICTTAATGA ATACTACTAA ATCATCATCT	120
	ATTGAGITTA TATTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA	180
45	TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGF TAGTGCATAT AGTTTAATTG	240
	GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300
50	ATCATTAATA TAATAACTCT TTAATTAGAG TOGTACCACA AGAATOCTGA AAGCATTAGG	360
	GGIGIGIACC TIACCICICT AATTAAAGII ATAAAATIAT CTTAACTAAT AAAAATAATT	420
55	AATTAAATAA ATAAATAATT AATTAAATTT AAAAAGTAA AAAAAAGAAA TAAATAATAT	480

	GITATATITA AATAGATCAA AATITCAACA ATITCCATTI CATTIAGTAC TACCATCACC	540
5	ATGACCAATT GITACATCAT TEAGTITATT AGGITTACTA TEAACTTEAG CETTTACTAT	600
	ACATOGIATI ATTOGIAATA TITATCCITT ATTATTATCT TTATTAGIAG TITITATTACT	660
10	AATAACTITA TGATTIAGAG ATATOGTAGC TGAACTTACT TATTIAGGIG ATCATACTTT	720
	ACCTGTAA	728
15	(2) INFORMATION FOR SEQ ID NO:703:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 688 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25		
23	(ii) MOLECULE TYFE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1463RP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:	
	CATCCCTCAG TCTGCTACCA AGGAGGTCGA GGAGGAGGAC ATGGATATOG AGCAATTGAA	60
40	OCAGGAGATE AAAGOCAACA AGGAGGCCTC TGCTFTGTAA GCTTGCTGTT TGCCGCTTGT	120
	GCTAGCCAAT CGTTGCTGAG ACTATCTAAC TIGHATACAT GCCGCTATCG CGGCACGCGA	180
45	ACCCAACACE AND ACCOUNTY OF THE ACCOUNTY ASSESSMENT ASSE	
45	AGCGAACACT ATAATGTATA TGTCAAGTTA AATACATCAT ATATTATCTT GTGCCTCAAG	240
	OGTOTTAAAG ATGTCATAGG ACAGTCOOGT OCTCAGACAC ACGAATATAA TCATAATAAT	300
50	AAATATATOG COGTICACCIT CATGACCACG TCAAGCCTTG ATACCAGAAG ACACTTCTAG	360
	CAATTTCTCA ACGOCACACA AAACACTAGG GIGIAGGIOG ICATTCGICA AGGACATCIG	420
55	CICCICOGIC CACAAGITOG CCICTOGIAC ATAGICIOGI TCACCGACAC CCAATAAGCC	480

	ACCUSIOCOCA OCCCAASICOC SIGACACGIGG AAGCIGTAGT GICTICCAGA OGTCATOCAT	540
5	COCCTCCAAT ACCACATCCG ACACCTCGTT CGTGTCCCCT CGAGTACCAA TCATACCCAC	600
	TETETEOGTE COGCGTGGAA COGTAGGAGT TGAAGGGCCT GTACGTAGAT GCGATGCTCT	660
10	CCATCAAAAT GTCGGAAGCA COCTTGOC	688
	(2) INFORMATION FOR SEQ ID NO:704:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 704 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1463UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:	
35	GATCAAACAG TAGAAGTATT AGADCTOCTT GCAAAGGGGG TCATAAACAA GAGACCTGTA	60
	ATGTOGACAA ATTAAACAGA AAAATATCAT TATTAGTOGA TAAATAACCA ACTTOCACTG	120
40	AGAGTATAGI TOTACATGIT TATTOOGTAA CAGAATTIOT ATOCAAATAG TITAATTOOG	180
	TTTTACTTAT CTACGGAGTA GCAGTGCAAG AACCTTGTAT COCAAAATGC TAGAGGCACA	240
45	TOCAGATGIA TAGIAAAGCA ACGICIGITT CITTOGATTT AGCAGOGICA GGOGAACAAA	300
	AAAAATAGAA AGTCAACAGG GATTGGGAAG TTATGAGAGT TGATATGTTT GTCCATTAGT	360
50	AAGICATTCA GITGATATGA GGTGCTTAAA TGITTIGTAAG AAGCAAGAAC GAAGAGAGAT	420
	ACAAAATGIG CAGTTGTGAA TOGTGAAATT GACACCAGAG GACGTCACTT COOGTTGCCA	480
55	CTGTTTGCCA ATTGCTTCTC GAGCTGCTCA ACCTTGCGCT GTAAATCTCT ATTGACTTTC	540

	TITIAGIAGIT CCAATICAAT AIGCGITICC TICGATCITC CATACCIGAG CAGITICCCC	600
5	ATCTCCTGGT TCTCTTTTGT CAACATTTCG AGTCGGACAA TCATCTTGTG AGGGAGGCT	660
	TCTTCGTCAT AACGGCCGAA TCGGGTAACG GAATTAGAGG GATT	704
10	(2) INFORMATION FOR SEQ ID NO:705:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1464RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:705:	
	GATCGAAATA ACTTCCGCTG AAAACGCAGC AGAGGCAGCC AATGGTCAAA TGGAGCGAGA	60
25	ATATOCACGA TATTTCTAGG GTACTGTTGC TTGCCAGTTG GTGCTCGGAA ACATAACCCT	120
35		
	CAATGOCGCC CAGTGTGTTG TACATACCCC ACACCGGAAA CAGACCCATG AATGACCCGA	180
40	AAACCACCAG CCACGCGCGT AAGCCGCCAT CCGGGTATTC GTTGGAGTTA TCGAGATATG	240
	COCCUTATION TO THE CONTRACT CONTRACTOR TO THE COCCUTATION OF THE COCCU	300
		2.50
45	TOSTIGOCCC ATCOCCAAAA ACCICITIST COCCCACACC TGIGOCICIG COCCIGICAG	360
	ACCATOGOCT CACCICTAGG OCTACOGOCT CATCOCCATG COGTACTICA ACCCIGIOCT	420
	ANNOUNCE GROWING CONTROL CONTR	920
50	TGTCGATGAC CACCATCGTT CCTAGCACGT ATGGGAGATG CTCCGAACCG CGTCAGCGCC	480
		220
	ACCACAGACC ATCTATCTAC TTAAATACCT AATTATCTGG TGTCCAGCTA AAAATCCGAG	540
5 5	TATCAGTCAT CCTGTGCCGG CCTTATCACC CATTAGGGTC CGCTTTGCGG TAGTGCATTA	600

	CCGICGGCG GATICATICCT CCAAAATGIC TCAAGCGATG CCTTGATTCC GAGTGTACAA	660
5	CCCCAGATT CCAACCCCCC AGGAGCCAAC TAATAGACG	699
	(2) INFORMATION FOR SEQ ID NO:706:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1464UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:	
30	CATCHICCOC THITTCTICA CACCOCCTIG GEIGIAGIAT TETTCCTCCT TAAIGHTCCA	60
	CITCACCCC CACCAACACC CCCCACACCCC CICIOCCCAC CCACCCCICC AAACCCCCCT	120
35	GICCIOCOCCIT TOCACCIOCCA GOOCOCCICIC GICCIOCICCA TAGICCICAT GITICOCCICCA	180
	COCCUCACION COMPOSCIO COCCUCACA COCACOCCO ACAMONOCO	240
40	GTCGCGGAAC TCGTACTCCT TCTGCGGGGTC CTCGCGGGCGG CGCTTGGCCG GCGGGTCCAC	300
	COCACOGCO GOCACCTTICA COCCOTTOCA GATAATICAAC TTGTGTTCCA COCAGCCCTT	360
45	COGATOCTIC TITICOGCCAT TOOGITTOGG COCCOGCCTIC TOCCCGTCCG CCACOGCCCC	420
	GOCCGCCCCC GCATGCAATT CGTTCTCGTC TGGCCAGACT GCGCGCGAT AAACTCGCCC	480
50	AGGATOGOGT CCACGITAGT GAGGICOCOG TIGOCOGTOCT CIGOCOGTOC GIGGIOGIGG	540
	THEOCOCCOT CACCOCCATE CACCOCCATC TOCHCOMES COTTOCCATC CHECHCOCCC	600
55	ATGCCCCGTT COOCTOCATG CCTCCAATCG ACTTCGACGT CGTACGATCC CATCCAACGA	660

	ACCCOTANC TIAICICCAR GIAIOCCIOC RIACCTRIAC TOSICOTORA	710
5	(2) INFORMATION FOR SEQ ID NO:707:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 703 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1465RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:	
25	(XI) SECTION SECTION. SEC ID NO. 101.	
	CATCCACTIC TITICOCCACA AGACATICGA GCCCGCCAAC GACTGCCAAA TCTACAACCA	60
<i>30</i>	CCCCCCCACC ATCCCCCACA GCCTCCCCCTC CCCCCACCAC ACCCTCACACA TCCTCACACA	120
	OCTOTICGAC CIGIAGOCOC COCCOCIAGO TAGITICITIG TAATTOCTOG ACATTITACAA	180
35	TGCATATTCC TATATACACC GCGCGCAGCG CTCAGCTGAG CAGCCGTACG TACGCCAGCA	240
	OCACOCCAAA COTACCCOTG CACACOCCGA TCACCCACTG CATGACCTGC GTCTTGACCG	300
40	AGICCATTIC CATCITCATA TTACTGACCT CCTGGTCAAT TCGCGTGTCA ATCTCCTTGA	360
	TCTGCAGATT GTGGTTGCTG GACTCCTCCC GGATGCGTCC CTTTTCCAAC GAGAGATCCA	420
45	OCTICAACCC TECCTICOCC TICCTICATICT CCTCTCCCAG CCCCTTCCCC ACCTCCTCTA	480
	GETCETTTCC AATCCCCTCC TGTTCGTTCT CCATCCAGIG CATCTCCCTG CCGTCCCCCG	540
50	TCAGCAGTIG GIOCCGCAGI TITGCAAAAT CCACCGCTG CTGGTACGTC AGCTICGTAA	600
	OCTICIOSCE GGACGCTAGG TOCTGCCAGA CATGCGTCAC GCCCCGGGGC AGTGGGTGGG	660
55	ACATGATATC CACGATCOCA TICOCCIOCT GOCTTOCIGA AGT	703

(2) INFORMATION FOR SEQ ID NO:708:

5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 619 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1465UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:	
25	CATCCCCCAA TAGCTTCATT CCATCCTCTC GTCCCCGTACC TCCTCCACTT CTCTTGCTCT	60
	TCTCTATGTT CGTTCCTCAC GCCCCCAAAA CCACTACACC ACAAAAAAATT CACAAGGTCC	120
30	GCCGCACCAG CCTTTTTAAT TAGCCCAATG GCAGCGAGTC CTGGTATATA AGGCAAAAGA	180
	COCCACCCC ACACCTACTA CACCCTCATC CACCCATCGT ATCTTCCCCC ACACTCCCCC	240
35	CAGGGGCAG GACTAACCTT GATGITICGAT AGAATGCGIT GTACAACCAC GCGGTGAAAC	300
	AGAAAAAGTT GUTGGAGCAG GAGUTGAATU GATTTGAGUT CGGGGTGGGG GCGCCGGTGG	360
40	GOCTOCAGOG TICCATIATOS ACGOCACIOGO TOOGACIOGA OCOCACAATT GAGCAGTATC	420
	AGGCGCAGGT GGCGCAAACG GGCAGCGGGG CGGAAGCCGG CAAGCATGCG CAGCGCGTGG	480
45	GCGAACTGAC GGAGTGCGCA ACGAACGCGC GGGGGGGGTT GGAGGGGCTG CGGGCCTGCGA	540
	CONTOCARCO GETCOCCTTC CACACCROCC COCCARCOCC GCACROCCCC GTCAACCARC	600
50	COCCOCCOCCOCCAC	619
	(2) INFORMATION FOR SEQ ID NO:709:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 715 base pairs

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10		
	(vi) ORIGINAL SOURCE:	
	(A) ORCANISM: PAG1466RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:	
20	GATCTCTTAC TTTTCCTACT CACCAATGTC TTTAACAGAC ACCCAGAGTC ACGCCCGGCA	60
	GOCTATCTOC CGTGCTGGGG CCATGCCCCG CCCCTGGTAC TGGCCCGCTC GTGCTCGGGC	120
25	TAGICTCACA GCAACGGAGC TROCTCCAAT TGGGCTGCAT TCTCCCGACC ACAGTCTGTT	180
	TGICAGGIGA CTCTCAGCCG TCCCGAATGT ACATTTCTAT TIATCTACIT CTTGCCGCCT	240
30	TECCECCACC ACATCOSCIE COCCECCACCA CACCEACCCC GCATCGCCCC CCTCGCCTITC	300
	GIACAACIGO GCACAGCACG TGIACAGIGO CTOCACIGOO GCCCCCAAC GGCCCIGOTO	360
35	GIACCCIGIG OGTITICAGAC AUGOCTIGGAT OGCACAUGCC TIGGGCCTTGC AUGGGGGCTIG	420
	TCCCICIOCO CTOCOCCOCC TATUGICCAT GITTIGIGIT CTATCIGITG GCCCGTACCA	480
40	CGITGITGIA CCAGAGIACA TIGICOCCGI GACCCCGIGI AATGICACCC CGIGGGCCAC	540
	AGATGACCCT GCCACATGCC TCATTTCTTT GACCGCACCG TGCCGCGAGA CCGCCGCACAT	600
45	GGGCCGTIGGG CACTCCCGACG ACACCCACGG GGGGGCACTG CAAGGGTIGGC ACGTIGGGGAT	660
	GAGTCAAAAC AAACCAGGTG TGGCGCTGGG CGGGTGAAAA TCGACTCATA GAGAC	715
50	(2) INFORMATION FOR SEQ ID NO:710:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 694 base pairs	
55	(B) TYPE: nucleic acid	

(C) STRANDELNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(12) TODACOLL TIPL. MA (GENNIC)	
	(vi) Original Source:	
10	(A) ORGANISM: PAG1466UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:	
	GATCITATTA ATTITICATOS TOCTATATIC TAAATICAAS TAATGATAGO GOSTGATGOS	60
20	GIACGIACCI ATACATATAA COCACAGITC ACCATCGICT ATGOSIGIAT GAAAATCACT	120
	CCACCCGIGC GACACGCCAC GIGIAATCTA GIGAGTTICA AGITCTICCT CCTCATCGCC	180
25	AGAAAGITOG CCCGCGGGG TGAGGITCIT GAGCGGCTCC TTGAGCTGCG CGATAAGGCT	240
	ATTOTOCOTT TGAGCATGCA TGCCGATACC CTCTAGAGAC ATATGAGCCG AATCTGCACC	300
		300
30	ATCIPARACCA TETTCOCTET TECTGCCAGT GOCAGCTGCC AGTITGGGAC TGGACAGACC	360
	TGICTGTCCA TCTTTGTAAG AATCCTCGGT CGTTGCCCAG TTGGAATTCA TGGTTCCCAT	420
<i>35</i>	AGTGTGCAAG ATTTTCTCCT CTTCTGTTAG TTCCAGATGG GTACCTGTCA GATTGATCAA	***
	THE PROPERTY OF THE PROPERTY O	480
	GGACCIGCCC CTITIACCCC CCCAGACCTT CCCCAGAGACA GAGIGCCCGC TIGCCCICCC	540
40	TICACCAAGG TITGIPATGG AGGIGIGAGA TCTCGCAGIC CTTGGTAGTC TCAGACACCA	600
	AGCACCOGCA TCATGTATCC ACTICOCAAC AAGCGAAGIC CAGCCACACT GGTGTGATGC	660
45	GCCCAAGCCC CTACCAGTGT CACCATGGAA GTAT	694
	(2) INFORMATION FOR SEQ ID NO:711:	
50		
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 690 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
<i>55</i>	(D) TOPOLOGY: linear	
	THE RESERVE AND ADDRESS.	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1467RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:	
	CAMICYCACAC MICTORYMC ACACHINANA ACACHINA ACACHINA ACACHINANA ACACHINANA ACACHINANA ACACHINANA ACACHINANA	
15	GATOGOAGAC TOOGOOGGAG AGACTITICOC ACCTOGGGCA CAGGTCTTGA AAGAGAGCTC	60
	COOCCUTICC GIOCCACACT CTIGITIATC AUGICCOUAA CAGCAGCGIT CGIOCCACGI	120
		120
20	ACCCCTICT TGTTCGTGTT TCCACCAATT GATGGAATTT GAGACGTGAA CCTCTGCGCA	180
	TICRRKCIAT TGAGCACACC ATTGGCACCA CTTGAGCCCC TTCGCTCTGC CATCCCTAAT	240
	CALLACATIVE MACACATANA MATATANA CANADA CANAD	
25	CGTCCTATCC TACGGCCGGC TAATAAGTTA CTACCAGACT CTGGCCCTCA TCTGGCACTG	300
	ATGITATOGT CTOCAGOCAG ATOCTGTTTG TGACCOGATC GAAATCATOG AGTACGAATA	360
		300
30	ACCACGICAC CATTATICAC GIGATGAATT TOCCOGICCC TGITGCCGAC TCTTACTCCA	420
	GGTTAACCAT GACTAGATOG GCATACCTCA GATACGTTAT TCATGGGATC CGGAGTTGCC	480
	GCGTCGGCCG AACCGCCCGG TGAATCTGTG CTGACGACCT AAAAAAATAGT GTGCCCAAGC	F 4 D
35	TOTAL TOTAL CONTROL OF THE PROPERTY OF THE PRO	540
	TTCCTTAATC TGTGAGATGC ACACTGACAA ACTTGAAGGC TGAACCATCA AAGCGATACG	600
40	CCTCATGCAC GTGCTCAATA AGGTCCAGGA AGTCTCGCAA TGGGGGCAAGC AGACGGTAGA	660
	TIGCAAGACA CAGACGATIG GGITGIGCCA	690
45	(2) INFORMATION FOR SEQ ID NO:712:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 700 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	
	(and reservoing seems reas (ACTVERTE)	

	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1467UP
5	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:
	CATCGTCCGA GTGCAAAATCC ATACCAAAAA TGTGGACCCCA GGTACGGGAT TCGAACTTCT
15	CGAAGAAAAA TAGOCTCAGT GAAGTGCCCA ATTGCCTTAT AGTCGTTTTG CAGAGCATAT
	AGAAATGTOG GACAAGOCOG TOOOOOOCT TGTOOGACOC GACOGAAGAA GOGATCTOGG
20	COOCHANTIAC GOOGGIGACA GOCHGOGGIG COGANGAGAA AAAGGIGAAG CGAGITGITG
	CCATGAGGGA GATGCAGCAG CCAATACCTA TCCCAATGGT AAACGAGGG GTCCAGATGG
25	CCCAATIGGCG GAGGGCAACA GGGCCCGGCT CCTTTTTIGGG CGGTCTGCGG TGCTGTTTCT
	TOGACTICAC GGICAGCIOG GITTCATAGC COGACTOSGA CICGITGCAA AGGITGTGCA
30	GGTGCTTGAG CAGGCGGTGC TTCTCGGTGGT GGTTGGACAT GATTATAGGG CTGCAGTATA
	CTCGCATGCA TITIGCGTGCG GTGTAGCGCT TCAGGAGAGC CGCCAGCGTG CTCTTCTGGC
35	CCTTCTGGCA CACGGGAATC ACGGTGGGGC AGGGCGCCTT CTCGCACAGG CGGTCCAAGA
	GCTCTGGCGC CTGCGCTATG TCGTGGAAGA CCACCATAAC CGCGAGGTAC CGCTGGCCCA
40	COTOCCAGOG COTGACCATG COGAGGITCT TCACGICAAA
	(2) INFORMATION FOR SEQ ID NO:713:
45	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 689 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEINESS: single
50	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1468RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:	
10	GATCTOGTOG CTCATTGTOG ACCTGCAAAA AGTGTTCAGA AGGAAGOCAA CATGTGTTTT	. 60
	TAATCCTACG OCCGTGCCCT CAGAGATTGT TCACTCAATG TCGTTCATCA TTATGAATGG	120
15	GIOCOGGGG CCIGCOGGCC ICGAACCGGC GCCACACGGC CICCGCCGGG CGCIGCCCCG	180
	CTGGGCCACG CAGGGTGCAA AACGCACCCCA AACTCACCGC GCGCACCGGG CTACACCGGC	240
20	GCCAGCACGI CACGIGCOGI TACCCOCCCT GCCGGCACIG AAAATITTIIC GCCGCCCAACA	300
	CTATCGCGCC CGAAAAAGCA ATTTGCCCGC CAACCACACA ACGATCTGTT ACCGAACAGG	360
25	ACAGGACTCA TOCCCCGTTC CCTTCTTTAT TTATTTACIA GCTCCACATA GATATTTTTG	420
	ATATTATAT GGIGIGITTT CCTCCGCACG CCGCAACCCA GCACTIACCA GACCACGGGG	480
30	GCAGGGACTG ACACCCAGCC AGAACAGAAC AACAACAGGC GACCTTACAA TGAGCATGGA	540
	AACCCCCCT GTAGATATCG ACAACATCAT CGACCCCTTG CTGCAGGTGC GGGCCTCGAA	600
35	CCCCCCCCACCCCCCCCCCCCCCCCCCCCCCCCCCCCC	660
	CAGCATCTTT ATCAAGCAGC CCATTCTTC	689
40	(2) INFORMATION FOR SEQ ID NO:714:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 620 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG146BUP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:	
5	GATCTCAGAA TTATCCCCTA CCAATTGATA TTACCATACT TAATTCCTGC TAAATACTTT	60
	GGCATCGCAT CTAGACATAG GAAGTAACCT CAAAAAAAGCT ACGCAGATAG TAAACCTGGA	120
10	ACAGAGATTG CGCAACAACA ACGGCCAGTT GGAAAATAGA CCACCACTTG ACCCTGTCAT	180
	TTGTAGACTC ASCAGTGTTC CTGTGTGTGC GTTCGCCAAT CTCCATGTAC TGTTGCTCGT	240
15	TEATHACTIC CATTGIGAGE ATGGAGAGCT TGCGCACCGC ACCCTCTAGC GICTCCGAGC	300
	TOGAATCASC GOCATCOGOG GAGAGAACAC OGTAGGTATT AAACGTGACA TOCTTAGTCA	360
20	GGTAGCCCGA ATTGTCGTTC GCAAAGCAGT ACTGGTATTT GCCATCTGTA GGCGCCTTCA	420
05	AGGICAACTC ACCGTGCGAC GACGCACCCT GCGCATCCAG CACTGACCGT CCGTCAATCC	480
25	CGTACACCAG CAGGICICCA GACAGCIGIT CAIGIGATIG TOSCICICIG TOSCOGAAIT	540
30	CATANGICAT TGTCAGCACG TCCCCGCCTT TCAACTGCTC ANAGAAACAG CGCCGCCCGT	600
30	ACCOCCAAG AAGTACATTG	620
35	(2) INFORMATION FOR SEQ ID NO:715:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 686 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: single	
-	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1469RP	
50		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

	GATCAACTIAC ATCTOCCAGC ACCAGCOGAA TIGIAAGGIG GCCATCATAG CATATGACAA	60
5	GIGGCIGCGT TICTICAACC TGCGCCCGGA GICCAGCCAG GCACAGGAGC TGATIGIGIC	120
	CGAGCTCAGA GAAGTCTTCC TOCCGCTGTA CAGCOGCCTC TTCGTGAGGC CTGCGGAGGC	180
10	AATGCATGIC ATACAGGACA CGTTGGTCAA GCTCGAGTCG TTTATCCAGG ACGACAAGCT	240
	CTCGCACGOC GCCCAGOCCT GCTTCGGGGTC GOCGCTCGAG GCCGCGCTGC TCGCCCTGCA	300
15	CACTOCCACC AATOCTAATG GCGGCAAGAT CATTGCGACT CTGAACACGC TGCCCACCGT	360
	GGGCAACGGC AATCTGACGC TGCGGGGGGCA GGACGGCCTC AAGAAGAGCC TGAAGTGCCGA	420
20	CAACAGCTTC TACACCGCGC TGGCGGACAG GATGCTGAAG GCGTACGTCG GCCTGGACCT	480
	CITICISCACA GOCAGOGOCT TCATGGACTT TGCCACGGTC GOCGACCCCG TGCTGGCCAC	540
25	CTCCCCCACC TTCCCCCACT ACTCCAACTT CCACCTCCAC GCCACCACTT CCCCCTCCCT	600
	CAACGACATG CTGCACGCCG TCAGCAGCAC CGTCGGCTAC CAGGCGCAGC TCAAGGTGCG	660
30	CTGCTCCTCG CGGCTGTCGT CAGTCG	686
	(2) INFORMATION FOR SEQ ID NO:716:	
35	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 572 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(V1) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1469UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:	
	0170000000	
	GATCGGGCGA GCAGGACTAG ACATGAGCAG CAATGACAGT GATTATCTCC TGGTTACCTT	60

	CARACTETIC ACTETICAL AGAMENTER ACCIGATION TOOPTOPPAT TEICHETEIC	120
5	ACGCGCGCCC GIGHAGGCGT CTTCGTCGTC CTCCTTCTCG TCCTCAACAT AGCCACAGTG	180
	GETCTTAGTC ASCITICAGET TOCCUTTCCT GEGGTCGGGG CCAATGGGGG ACGCGGAGGG	240
10	AGGGCTTTTC GCCAGCCTGT GGCTCAGAGA CTTCTTCCTG CCCACGGTGC TCTGCTTCAT	300
	COCCTCTATA CCCACACOGC CCCCCCCCCC CCCCTCGACG AACCTCCTCG ACCCAACCCC	360
15	CHERERCACE GOCCCATOCA CAAGGICCOC GGITACCTTG GCGTCCAACT GCGTCACCTC	420
	CCAATGGTTC TIGATAGCGT TCACCGTCGA CGACCAGCGC TCGCCGCACGT CGCCGCCCCA	480
20	ATACAGGTAC GAGTOGTOGT COTOGTOGAT GCCGAAGACC TOGTTCATOG CAGACTTGTG	540
	TOCOGREDOCC CCCACAACCT CCACITICOCC CC	572
25	(2) INFORMATION FOR SEQ ID NO:717:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1470RP	
45	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:	
	GATCTTOCTC CTATCCAGAA ATGGGAAGTT CTTIAGACRAC GGGGAATTAA GCCCCTTTTC	60
50	CAATATTTTG AGGGTCGTTT CATAGCTCGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT	120
	CIGITCATGI TOGCICATGA AAGGIGICIC TATCAAATCI AGCICCATCA TOGCAGAGIA	180
55	GITATTATCT TICTTCCAAG ACAGACGCAC ATGCCGCAAC TTCGTCAGGA TTACAGTAAA	240

	ATANTOGING AACCOCCEAC TCACACAATC GACCACCOCT CEANATGAAG TOSSCOCTA	300
5	GANGATUGIG COCCCCIOCT TCTCTATCAC AAGATOGAAC TOCGAAAGIC TGTTCACOGG	360
	GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
10	CCGCGCGAGC TCAGTCTCAA GCTCGTCGAT CCGTCGCAGC AGCTCCACAT TCGCCGTTCG	480
	AGCTGAACAG CTCCCCGTGAG TTCACGTCGT GCGTAAACTC AGACAGGTAC ACACACTCGG	540
15	GCAGGCCCTT CCCAATACAT TTAGAGCACT TCGGCCCCCC CTTGTTGCAC TTGACGCCCC	600
	CCTTCCCCCA GAACACCCAC GACTTCCCTGA CCTTCCCCCCT GCTTTTCACA ATCTTGCCAT	660
20	COGACTICTOC CATCCCOCCA OCTTICACCAA AATGACTAG	699
	(2) INFORMATION FOR SEQ ID NO:718:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 655 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(b) lorologi: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1470UP	
	(A) CARREST. PROJECTOR	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:	
45	GATOGOGGAC GTGGAACACT GGCCGGAGAT GCCCGCGGGC ATCCTGGTGG TTTCTGCGGA	60
	CCGCAAGGAC ACGCCATOGA CGAGCGGTAT GCAGCAGAG GTGCACAGGT CGGACCTCTT	120
50	CAAGGAGCCC GTCCCCCACCCC TGCTCCCCCCC GCCCGTACCCCA GAGATCCCCCC CCCCCGATCCCC	180
	CCCCCCCCAC TICCCCCACCT TICCCCCCCCT GACCATCCAG GACTCGAACT CCTTTCACCC	240
55	CACCIGOCIG GACTCATTIC COCCCATCIT CTACATGAAC GACACITOGC GCCGCATTGT	300

	CAABCIGIGI CAICIGATCA ACGAGITCIA CAACGAGACA ATOGTOGOGT ACACGITICA	360
5	COCCOCIOCO AACGOGGIGO TOTATTACTT COCCEAGAAC CACCOCCCCC TOTOCCCTT	420
	CCIUTUTOCC GICTITOSCG CCAACGACGG CIGGGAGACC ACGITICIOGA CGGAGCAGCG	480
10	COCCACTICG CCGCGCAGTT CGACGAGTGC GTGCGCCGCAA AGCTTGCGAC GGACCTGGAC	540
	GACGAGTTOC ACAGAGGAGT TECCCOCCTC ATCTTCACGA AGGTCGGGCA GGGCCCCAAG	600
15	ACACTAAATC CTCGCTCATC GACCCCGAGA CGGGCCTGCC CCGCTGACGC TATTC	655
	(2) INFORMATION FOR SEQ ID NO:719:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 708 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1471RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:	
40	GATCAATTAA CIATCTAGAT GAGICTAATT AATTAATATA CTTAAAAGTC COGITAATAT	60
	CAPTAGCTAC CCTATCOGAA CAGACCGTCT CCTACTAGOC CGAAAGGGTA AAGCAGTTGT	120
45	CAGTCAGTAC TIGCTGTTGC TTATGGAATG CCTGTCATAT GCCGGCAGCT TGTTTGTCAC	180
	TOGAGTACOG COCCTOCCOC CITOCACAGO GTACCCATGA TICTGAACOC CAAGGTACCA	240
50	CACCITCCIG CCACATCICC TCGACCICTY CCAAAGICAA ACCCITIGIC TCGGGGACAA	300
	AGAAGAAGAT GTAGAAGAAC OCAAAGATCA AACAACOCAT GAACACGTAG CCGTAGTAAA	360
55	ACCIGATOGC ATTOGTANTG TATGGTGTAA AGAAGOOGAT CAAAAAAGOOC CATATCCAAT	420

	recederal escentiasee Misceeties Citiencies Tambocama Gietettama	480
5	CANTGACATA COCAATTOOG OCCCAGGTAG TIGCAAAGAA GAAAAATGTA GAGGCAGGTA	540
	AAAACAATCA TAGCATTGCC TGCCGGTCTG GAAGAAGGCT GATCGGGTCC ATTGGGCCAT	600
10	AGTOTTOTCA CACCAACOGA GOCAAAAATA ACCATACAAA COOCCATTOC COCOOCACOG	660
	TAGAAGCAAA CATTTCCTCC TGCCAAATCT ATCGACAGTG TTACATTG	708
15	(2) INFORMATION FOR SEQ ID NO:720:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1471UP	
30		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:	
35	GATCTTCGCC TTCTTCTACA TGTTCTTCTT TGTCCCAGAG ACAAAGGGTT TGACTTTGGA	60
40	ACACCICCAC CACATGIGGC ACCACCGIGT OCTOCCATOS AAGTCCCAGT CCTGGACTCC	120
	TICCIACAAG AGAAATGCTT ACGAGACTGA GGAGGTGAAG CCAGAGAAGA CCTGGGCTTA	180
45	AAAACTITAA ACTACAAACT TITTIGIICT GCTAATCATC GGGTTAAAAC CTAAACCTAA	240
	TCTATGTTCA TTAATATTGT TATGACGTTC ACGAGATACC ATATGTAAAT TACTATTAAA	300
50	AATATGCGAT TAATCTGTAT TTATTAGTTG TAATTGCAAT GCCATATGAT ACTGCAAAGC	360
	AATACATOCC GAGATAACCA ACOCCACTGA GOCGGGACTG GOCCCCTTCT CCGGCCCGCC	420
55	CHACALOCCI, CLOCALIGGIC GOCCOCCIOC COGLOCOCC CCACCOCCATA COCCGLOCIC	480

	GGICALCOCC CCACITICAA ACTITIGTAAT CGAGCAGGAA ATTAAGATIC GTTATAAATIG	540
5	ATATCAAATT TTTCGTCGTT TCTTTTCAGT GAGTAATATT GTTCCGGCAC CGCACGCCGA	600
	TGATGCCGCT ACATCGCACA GGGCCAAAGC ACAGGTGCTA AACTATTGCT TAGTTGGGGT	660
10	CGTTGAGCTC GTTTATCCTT AGTGGAATAT CTGCAGCATA TTCAATATCA AGTCTGAA	718
	(2) INFORMATION FOR SEQ ID NO:721:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 695 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1472RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:	
3 5	GATCTATCTC CCAGCTTAGA GAGACOGTOC GCATGTAAGT GATACOCAGA CAGCCAATGA	60
	TACTOGICAA GITTIGIAGI TITTATAAGAA AACATATATI AAACOOCTAA AGACAGAAGG	120
40	CGAAAAGCCC GACTITTATG GGCGTAGAAG TCGTGAAAAA GGCCAAAAAC TATATTTCCA	180
	CITAGOSCIC CICCITCCIC ACGIAAACGC GCATCAICAT ACGCCTICIG TGAGICAAGA	240
45	GCACTACGAC ACGCCGTGCA TTCCCTCATA CAACCTTGCC AACACATGAT CATGTCCAAG	300
	GATATIGCTA CCACCCCAGA ACTOTCCCAA CCAGACAAGT ACTICGITGA GCAGCCCCAT	360
50	TIGCIGCIAC AAGAAATCAC CICCACGITA GACICCATCC TGAACAACTT AAATGGCCTG	420
	AATATTICOC TOGAGAACIC CATCOCAGIA GOCAAAGAGI TIGAGAGCGI GICCGAGCIT	480
55	TOGAAGGICT TITACGAGGG ACTOGOGAAC GGAGCGGCTC CIGGAGTIGC CGCAGCCAAC	540

	COSTOSTCTC ASSACCTSCC CACTGASCCC GTCGCCGCGC ACCAGAATGC TGCAGCGGGC	600
5	AATAGIGACG CACCAGCGCC ATCGCAGTAG CGITTGCACT CTGCCCTGGC TITIACACCGG	660
	TOCACCCACA TIGOGCICTA CITTIATGIG TCATC	695
10	(2) INFORMATION FOR SEQ ID NO:722:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 719 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1472UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:	
	GATCTCGATT GAATGCCAAT GAAGGTTTAT GGCCGTCACG GCAGGTATAA CAGACTTGTA	60
35	ACCACTITIG GIAAGACCCA COGTGAGGAA GATAGCTGGT TTAGCAGCGA CGATGAGAAC	120
	CACGGCAGAC CAGTTAGGGA GGACACAAGC AAACTCAGGC TGAGGCCAAGA TGGATGCAGC	180
40	GAATTACCGC AGGAGACGAT AGGTGCGAAT AGAAAACGTC CCCCCGAGCG AACGCAGACG	240
	CATCCCCTICT CCCACTTTICT CCAACCCCCC CCATCCCCCC ACAACCCCAC AACACCACCA	300
45	ACATGCGATT CTACAGAATA TAGAGAGAGT GCCAGTCAAG AGITTCTAAA CGCTGTGAAC	360
	GITGIGCAGG GCATAGIGIC TICTICTICAAG CCTGCAAAAG AGGTAGTIGA GCACTGGGGG	420
50	GASCITICAGG ATGTGCCAGA GGATCGCCCC AATAACGGGC AGGCGGTCTA TGGCAAAACA	480
	AGAACATOCT TOCAAAAOCG GAAGAGGATT CTGACACCGA ACCTOCTOCA CATGAGTCTG	540
55	ACGAACCOCT GCACAGOCG ACGAAGCACT ATCGCCGCAC TTTAATGAGC TGCGTACGAT	600

	CCCCAGACI CITAAGTACA CCCCAGACATCT CGACTITIATA TTGTCCCGACA ACTCCATGAC	660
5	GACACCOGAA CATAGACOGCA CCACATOCTO COCTTIGTOTO TOGATATICAT GAACAACGA	719
	(2) INFORMATION FOR SEQ ID NO:723:	
10	(i) SEQUENCE CHARACTERISTICS:	
,,,	(A) LENGTH: 675 base pairs	
	(B) TYPE: mxcleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1473RP	
25	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:723:	
	GATCGCATCA TCCTGTACAC CAAGCGCCAC GTCTGCGGCG CGCCCACCCC CGCCGCCGTC	60
30	CACCOCTEGE ACCCCCAGAC COCCCCACCAC TACATOCTCC TCGACCOCCC CACCOCCCCC	120
	GACCOCCCC COCTECTICCC COCCCTICCCC GCACCCTIACG ACCCCCCCCC TECCCCCCCCC	180
35	GOCGCOCTOC CCCTGGGCTA CCCCCTGCTC GTTGCGGGCA TGCCCAAGGT CGGCAAGTCC	240
	ACCCTICGTICA ACCCCCTCCCC COCCTCCCCCC ACCCCCCCCCC CCCCCAACCT CCCCCCCACCC	300
40	GEOGCOCACO COGGGGTCAC GOGCGCTACO AGTGAGTGCG TGCCCATCOC CGATCACCCC	360
	GOCGGGGGTCT TCATGCACGA CACCCCCGGC GTCGCCCCTGC CCGCCCGGGC CTCCTCGGTG	420
45	CECCOCXIOC TCCCCCTTOC TCTCCCCCCC TCCCTCCCCC CCCCCCTCCT CCXCCCCCTC	480
	ATCCAGGOG ACTACTGCTC TACCTCCTCA ACCTTCAGGG CCTGGCCCCC TCCTAGGCCG	540
50	CCTIACAGCCC CCCCACCAAAC GACATGGCGG CCCTGCTGGC CGCGGGGGGC ACCGGGCACC	600
	GOCTACOCTC CGAGACCCCA GOCGCCCTGC ACTGGCTTGC CATCCGGGCC CCGGGCCTCT	660
5 <i>5</i>	GCCTGCAACC GCAAC	675

	(2) INFORMATION FOR SEQ ID NO:724:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 703 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1473UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:	
	CATOTINO CASO CASOTINA TINA DI CASOCIO CASA DI	
25	GATCTAGACG GAGTTATTAT OCCOCCOCCAC CTCCACCCAC TGATACTCAA GAATGTOCCC	60
	TCCGTGCGGT GGTGGAGGTT CCGAGAGATC CACGAAATTA CGCTAGATCC TAATACGTTT	120
	The state of the s	120
	ACCAAGAAAC AGGCTTTGT GGGAACTATA CACGGGCCAG ATCAGGATCG GGTGGAAGTG	180
30		
	COOCAGATAA ACAGOOCTGT CATGAGTCAG GACACATACT TOCACTTTGA TAGTCTTTTG	240
	ACCOMPANIES ACCORD CONTROLLED ACCORDING ACCORD	
35	ACCOCCAGGI TOCAGAACCT CAACTACATC AGTCTOCACA ACGTTTCCGA GGAAATTACT	300
	GOCATCATAG TOCCTCACCG ACTETATTOC AATGOCGCA TCAGCATTOC AGGCTGCGTC	360
	The second in the second	500
	GIGARGGGG TIGIRATGAT CTARACTICC COGGATATOC CTATIGAGAA ATARACACAT	420
40		
	COCTICAACTT ATACATACCC COCCAACAAG COCCTTGAAT ATTICATACAC CCAATACTCC	480
45	GATCAATGIA ATTAAATAGA TAGGTTACAG CCCTACCGGG CTGGCATTTG GTCCGAGATT	540
	CONTRACTOR IN COLUMN CONTRACTOR C	
	GETCTGCCTC TACCAAGTCA GCCAGTTACC GGAGGGTGAA GTAGTAGGAC ATCATAACTC	600
	ATAAAAAACG TTACATTCGT TGTGCTTGTC GGGAAATCAG TAATCATGCA GGTGCGTCGT	660
50	The state of the s	300
	GAAACCGAAG GAAACGTAAT GOOGTIGGAAT AAGTAAAAGA TGC	703

(2) INFORMATION FOR SEQ ID NO:725:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1474RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:	
	GATOGITCAG TITAATCACC TOOGACOCAC TOOCTTOCOG TICCAGCACT GOOTGAAACT	60
25	TESCCASSCS THECATCACS SCATTAAGCT CCTGTACATC SCSCTCGTGC TESSCCTCCA	120
	SCTSCAASCG CASTTCASCG CTGATATECT TCCCCCCCCCC TGTAGACATC TGCCGCCAAGC	180
30	TAGGGTAGCT GCCCCACCGC CGCAGCGGCG AGCTGCCGGC GCCCTTGTCA GCCGTCTTCT	240
	GTGCCCCCAT TAGTGGCCGT ATCATCGTCT CGATCCCGCC GTTTGCCATC ATCGGTATGG	300
35	GIGIGITIGIA ATCGICAATT ACCCCACIOC AGICCTOGIC CAGGICCGIA AAATACTIGI	360
	CTTTTTTGCC GCCAGOGTGG TTAGACCOGC CCGTGGTGTT GCTCCGAAGC GGGCTCAAGT	420
40	GCACGCCGCG GTGGCTGCTG CTGTGGCTCG ACAGGCACGC TGCATAGTCT GCCACCTCCT	480
	GATGGCGCTA ATATTCCCCAT COCTATCIGC AGGCTCCAGC GATGGCGACG CCAGCTGATT	540
45	CGACTTOSCC GATGACGCCG TCTTCCACGA CTTGATCAGC GAGCCCACAA GCGACGAAGA	600
	TGATGAATIT GACTITIGGT ACATTICTIT GGACCCATIC CCATTATIGGG GAACCGICCT	660
50	GATAGCCATC ACAATGTATA GCTCGCTACT CTGAACCGCG TGGCAACCAC TGCAAC	716
	(2) INFORMATION FOR SEQ ID NO:726:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 699 base pairs

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1474UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:	
20	GATOGAATTC TCACAGGCCA GTACCTGCGT ATTACAGGTT TGCCATAGTA TGATTAGAAC	60
	CGTAAAGCCC AAGAATGCCA GGGCCAAGAG AGCTCTGGAG AAAAAAGAGC CGAAATTGAC	120
25	GGAGAACGIG AAGCAAGCGC TITTIAATTCC TGGCCAAACT TCGAATAAGC TCTTGCACGA	180
	TETTIATOGIG GACCITOGIG GACTCAAGAA GOCTGATGIG AAGCOCTTCA COCCGAAGAA	240
30	CCACCTTCGT CCCTTTCACC ATCCCTCCCCC TGTCCAATTT CTCACCCACA ACAATCACAC	300
	CICCITICGIG GIGGICTCCT CCAACTCGAA GAACCCCCC AACAACTICA CATTCATAAG	360
35	GACCITITOCC TACAACCITT ACCACATGAT OCACCITCAG ATTICCAGAGA ACTACAAATT	420
	OCTAGOGGAC TICCOGGAAGC AGACGITTOC AGIGOGGITG AAAACCGAIGI TITICCITICCA	480
40	AGGIGCOGCA TICCACICIC ACCCAGIATA CAAGCACGIC AAGICTITGI TCCTCGACTT	540
	CTTCCCCCGT GAGGTGACCA AGCTCCAAGA CGTTCCAGCGG CTTCAGCATG TGATAGCAAT	600
45	GALGATCCAG GOOGACTITG AGGATGGOGA GOCATTGCCC AAGGTCCTTT TCCGCGTCTA	660
	CAGGCTTANG ACGUACAGAA GCAGCCAAGG TOGTAAGAA	699
50	(2) INFORMATION FOR SEQ ID NO:727:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 749 base pairs	
	(B) TYPE: nucleic acid	

	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1475RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:	
	CATCOUNCEA ACCAGCOCAT CTOCAGCCAC ATCOTTCATA ACCTCACCAT GATCCACCAA	60
20	ACCURAGEAGG ACCAGGGCGC AAAGAAGGGC GCCTTTGCTG TTTGAAGCCG GATCCTGCGG	120
	CGITCAACCC TAAATAGTCT TATAGCCAGC ACGCCAGGCG CCGGCCGGTT CCTATGTAGT	180
25	CCTGCAATCG CTCGCTTGCT AGCCGCACGA TCACAGAATA CAGCTACTTT ATCCTAAATC	240
	CACTOCTATO AAAATATOOA GOOGGACAT TIGTICICIG TOTOGTOGGA TGTOGOOGIC	300
30	GOCATTOTOG AGTAGGOCCG CAACTOGGAC AGGGACCACA GGTGGCCATC ACAGCTGCCG	360
	GICCOGIGIC CGICCCIGGA ATCCIGCTCC AAGCCCTTCT GGICAAAGCC AGCCAAGCIC	420
35	CCCTGTCTGA TGGCGTCCTC GACCGCTGCG TCCAGCAAGT CCTGGTATGG ATCTGCGCCG	480
	ACCCUTCIGG COCCCCACG COTTGTGTGA ACCCAGTCCC ACAGAGAGCG TGTCCCTGTT	540
40	ACCOCAACAG ACGAGOCOCC TGTGCCCCCC GCATGGGCCG CCCTGCCGAA TGCCGTGCCG	600
	TICATGIAAT TECTECCCIG GICCCATGIG TATTGIGICT CCCAACCGCA AATCCCCCAC	660
45	GCAGGAACGI ICGCCIOGCC GCCATCGITC TCGCAGCICT TCGGITGCGG CACCAAAGCC	720
	TOCTTOTOCA GCATCOGCCC TGAGCCGTT	749
50	(2) INFORMATION FOR SEQ ID NO:728:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 740 base pairs	
<i>3</i> 3	(B) TYPE: nucleic acid	

	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) CRGANISM: PAG1475UP	
15	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:728:	
	CARCHITYCE CONTRACTOR OF THE CARCHITY OF THE CARCHITYCE CONTRACTOR OF THE CARCHITYCE CONTRACTOR OF THE	
	CATCHICOGI COCCAGIACG GIOGICICITI CGAGATATNA GCACGCIAGGG CAACIGHATC	60
20	AASCTAACCA ACACAGTKOG CACOCTTTTC GAGCOGAGCT CAGGOGGGAG GTGAACCAGC	
	GRANCIACE CARCUSCIAG GIGNACCACC	120
	TCTGAGACAG ACAGACGCCC CTTGTTCAGA AGTAGCTCAA TAACACGTCC GCCTCGCTCG	180
05		160
25	CCGAGGIGCG ACCGCGCIAC CICIGIGIAC AGGAAGGITT CAGGACICAA TGICCICAIC	240
	TCCAGRGRES ATACTESCAC CRESSOR	
	TOCAGTGIOG ATACOGGCAC CTCCGCAGCA CGCTCGTTTT CGACTTGICC ACCTGCAGCA	300
30	CCCATAGATC COTTCATTAT OCACTAGGAC CTCGCCCTCA CTCAAGCCCA GGGCCGTCTG	
		360
	GAACGCAATA CICGCTAGIG CTAGITCCCA CCTAATATCT ATCTCATCGC CCATCGAGCA	420
35		
	GCGGGCCAGC TAAAAAATCA CCACTGCGCG CTCACCACGC ACGGTTCACT AAATACGAAA	480
	CASTIGITOS TCACGIGITIS CICACGIGAT TITACCCOSC COGTATAATA TCGGGTTCTC	
		540
40	AGCCCCCCGA CCCAACCACA CITCCTIGTAT CATAACAAAC CACCACAGGC CGTAGGACCT	600

	ATCOSCAÇÃO TCCCAATACC CITISCIACIO TICACATIÃO GIOGITICAAA TGAGIGICIO	660
45	TITIAGIGGIT ACCAAGAGIG TGGCGACAGC CACATTGGGG ATCTACACCG GGATGGIGGI	
	CALITOCOG ALCIALACOG GGATGGTGGT	720
	AACGCGGCAG TIGGICCITC	740
50	(2) Differences	740
	(2) INFORMATION FOR SEQ ID NO:729:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 707 base pairs	
55	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAGI476RP	
10		
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:	
	GATCGIAIOG CTAACTGIAA TATOGAAAGA AGCACAGACA TCCCCGAAAA ATGACATCTC	6 0
20	AGIGACACTO TICAACAAAT CATAAGAAGA AAAGIAIGIG ACTAATGCTT GCAGAAAAAT	120
	AAATTOCTCG CTACCAGTAA GCGATGTTAG TAGCGTQCCA TGGCATTCAA TAAATCGTAA	180
25	CACATACGIG GGIGGIATCT CCATGCTITT GAGGIACGCA AAAATIGGGC CATATAAATC	240
	GATCHICAAT OGTACCCITT TOCATATOGA TICHTCAAGA AGTCTGITTA TAAGTTCHTT	300
30	ATCAGAATOC TOCATAGACT GATOCAGGAG AGCACTUAGC ACATOCCCTT TATUCCUAGG	360
	ATAGAGCAAA TATTCTTTGA ACGAAGCTGG GTCTTTCCGG AAGTCAGGCT TCATACCATA	420
35	AAGGIACATG TATACATICC TIGGGACATC CATATCCTCA ATACIGCTIT CAAGCATCGC	480
	AAGSTAAAAT TOGTAGGAAA ATTOGGSTAC OCAGGAATGC TGTTGAAATT GOGTCCAGAG	540
40	THTGTATECT GECTIGOGOT GOTTOCTTICC CACGOCCAAC AGGAAGTTICG GACAGAACCA	600
	GOGTOTOACA GOGAATOAAG ACCATOTOTT CAGOGAATTT GOGTGAGAAG GOGATOAAGO	660
45	ASCITICACAG CAACITICCAG GGAATCTAAG CIGACAAGCC CAGCITAC	707
	(2) INFORMATION FOR SEQ ID NO:730:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 635 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: INA (genomic)

5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1476UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:	
15	CATCTGAAAC TAACAACAGC AGTGOGTGAA OCAAGAGGCA TTGGAGGCGT ATGACGGCGT	60
	GICGCAAGGC AAGTACACTA TOGGCTTGGG CCAGACCAAC ATGAGCTTTG TGAACGACCG	120
	CGACGACATC TACTOGATGT GITTGACCCC GTGCTCGAAC TTGATGAAGA ACTACGATAT	180
20	CONTROL INTO GITTEROOF GIOCIONE TIGHTONEN ACINCATA	100
	CAAGCCGGAA AGCATCGGCC GCCTCGAGGT GCGTIACGGAG ACGTTGCTTG ACAAGTCGAA	240
	GICCGIGAAG TCTATTTIGA TOCAGITIGIT COCCGAGAAC ACCGACTTOG ACCGIGICGA	300
25		
	TACOGTICAAC GCCTGCTATG GCGGTACTAA CGCGTTGTTT AACTOCTTGA ACTGGATTGA	360
30	GTCCAGTTCG TGGGACGGTC GTGACGCAAT CGTTGTTTGT GGTGACATGG CAATCTAGGA	420
	CAAGGGTGCC GCCCGGCCCA CTGGCGGTGC GCCAACTGTC GCTCTCCTGA TCGGTCCAGA	480
		E 40
35	COCCCCAIT GICTITGACT CTGTGCGTGG CTCGTACATG CAGCACGTCT ACCACTTCTA	540
	CAAGCCTGAC TTCCGCAGTG AGTATCCATA CGTCGACGGC CACTTICTCAC TAACATGCTA	600
40	OGTCAAGGGC CGTCGACCAG GCTTACCGGCG CCTTTA	635
	(2) INFORMATION FOR SEQ ID NO:731:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 719 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(may remove the same same)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1477RP

5	
	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:731:
10	GATCTTTOCG AGGGACCACT CTGCAATCCA AGAAGACTAG AGGAGTTGTC TAGGACAACA
	AAGIPTATAA GCAGACTICT GGIGITTTAC CGICCITTIC GATACCGATT CICGACAGIA
15	TATTCAAAGG CCAATAACGC CAAACAATAC GTTAAAGTTG GCTGCCAGTT TTTCAACACA
	CTACTACAAC ATTATGAGGG CATAAAGGTG CTTCTAGATG ATAGCAAAAT CATTCCTCAG
20	CTCCCCAGTA CTCTCTATAA QCCTATUCAA QCCCATATTT TACCCAGTAA CCTCTTCTCC
	TOTTOGOCTO TOCAGAATAC GITATGIGGO TOCTACITOA AATTOCTOGG ATTOCTAATG
25	AAATCTAAGG AAGGAATCAA TATATTAGAA AAATGGAACA TGTTCACTGT CATCTATAAA
	ATGITTCAGC CATCACCOCT AGCGGAAGAA TATTTGTTAC TCATGCTTCC AGAGTTGCAC
30	CICICICACA GCATACATTG TAGGATTATT TTTAGCAAAG CGCTAGTCGA CAGTAGAGAA
35	GICATAAGGA TCAATGCTAC CAGGGITTTA GGCGAAATGA TCAGCAGOGI CAAATTATCT
	CATCCCACTC TOGAAGAGIT CATGITAAAC CIGITOGICG CICAGITGIA CGATTIATCG
40	AGICAAGIOG TAGCAGIOOC CCACCAGATA CIGIACCATT ACIGITTAAG TCAAAGIAT
.2	(2) INFORMATION FOR SEQ ID NO:732:
	(i) SEQUENCE CHARACTERISTICS:
45	(A) LENGTH: 726 base pairs
	(B) TYPE: mucleic acid
	(C) STRANDEINESS: single
50	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)

(A) ORGANISM: PAG1477UP

(vi) ORIGINAL SOURCE:

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:732:	
5	GATCCGAATG TCCTTAGTCT GTGGGAAGGA ACCGATGGTG GTGGTTGGCA ATAGCGGCAG	60
10	CTIGAAAAIT GOCTGCTGCT CCTTGAGACG CTCCCCGAAT GGTGCCGCTC TCGTGCATAG	120
	CTTCTCGTTC AAACCAGCAA CACGTCCTGG ACAGCAGGAT CGTTGGTGAT CGCAGAGGGG	180
15	GCACGOGCAG CAATOGAGIC TOCATTIGOC TICAACTCAG AGGAAAAGIC TICGGCCAGAA	240
	GCCTTCTTAG CGAGGACAAC AACCTCATGC AGCTTCTGGG TTGCAAAAGA GAACCAGTCC	300
20	TIGATOTOTO COTOCCAACOO ACACTOCTITI TOCCAACTICAA CTOCCACTICTO CAACCAACGAA	360
•	GACCACCTOG CAACAATAAC GOOGTOOOCT CCTAGTTTCT CAATTOCCTT ACAAATAGTG	420
2 5	GCAGCCGACT TOGOGRAGIC ATTOTTOCAG ATGITTCTAC CGTCAACAAC ACCTACAGAC	480
	AACGACTEGT TITCGCCAAC GATOGCTAGA ACGTOGTCCA ACTGCTCTGG GTTTCTCACC	540
30	AAGICGAAAT GTAGGCCAGC CACTGGAAGA TCCACAAGCG CCTTCAAGTT CGGAACGACT	600
	GICCCGAAGT AGGIGGICAA CACAATGICG AGAGACITTIT CCGCACCTAT ATGITCATAA	660
35	GOSGICTIVA ACGUAGACIG TACGICCICT GUAAGAICIA AGACCAACAC AGGUICATOC	720
	AGCTGA	726
40	(2) INFORMATION FOR SEQ ID NO:733	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 675 base pairs	
45	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1478RP	

5	(MI) SEQUENCE DESCRIPTION: SEQ ID NO: 733:	
	GATCATTATG CATTITATGA TATACACTOC TATCAAAGAC GACCAGTOOG TAGTGAATAC	60
10	ACACCOOCTG GCAGACACAA CCAATGCCGA GGATGAGGCT AGTGAGGACG AGTTAGAGGA	120
	GCTCGTTAGT AGCACTOCAC ACAGCGGCGA TGCTACTAGC GAGTGAACAG GTATTTTACC	180
15	TGAGCTTTGG AATATATAGG TAGGTGATGA GCTTTTACAAT ACGTATTCGC TAACAATGAA	240
	ATGCAGGAAC TOCTCAAGCT CTTTAAGTTC TGTAAAAAGG GTATCAAAAA CCGTTTTTCC	300
20	ASCOCIGICT COGIAAATGA COTOCATTAT COCATTOCAA TAGITOCTOC TOTTCAACGT	360
	CAGATCTATG ACCCCTTTTG CCCCCAGCCT GGTACCCAGT TCCCTCCGTG GCATCCCGAG	420
25	CATCTIGICA AATAGOCCIA TCIGITIGIT TAGOCTAGOG AIGITOGOCT CACGAGCAIG	480
	CASCETATOS COCTOCCTTO GITGTOCCAG CACCTOCCATO CACCAACCAG CAACAATGIT	540
30	CAACACGCAC TOOGTAACAA CTCTTTTAAC CACCTGTAAG TAGTTTCTAT GCCTTATTCT	600
	ACCCAAAACA GGTCTTAATA GGAGAAGGTC ACCATCAGCT CTATATTTAT GCTTGGAAGT	660
35	TECTOSCTIG ACCCC	675
	(2) INFORMATION FOR SEQ ID NO:734:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 706 base pairs	
	(B) TYPE: mucleic acid (C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genamic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORCANISM: PAG1478UP	

(xa) S	EQUENCE:	DESCRIPTION:	SEQ	\mathbf{ID}	NO:734:
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5	GATCTGAGTA TCAAGATACC ATGAGGGATT CTTGCTCACT CTTGTACGGG ACTGCCCCGC	60
	TTATCCAAGT GCAGACAAGA TGCAACATOC ATACTGGCAG ACCAGGCCCT CTGGATCATC	120
10	GAGTIOCTIT AAGCAACATA GTAGGAGGCT TCGAAGGAGG AGTICTTCGG CTACCTATGT	180
	ANGAGATIOCA GOGGATIGGTT ACTIGCTIGGTIC ACGIGCTAGA ATCATATACC ACGIGAAAAGT	240
15	GGATATGTTG CTTGCCCTTT ACATATGGCA GTTTTGCCAC CCTACTTGAC ACAGCTGTAA	300
	CAACGITICAC TAAGGATAAA CAAGAGCTAC TGTCAACOGG CTATCCATAC AATGACATCT	360
20	CATCTAATOG AGGIGGACTC GOCCCATACA CCGCATGTTT ATAGCGCAAG CAAGGACAAC	420
	GITGACAAGT TIGIOGATOT GOTTOGOCAG GTOTOCAAGA CTACTATAAC ATTIGGACTOC	480
25	CGCTATGTGT GGAAGTCTCT TOGCGAGCTA ATGTCTTTGC GCAAGGAGCT GCAGCAGCAG	540
	ACCCTCACCA TOCTTATCAC GCTCCTATAT COGGACGACT CGGCATTCAA GGTGCCATTG	600
30	CTTCGTGTGG TGAACCAGAA CTCAAAAGCA GCGTGGACGA TGCGGGAGCA TTCCAGGGCA	660
	AGUACCCCCC AGACUTUATIC ACCTGACUCC TGACGGCAAG AUTGAC	706
35	(2) INFORMATION FOR SEQ ID NO:735:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 695 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

(A) ORGANISM: PAG1479RP

	CALCORE IN CHEMICATT GICICOSCAG GITGOCTGOC TCAATTITAT CCCGGCCCTC	60
5	GAAGAACTOC AACTOGAAGA GGAAGITOGT GOGGCACTGG CATAAATTGT CTATGOCCAG	120
	CCCCTGTTGG CAGAACGCAT GCTTGCACTC TGCAAACTGC TGCACCTCGA ATTGGCGGAT	180
10	CAAGAGCTGT AGCTCCACGA GCGCATCCTT GGTAAGCCTG CTGCCTCCGG AGCGGTCGGC	240
	SCACOSTITE TOTATECATT CETTERITCTC CICIETTAGE TIECOGICTE TOTATOGECCA	300
15	ATTOTOGAAA AGOGTOGGGC GCACTATOTO COTGOCTIGAA GGCACOTTGT TOTOCTTGTT	360
	COSCROGICG THTCGIAGG GOGAGGICAC TGATGATGAA TCATTCATAA AGCTGHTTTT	420
20	ATTCCGGAGG CTGCGCTTGC GCTGCACGTT CACGTCAAAT TGTTTCAACG CCCTCTTATA	480
	AGGICTITIC TOCATTATUA TAGCACTATG CCAAGATCCA GATGIGOCAA TOTGOGATTA	540
25	CTAGACCIGT TOCOCCAGCA TOCAGITICIC TIATATACAC TOCCAGITIG TGICTGACAC	600
	AAAGACGIAA AATTOOGACT ACGAAAAAGGG AGTOOCCAAA CAAGTOGCAA ACGITGIAAA	660
30	AGGATAGIGI ATATTIATAC TATPAGIAAT TAIGI	695
	(2) INFORMATION FOR SEQ ID NO:736:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
	(B) TYPE: nucleic acid (C) STRANDFINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1479UP	
0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:	
5	GATCOGGGCA TTACGGTGCC CATCTACGAG GAGGACATTG TOOGGGACCA GGGCGGCACG	60

	GACGIAGACG GOCAGCCOCA GAAGCIGGGI TOGIACCOGG GGGGGGCGG GGGCITCICG	120
5	AACACGCTGT CCAACCTGCT TCCCAGTATC AGCGCGAAGC TGCACCACAA CCGGAAGGCC	180
	COCACCOCA AACTICGCCCC CTICTOCTCCC CACCCCCACC COCCACCCCC CTICTIACCCTC	240
10	GTT0CCGCEAG AGATGCCCGC CAGCATCACC CCTCCCCCAGG ACCTACATAA CGTGGTCAGC	300
	TTCCCCCACC CATACCCCCT TCCACACCCA CCCACTTCCA CCCAATCCTA TACCTATCCT	360
15	TCTOGATACA GTOCOCACCT GCACCCCACA GTCTCCAACC CTGCTACGCG GACTCGGAAT	420
	AATACIGTAT CITCOCAGAT TACITCOCTT TCAAGCATGG GCCAGCTGGG AACCCCCAGC	480
20	ACGAGCAACA TCTGGACCAA CAATGCCTCA AGCCCGGCAG ATCCAATCAG CAACATGCTC	540
	ACCACCACT TCAACCCCAT CCCCCTCCCC GACTTTGGCC AGTCGAACTA CTACGACGTA	600
25	ATCACGCAGC AGCAGCCTCC GCAGTCGACG AACTCACTGA ATGTGCCCTC CGGGGGTAAT	660
	ATTICIOGGA AAAACGIACT CGITCICAAT CTAATGCTTC TAGCATATAC GCAGAT	716
30	(2) INFORMATION FOR SEQ ID NO:737:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 748 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1480RP	
45	CONTRACTOR PROJECTION OF THE PROJECT	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:	
	GATCUTCTGA GOCGAGCCCT ATCCCAAGIT TATTCCAAGT TCTTGCCGAA AGGTAACAAA	60
55	COGTITATIT ACAIGAGITT ACACATAACA COOGAGAAIG TIGAIGITAA TGIGCAICCT	120

	THE PARTY OF THE P	180
5	CICCATGAGC GETTATCTCA GCTGGATACT TCGCGAACTT TTAAACCGGG CTCTTTGACA	240
	CCTGGGAAAC ATAGITCAAC TGIGICCTCC GCATTCCGJC AATCAGCGAC CCCGCAAGT	300
10	ACACAACCAA AGGCAAAAACG TOCAGAAAAC ATOCTTOTICA GGACTGATOG TAGGCAAGCT	360
	AAAATTACTA ATTATGICAG AGCAAGTCAA AGCTCTACCA GCTCATCCTT TTCCACTTCT	420
15	TIAAGAAAGA AATCACATOC GOCAGCAAGT GATGAACTIG GCAGCATIGG GGAGGACTCC	480
	CAAGATACAG CAACATOGAT GACAACOTOT ACACAAGAGC CTAATCATAC CAAGTOTAGA	540
20	GCCATITUAA CCITATUCAA TAAUGAGUAT GAAGUCGUAC AGCCGGAAAG AACGGAAGUA	600
	AATCTCACCA GCATCAAAAC TCTAAAGCAG GAAGTAGACG AAGATATGCA TAAGGGAATT	660
25	AACAAGIGIC TITIOCAGATA TGACCTATGT TGGIGTCGIT GATGCAACAA GGCGACTTGC	720
	ATCIATAÇAG CATGGITTAA AGITIATITT	748
30	(2) INFORMATION FOR SEQ ID NO:738:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 727 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
40		
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1480UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:	
	GATCOCGICA TOOGATACAT AAACCACOGA ATCAATGAAA AOCICOCTTA CGAACAGITT	60
55	GGATCTGTAC COGAGAAGGG CTACTATATT CCTCCCACAA TATTTCTGGA CGTTCCTCAG	120